COLD SEASON TOLERANCE AND PREVALENCE OF SEEDLING BLIGHTS IN SWEET CORN IN THE COLUMBIA BASIN OF WASHINGTON

By

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A thesis submitted in partial fulfillment of
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To the Faculty of Washington State University:

The members of the Committee appointed to examine the thesis of RYAN KEITH SOLEMSLIE find it satisfactory and recommend that it be accepted.

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COLD SEASON TOLERANCE AND PREVALENCE OF SEEDLING BLIGHTS IN SWEET CORN IN THE COLUMBIA BASIN OF WASHINGTON

Abstract

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Washington State is a major producer of sweet corn in the United States with ~36,400 ha planted in the semi-arid Columbia Basin annually. Cold spring soil conditions and soilborne pathogenic species of *Fusarium*, *Pythium*, and *Rhizoctonia* can cause significant losses. In 2018, conventional (n = 31) and organic (n = 16) sweet corn fields were surveyed in the Columbia Basin to assess the prevalence of seedling blights. Stand losses ranged from 3.3-47.5% (14.9 ± 10.9%, mean ± standard deviation) and the incidence of stunting ranged from 3.7-23.4% (10.1 ± 5.3%), demonstrating the opportunity to improve sweet corn production. Of 14 species identified from 350 *Fusarium* isolates obtained from stunted seedlings, *F. oxysporum, F. verticillioides, F. solani,* and *F. equiseti* were the most prevalent. Five species and anastomosis groups (AGs) were identified from 66 *Rhizoctonia* isolates, with *R. solani* AG 4 the most prevalent. *Pythium ultimum* was the most prevalent of four species identified from 63 *Pythium* isolates. Approximately 60% of the *Pythium* isolates were resistant to the fungicide mefenoxam at 10 and 100 ppm, which might account for some stand losses. Isolates of *P. irregulare, P. ultimum*, and *P. sulcatum* were highly virulent on the sweet corn cv. SuperSweet Jubilee, as were isolates of *R.*

solani AG 4 and AG 2, and *F. acuminatum, F. graminearum, F. fujikuroi, F. oxysporum, F. proliferatum, F. solani*, and *F. verticillioides*. There was variation in virulence among isolates of a species.

Seed germination and seedling vigor are impeded when sweet corn seed is planted in cold soils. Accessions from the sweet corn breeding association panel of the USDA National Institute of Food and Agriculture Specialty Crops Research Initiative Project No. 2018-51181-28419 were planted in the Columbia Basin in spring of each of 2019 and 2020 to screen for cold tolerance. In 2019, 24 of 182 lines tested had greater emergence and vigor than the processing *sh2* hybrid GSS 3071. In 2020, 223 of 580 lines evaluated displayed better emergence and vigor than the processing *sh2* hybrid GSS 3951. The trials demonstrated significant potential for improving cold tolerance in sweet corn cultivars.

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For my loving parents, brother, and grandfather, Marilyn, Keith, Alec, and Allen.

CHAPTER ONE

LITERATURE REVIEW

1.1 Sweet Corn

Sweet corn, *Zea mays* var. *rugosa*, is a subtropical, annual, monocotyledon in the family Poaceae that is grown as a vegetable around the globe for its sweet kernels with good eating quality (Dias and Ortiz 2011; Hassell et al. 2003; Shultz 2008). Most sweet corn varieties require average air temperatures of >13°C for good growth and development, with an optimum air temperature of 20 to 22°C during the seedling stages, and optimal temperatures of 25 to 33°C by day and 17 to 23°C by night during subsequent vegetative and reproductive growth stages (Pothour et al. 2002). Sweet corn generally has a significant demand for water over the cropping cycle, about 45 to 50 cm (Grecu et al. 2018; Nield and Newman 2016). However, due to an extensive root system, sweet corn plants typically can access lower profiles of the soil effectively, resulting in a greater tolerance to temporary water deficits compared to other commonly grown plants (Grecu et al. 2018).

Corn (*Zea mays*) can be traced back to its closest wild relative, teosinte (*Zea* spp.), which is widely distributed in Central America (Mangelsdorf et al. 1978). Corn is thought to have been domesticated from these wild relatives around 7,000 years ago in what is now southern Mexico, and was subsequently spread throughout North and South America (Hilaire 2000; Mangelsdorf et al. 1978). Mutant selections of field corn, or the dent and flint corn types, were the first sweet corn cultivars grown and are similar to sweet corn mutants found today. These cultivars were believed to have been grown commercially first in Pennsylvania in the mid-1700s (Agricultural Marketing Resource Center 2015). However, there is evidence of other independent origins of sweet corn in the central and southeastern United States and Central America (Hendry 1930;

Tracey et al. 2006). Archeological evidence also shows that sugary forms of corn were grown throughout the Midwestern and Northeastern areas of the United States up to 700 years ago (Erwin 1942; Hendry 1930; Will and Hyde 1917). There is also evidence that sweet corn was derived through a mutation in corn grown in at least one instance in Peru prior to 1534 C.E. (Hendry 1930). These corn varieties carried a mutant variant of the gene that is now known as the *Sugary-1* (*Su1*) (Tracy et al. 2006). The recessive version of this allele, *sugary1* (*su1*), alters the starch synthesis pathway in the endosperm and leads to an accumulation of phytoglycogen and disaccharide sugars rather than starch in the homozygous genotype, which imparts the kernels with more desirable sweet traits for fresh consumption (Allam et al. 2016; Tracy et al. 2006). Ultimately, this results in an accumulation of significantly more sugars in the endosperm compared to field corn (Doehlert et al. 1993). Since the discovery of *sugary* genotype (*su*) other sugar enhancing mutants have been identified and incorporated into commercial cultivars, including the sugary enhanced (also known as enhanced sugary) group (*se*), and the super sweet or shrunken group, with the *shrunken-2* allele (*sh2*), both of which result in significantly higher sugar content in the endosperm during the kernel filling stage compared to *su* cultivars (Brandenberger et al. 2017; Grubinger 2004; James et al. 2003). Combinations of these genes have also been used in sweet corn hybrids, such as sugary × sugary enhancer (*su1se1*) (Brown et al. 1985; Ordas et al. 2008). Other kernel sweetness modifying genes have been identified, including *brittle* (*bt*), *brittle-2* (*bt2*), *shrunken* (*sh*), and *shrunken-4* (*sh4*) (Brown et al. 1985). However, these genes are not found as commonly in commercial cultivars as the *su*, *se*, and *sh2* genes.

Currently, the supersweet sweet corn cultivars, i.e., those with the *shrunken-2* (*sh2*) genotype, dominate the fresh market sweet corn industry in the United States due to the longer

shelf life and desirable eating quality of ears harvested from cultivars with this gene compared to those with other sweet corn mutations (Hartz and Caprile 1995). Typical ears of *sh2* hybrid's maintain eating quality longer than *su* and *se* sweet corn because the conversion of sugar into starch at ambient temperatures is slowed significantly (Dias and Ortiz 2011). Other genotypes, including *su,* are still important and sweet corn varieties with these mutations are planted on significant acreage annually even though the kernel sugar content typically is not as high as that found in *sh2* varieties (Styer et al. 1980). The decreased starch content of the endosperm in these popular *sh2* and *su* genotypes compared to field corn has been associated with reduced endosperm weight, reduced carbohydrate reserves, and poorer pericarp integrity, all of which can affect seed quality and vigor adversely (Revilla et al. 2003). In particular, kernels of sweet corn cultivars with the *sh2* allele weigh 33 to 50% less than kernels of *su* cultivars (Viesselmann et al. 2014). These cultivars also, as a result of the reduced starch content, develop a collapsed endosperm, cracked pericarp, and air pockets between the aleurone layers and the pericarp as the seed dries on the ear (Juvik et al. 1993; Styer and Cantliff 1984a).

Unlike field corn or popcorn, sweet corn is not harvested for eating at physiological maturity since sweet corn ears are harvested for maximum sugar content before starch accumulates in the kernels (Shultz 2008). Rather, these ears are harvested during the brief period of the R3 growth stage or milky stage, i.e., when the kernels are still soft and sweet to the taste (Williams 2014). Both fresh market and processing sweet corn are harvested in this manner. Once harvested, however, sweet corn kernels continue converting sugars within the kernel into starch, which affects both fresh and processing quality (Tracey 1997). Different sweet corn genotypes differ in the duration of shelf life of the ears. The *su* genotypes undergo a rapid conversion of sugars if not refrigerated shortly after picking and need to be processed or

consumed within a few days. In contrast, *sh2* cultivars have a higher initial sugar content coupled with a slower sugar conversion rate so the ears last longer while maintaining a decent eating quality, even under suboptimal storage conditions (Tracy 1997). For crops destined for processing, this is less of a concern as the ears typically are processed on the day of harvest.

It is worth noting that processing sweet corn crops typically are grown under contracts with processing companies. As a result, the processing company personnel make several crop management decisions for the growers, such as the cultivar to be planted, planting dates, and harvest dates so the processor can facilitate harvest of thousands of acres at optimal dates for eating quality (Williams 2014).

1.2 Sweet Corn in the United States

In the United States, sweet corn is one of the most important and popular vegetable crops grown (Grecu et al. 2018; Revilla and Tracy 1995). Per pound per person, sweet corn is the fourth most consumed vegetable in the United States, at an average of 12 kg per person annually [Agricultural Marketing Resource Center (AgMRC) 2015; United States Department of Agriculture National Agricultural Statistics Service (USDA NASS) 2018a and b]. Sweet corn is grown in every state in the United States (Lizaso et al. 2007). According to the USDA (NASS 2018a) 252,097 ha of sweet corn were grown in the United States in 2007, the most recent agricultural census year for which these data are available, on 28,241 farms. This equated to $835.8 million of fresh market sweet corn and $335.5 million of processing sweet corn for the 2009 calculated value (USDA NASS 2018b). Fresh market sweet corn can fetch premium prices, and the production of fresh market sweet corn occurs primarily in southern states where warmer air and soil temperatures enable early planting and a longer growing season (Lizaso et al. 2007). California, Florida, and Georgia are the states with the largest production of fresh market sweet

corn (USDA-NASS 2012a). However, fresh market sweet corn production only accounts for 31% of the total sweet corn production in the United States, with the remaining 69% attributed to processing sweet corn (Lizaso et al. 2007). The primary processing sweet corn production states are Minnesota, Washington, and Wisconsin (USDA-NASS 2012b). Globally, the United States is one of the top five producers, along with China, Mexico, Peru, and Thailand (Dias and Ortiz 2011).

1.3 Sweet Corn Production in Washington

Washington State is one of the largest producers of sweet corn in the United States, similar to Wisconsin and Minnesota (Sudermann 2013). In Washington, sweet corn is grown in rotation with other vegetables such as onion (*Allium cepa*), carrot (*Daucus carota* subsp. *sativus*), various cereal crops, and potato (*Solanum tuberosum*), as sweet corn functions as both a high value cash crop and as a rotational crop to break plant disease cycles, particularly in potato rotations (Pelter and Sorensen 2003; Van Denburgh 2001). Most of the sweet corn grown in Washington is located in Adams, Benton, Franklin, Grant, and Yakima Counties in the Columbia Basin, where access to abundant irrigation water combined with the warm, semi-arid region allows for irrigating optimal amounts of water at critical stages of the sweet corn crop cycle: tasseling, silking, and ear fill (Sudermann 2013; Van Denburgh 2001). In 2017, for example, 553,147 metric tons of sweet corn were harvested on 35,500 ha in Washington (USDA NASS 2018b). In the spring of 2018, 36,400 ha of sweet corn were planted in the Columbia Basin (Kevin Moe, Syngenta, *personal communication*). In a typical production year, sweet corn crops in Washington average 27 tons/ha for processing sweet corn and 19 tons/ha for fresh sweet corn (Granatstein et al. 2015; USDA NASS 2018; Wheat 2015). By comparison, Minnesota and Wisconsin, other major sweet corn production states, typically average 19 and 22 ton/ha for

processing sweet corn and 15 and 16 ton/ ha for fresh sweet corn for each state, respectively (USDA NASS 2019a; USDA NASS 2019b).

Washington State led the nation in organic sweet corn acreage, value, and production in 2011 with, 39,140 metric tons harvested that season (Granatstein et al. 2015; USDA NASS 2012). In the spring of 2018, 4,900 ha of organic sweet corn were planted (Kevin Moe, Syngenta, *personal communication*). Most of the organic sweet corn grown in Washington State is concentrated in Grant and Franklin Counties, with about 70% of organic sweet corn producers and 98% of the organic production hectares (Granatstein et al. 2015).

1.4 Sweet Corn Emergence and Vigor in Cold Conditions

Being a warm season crop, sweet corn grows best at soil temperatures >10°C for optimum germination, growth, and development, with soil temperature ranging ideally 15 to 35°C (Hassell et al. 2003; University of California 2013). It is for this reason that sweet corn should only be planted after the top 10 to 15 cm of soil have warmed to ≥10°C (Grecu et al. 2018; Huelsman 2000). In cool soil conditions, sweet corn seed germination and seedling development is much slower than in warm soils (Hassell et al. 2003). As a result, poor vigor and emergence can be a limiting factor in sweet corn production in areas with cool springs, like the northern United States (Allam et al. 2016). However, early planting of field corn or sweet corn is generally favored by growers in dryland production areas because early planted crops can mature before high summer temperatures occur and are more likely to avoid drought stress during critical flowering and kernel development stages, both of which can cause significant losses in yield (Mock and McNeill 1979; Wijewardana et al. 2015). Early planted crops also benefit from escaping late-season pests and diseases (Mock and McNeill 1979). In addition, early harvested

sweet corn crops often command a greater price in the fresh markets and help to spread out harvest operations to facilitate processing of large acreages of sweet corn (Revilla et al. 2003).

Early planting can be problematic for sweet corn, however, which tends to have poor seed germination and poor seedling vigor under cold soil conditions (Styer and Cantliffe 1984a). Many sweet corn cultivars have poorer seed and seedling performance than field corn, even under optimal conditions (Styer and Cantliffe 1984a). Seed lots of some sweet corn, cultivars however, germinate, emerge, and grow well under relatively cool soil temperatures (Hotchkiss et al. 1997; Mock and McNeill 1979). Sweet corn germplasm can have a wide range within and among genotypic groups for cold tolerance that translates to impacts on seed germination and seedling development (Styer et al. 1980). Typically, cultivars with the *su* genotype have greater cold tolerance compared to other sweet corn genotypes (Hassell et al. 2003). In contrast, the *sh2* cultivars often have poorer seed germination and seedling vigor compared to other sweet corn genotypes; some cultivars within the *sh2* group can even perform poorly under optimal field conditions, depending on the seed lot (Styer and Cantliffe 1984a).

Two important factors that affect emergence and seedling vigor of sweet corn cultivars, particularly for *sh2* cultivars are: 1) the integrity of the seed pericarp and membranes, and 2) susceptibility of the cultivar to soilborne and seedborne plant pathogens (Parera et al. 1995). Poor emergence in sweet corn has been attributed to low starch reserves in the endosperm, dysfunction of the scutellum or carbohydrate metabolism, and poor pericarp integrity (Mock and McNeill 1979; Revilla et al. 2003; Schmidt and Tracy 1988). For sweet corn cultivars with poor pericarp integrity, the pericarp can become readily damaged readily during drying of the seed or during seed processing and handling (Callan et al. 1996). Damage to the pericarp can result in leakage of various metabolites during the seed imbibition process and enables potential plant

pathogens entry into the seed (Tracy and Juvik 1988; Wilson and Mohan 1998). Each of these factors can reduce the emergence and vigor of sweet corn seedlings (Wilson and Mohan 1998). These factors can be exacerbated further when seed is planted in cold soil because cracks in the pericarp can result in rapid imbibition, which can damage the seed, and leaked metabolites attract plant pathogens (Allam et al. 2016; Revilla et al. 2003; Zhao et al. 2007).

1.5 Cool Season Seedling Blights of Sweet Corn

Seedling blights and damping-off are worldwide in distribution for both conventional and organic cropping systems (Laemmlen 2001). These diseases affect juvenile, succulent parts of plants such as seeds, seedlings, and young roots (Laemmlen 2001; Lamichhane et al 2017). Infection of seeds and/or seedlings can result in the failure of seed germination and the decay and death of seedlings prior to emergence from the soil, resulting in pre-emergence damping-off, or post-emergence damping-off or seedling blight (Hendrix and Campbell 1973; Lamichhane et al. 2017). With post-emergence damping-off, emerged seedlings infected in the roots and/or on the hypocotyl develop water-soaked, sunken lesions (Lamichhane et al. 2017).

Seedling blights and damping-off are attributed most commonly to three genera of fungi and oomycetes, *Fusarium, Pythium,* and *Rhizoctonia* (Munkvold and White 2016). Many of the species of these genera are cosmopolitan and abundant in soils, have a wide host range including corn, and are active under the conditions that typically occur at the time of planting crops, including corn (Bakker et al. 2016; Miedema 1982; Munkvold and White 2016). Pre-emergence damping off under cool, damp conditions typically is associated with species of *Pythium* or *Globisporangium* (Hendrix and Campbell 1973). Infections by *Rhizoctonia* spp. often occur under warmer conditions and typically occur near the soil surface (Laemmlen 2001; Lamichhane et al. 2017; Sumner and Bell 1981). *Fusarium* spp. that cause seedling blights typically cause

root rots or wilting. They often affect older seedlings, and are more commonly pathogenic under warm soil conditions (Gordon et al. 2015; Inman et al. 2008; Lamichhane et al. 2017). While *Fusarium, Pythium,* and *Rhizoctonia* are the most prevalent genera that cause seedling blights, they are not the only fungi that can cause seedling diseases in sweet corn production (Munkvold and White 2016). Species of *Penicillium* cause seedling blights of sweet corn from both seedborne and soilborne inoculum (Halfon-Merire and Solel 1990). Some other fungi that have been reported as pathogens of sweet corn seedlings include *Alternaria* spp., *Aspergillus* spp., *Nigrospora* spp., and *Rhizopus* spp. (Munkvold and White 2016; Robertson and Munkvold 2009).

In cool, wet soils, especially between 5 and 15°C, germination of sweet corn seed and growth of seedlings can be affected greatly by seedborne and soilborne fungi pathogenic on corn, which can be a major contributing factor to reduced sweet corn emergence and seedling vigor (Miedema 1982). As stated above, corn seed germination is slow under these conditions, but some of the pathogenic soilborne and seedborne fungi can be active (Miedema 1982). This can lead to colonization of the seed or emerging seedling by pathogens and, ultimately, failure of the seed to germinate or death of the seedling (Halfon-Meiri and Solel 1990; Styer and Cantliffe 1984b). As noted above, many sweet corn cultivars, particularly those with the *sh2* allele, have a collapsed dried kernel due to reduced starch levels in the endosperm. This can lead to cracks in the relatively thin pericarp during the seed drying process (Schmidt and Tracy 1988; Wilson et al. 1993). The damaged pericarp results in a greater amount of electrolyte leakage during the imbibition process than from kernels without cracks in the pericarp, which stimulates and attracts various soilborne pathogens (Nelson 2004; Schmidt and Tracy 1988). A damaged pericarp also allows more rapid colonization of the seed by pathogenic microorganisms once the seed is

planted (Wilson et al. 1993). Not all seedlings infected by pathogenic organisms are killed or severely affected. Some may be affected moderately and survive infection. However, these seedlings are often less vigorous and produce stunted plants that may not develop marketable ears (Berger and Wolf 1974).

1.5.1 *Pythium* species as plant pathogens

One well-known group of seedling pathogens comprises species of the genus *Pythium* (Hendrix and Campbell 1973). *Pythium* belongs in the kingdom Chromista and the subphylum Oomycota (Kageyama 2014). Approximately 140 species of *Pythium* have been described currently (Kageyama 2014). *Pythium* belongs to the Oomycetes which have key features that differ from those of true fungi (Thines 2014). This includes: 1) the cell wall is formed primarily of cellulose and glucan, unlike true fungi which have a cell wall primarily formed from chitin derivatives, 2) the vegetative hyphae are diploid compared to predominant haploid hyphae of true fungi, and 3) oomycetes produce swimming zoospores and sexual oospores (Bartnicki-Garcia 1968; Kageyama 2014). Species of this genus are common around the globe and occupy a wide variety of ecological roles (Robideau et al. 2011).

Pythium is most commonly known for species that function as plant pathogens, which can have significant economic impacts (Domsch et al. 1980b; Hendrix and Campbell 1973). However, some species are animal and human pathogens while others are saprophytes (e.g., Calvano et al. 2011; Loreto et al. 2014; Robideau et al. 2011). Many saprophytic species are also facultative necrotrophic pathogens under the correct conditions (Thines 2014). Pathogenic *Pythium* species typically are considered to be necrotrophic colonizers which attack germinating seeds, young roots, and seedlings (Schroeder et al. 2013). Typically, juvenile or succulent plant tissues are the primary substrates of infection, including seeds and the radicle of newly emerged

seedlings (Hendrix and Campbell 1973; Schroeder et al. 2013). *Pythium* induced rotting of seed often leads to pre-emergence damping-off, but root rot caused by *Pythium* can result in pre- or post-emergence damping-off (Matthiesen et al. 2016). For both pre-emergence and post-emergence damping-off caused by *Pythium* spp., infection typically is favored by cool, wet conditions that slow the rate of germination and emergence, thereby increasing the window of susceptibility to infection (Schroeder et al. 2013).

The persistence of many *Pythium* species in soil is due, primarily, to production of oospores (Hendrix and Campbell 1973; Johnson et al. 1990, Schroeder et al. 2013). The oospore is the primary resting spore for many *Pythium* species due to the robust cell wall which enables the spore to survive unfavorable conditions, including in the absence of host plant tissue (Dick 1969; Johnson et al. 1990). Oospores can persist in soil for long periods of time, ranging from several months to years, depending on the species and soil conditions (Hendrix and Campbell 1973; Lifshitz and Hancock 1984). These spores also have varying degrees of dormancy and asynchronous germination, even in the presence of spore germination stimuli (Ayers and Lumsden 1975; Hendrix and Campbell 1973). The germination of oospores in soil is affected by many factors, including soil temperature, oospore age, cycles of wetting and drying of the soil, CO_2 concentration in the soil, and exudation of seeds and other plant tissues (Ayers and Lumsden 1975; Johnson et al. 1990; Lifshitz and Hancock 1984).

Complimentary to oospores are the asexual reproductive structures of *Pythium* species, including sporangia, chlamydospores, and hyphal swellings (Hendrix and Campbell 1973). The sporangia of *Pythium* species produce zoospores, which are motile, flagellate spores that are released into the surrounding environment (Walker and Van West 2007). The release of zoospores by a sporangium is mediated by moisture and temperature in the environment, with

zoospores typically released under high soil moisture conditions and temperatures <12°C (Walker and Van West 2007). Zoospores are motile asexual spores that show a homing response based on chemotactic cues in the environment which allow the spores to locate suitable growing locations or host tissue on which the zoospores then encyst and penetrate the host (Van Der Plaats-Niterink 1981; Van West 2003; Walker and Van West 2007).

Pythium species can infect many plant species, both above and belowground, e.g., bean (*Phaseolus vulgaris*), carrot, cucumber (*Cucumis sativus*), pea (*Pisum sativum*), potato, and sugar beet (*Beta vulgaris* subsp. *vulgaris*) (Alcala et al. 2016; Porter et al. 2009; Rossman et al. 2017; Schroeder et al. 2013). *Pythium ultimum,* is one of the most common pathogenic species on these crops. In sweet corn, many *Pythium* species can cause damping-off, including *P. irregulare, P. debaryanum, P. ultimum, P. rostratum,* and *P. vexans* (Munkvold and White 2016). However, seedling blights and damping-off are not the only diseases that *Pythium* spp. can cause on sweet corn. Species such as *P. arrhenomanes* and *P. inflatum* can cause stalk rots later in corn development (Deep and Lipps 1996; Song et al. 2015).

1.5.2 *Rhizoctonia* species as plant pathogens

The genus *Rhizoctonia* is widespread and common in both cultivated and non-cultivated soils, and the genus is isolated readily from diseased plants and soil (Ogoshi 1987). These fungi are found worldwide and include some destructive plant pathogens, saprophytes, and mycorrhizal symbionts (Leake and Cameron 2012; Ohkura et al. 2009). Species of *Rhizoctonia* belong to the kingdom Fungi, phylum Basidiomycota, class Agaricomycetes, and order Ceratobasidiaceae (Ajayi-Oyetunde and Bradley 2018). *Rhizoctonia* encompasses multinucleate and binucleate species that are subdivided into somatically compatible anastomosis groups (AGs) (Ajayi-Oyetunde and Bradley 2018; Ogoshi 1987; Otero et al. 2002; Tuncer and Eken

2013). There are 14 AGs for multinucleate *Rhizoctonia* (teleomorphs *Thanatephorus* and *Waitea*) and 21 AGs for binucleate *Rhizoctonia* (teleomorph *Ceratobasidium*) (Arakawa and Inagaki 2014; Carling et al. 2002; Ogoshi 1987; Sharon et al. 2008; Tuncer and Eken 2013). Species of *Rhizoctonia* traditionally have been characterized by their vegetative features such as the branching of hyphae at approximately 90° angles, constriction at the hyphal branching point, the production of monilioid cells and sclerotia, the basidial structure of the sexual state, and the number of nuclei present in young cells (Ajayi-Oyetunde and Bradley 2018; Otero et al. 2002; Sharon et al. 2006; Sneh et al. 1991).

Species of *Rhizoctonia* lack conidia and other asexual spore production (Arakawa and Inagaki 2014). The primary means of reproduction for many species is the production of hyphae, monilioid cells, and sclerotia (Arakawa and Inagaki 2014; Ogoshi 1987). Monilioid cells are specialized, short, hyphal cells that can form in chains and aggregations, and that act as propagules (Ajayi-Oyetunde and Bradley 2018; Ogoshi 1987; Ritchie et al. 2013). Sclerotia, which can be comprised partially of monilioid cells, are aggregations of melanized hyphae that are resistant to a wide range of conditions and can survive in the soil for many years (Lu et al. 2016; Ogoshi 1987; Ritchie et al. 2013). Sexual reproduction, through the production of basidiospores on basidia, does occur and provides propagules for infection and spread of some *Rhizoctonia* species (Arakawa and Inagaki 2014). The importance of basidiospores for reproduction in other *Rhizoctonia* species, however, is not well known as many of these species do not produce basidiospores readily under most conditions or in culture (Arakawa and Inagaki 2014; Ogoshi 1987).

Many *Rhizoctonia* spp. are common seedling pathogens on a variety of agriculturally important crops, causing root and seedling diseases (Ajayi-Oyetunde et al. 2018; Matsui et al.

2013). *Rhizoctonia* species also have the capacity to survive for long periods as saprotrophs without a live plant host allowing for the persistence of these fungi even in the absence of a susceptible host (Naiki 1985; Ogoshi 1987). *R. solani* Kühn is one of the most prominent of the plant pathogenic *Rhizoctonia* species, affecting many agricultural commodities such as barley (*Hordeum vulgare*), corn, onion, pea, potato, and others (Ritchie et al. 2013; Ohkura et al. 2009; Patzek et al. 2013; Sharma-Poudyal et al. 2015; Smiley et al. 1992; Sumner and Minton 1989). Within *R. solani*, isolates can vary in virulence, including among and within AGs, depending on the host plant and environmental conditions (Ogoshi 1987; Patzek et al. 2013). *Rhizoctonia* species were once not considered to be major pathogens on corn as *R. solani* had been isolated infrequently from leaves, stalks, and roots of seedlings and mature plants (Berger and Wolf 1974; Sumner and Bell 1982). However, in places where corn seedlings were grown in soil that was heavily infested with isolates of *R. solani* and *R. zeae*, the seedlings developed root rots (Sumner and Bell 1982). Isolates of *R. solani* AG 1-1, AG 2, AG 4 have been recorded as common pathogens on sweet corn seedlings (Munkvold and White 2016).

1.5.3 *Fusarium* species as plant pathogens

The genus *Fusarium* is comprised of diverse species, including saprotrophs and pathogens of plants, humans, and animals, and can be found in many areas around the globe (Domsch et al. 1980a; Nelson 1981; Chandra Nayaka et al. 2011). Within the genus *Fusarium*, there are many species and formae speciales which cause diseases on a variety of annual and perennial field, vegetable, and ornamental crops (Nelson 1981). Members of this genus belong to the kingdom Fungi, phylum Ascomycota, class Ascomycetes, and the order Hypocreales (Leslie 1995). Most species of *Fusarium* have a teleomorph classified in the genus *Gibberella*, with other groups belonging to the teleomorphs *Hemanectria* and *Albonectria* (Gräfenhan et al. 2011;

Leslie 1995). Traditionally, *Fusarium* species have been identified by morphology of the microconidia, macroconidia, chlamydospores, and conidiophores (Schroers et al. 2009; Gräfenhan et al. 2011). However, species-specific primers and polymerase chain reaction (PCR) assays have been developed for the detection and identification of some *Fusarium* species (e.g., Demeke et al. 2005; Spanic et al. 2010). Most species of *Fusarium* are soil dwelling, cosmopolitan in distribution, and active as saprophytes on organic material in the soil. However, there are species with many different lifestyles, including endophytes, saprophytes, and pathogens of plants, humans, and animals (Barik and Tayung 2012; Domsch et al. 1980a).

Asexual reproduction of *Fusarium* species occurs through mycelial growth and the production of microconidia, macroconidia, and chlamydospores (Chitarra et al. 2005). Macroconidia are septate, crescent-shaped conidia whereas microconidia are typically unicellular and usually oval, spherical, or allantoid in shape (Chitarra et al. 2005; Domsch et al. 1980a). Microconidia and macroconidia, however, usually are not long-lived in soil environments and not all species produce both microconidia and macroconidia (Chandra Nayaka 2011; Leslie 1995). Chlamydospores serve as the primary survival structure for many *Fusarium* species as they are thick-walled and tolerant of a variety of conditions, though persistence varies depending on species, formae speciales, as well as environmental conditions (e.g., Bennett 2012; Chitarra et al. 2005; Couteaudier and Alabouvette 1990). Some species can also persist as dormant hyphae in plant material (Burgess 1981). Ascospores are produced in perithecia on plant debris in some species and can act as a significant source of inoculum when released under optimal conditions for infection of plants (e.g., Manstretta et al. 2016).

A wide range of *Fusarium* species is known to act as pathogens on many agronomically important crops, including >400 plant species (Ma et al. 2013; Roncero et al. 2003). For

example, canola (*Brassica napus*), corn, cotton (*Gossypium hirsutum*), lupin (*Lupinus angustifolius*), pea, spinach (*Spinacia oleracea*), tomato (*Solanum lycopersicum*), and wheat (*Triticum aestivum*) are affected by various species and formae speciales of *Fusarium* (Chang et al 2011; Chang et al. 2013; Cianchetta and Davis 2015; Foss and Jones 2005; Glynn and Edwards 2009; Hwang et al. 2015; Larkin and Fravel 1998). Several *Fusarium* spp. can be significant pathogens of corn and corn seedlings. *F. verticillioides,* in particular, causes seed rots, seedling diseases, ear rots, and stalk rots of corn (e.g., Bacon et al., 1994; Murillo-Williams and Munkvold 2008). These pathogens can infect corn through seed and seedlings, silks at flowering, or through wounding on stalks or ears caused by insect or mechanical damage (e.g., Scarpino et al. 2015). Several species of *Fusarium,* such as *F. verticillioides* and *F. graminearum,* can greatly affect the quality of harvested corn seeds and can reduce yields by 10 to 50%, depending on the severity of infection (Gai et al. 2018). *F. verticillioides* can also behave as an endophytic fungus and be present asymptomatically in kernels (Lanubile et al 2017; Munkvold et al. 1997). *F. graminearum* is a major pathogen of corn in some regions, causing seedling diseases and stalk rots (e.g., Broders et al. 2007). Many other *Fusarium* species can cause seedling diseases and root rots on corn and wheat, including *F. oxysporum, F. solani, F. acuminatum, F. culmorum, F. equiseti, F. proliferatum,* and *F. subglutinans* (Munkvold and White 2016).

1.6 Management of Seedling Blights and Damping-off

1.6.1 Chemical treatments. Seed rots and seedling blights are a concern for both conventional and organic growers of sweet corn as they can reduce the plant stand of a crop significantly. The pathogens that cause seedling blights can also persist in soil for many years due to their persistent survival structures (Chang et al. 2011). Growers of conventional sweet corn commonly use site-specific and broad-spectrum fungicide seed treatments to protect

germinating seeds and seedlings from soilborne and seedborne pathogens (Hartz and Caprile 1995; Matthiesen et al. 2016; Rodriguez-Brljevich et al. 2010). However, seed treatments may only provide control for a short period after planting, after which pathogens can infect seedlings (Cook et al. 2002; Jaaffar et al. 2016). The widespread use of fungicides, such as captan, as seed treatments has increased stand establishment in sweet corn crops by ≥30% (Wilson and Mohan 1992). In the Columbia Basin of central Washington, the use of seed treatments on sweet corn has, in many cases, reduced the incidence of seedling blights to about 5% (C. Burt, Twin City Foods, *personal communication*).

Organic sweet corn growers do not have access to the effective, synthetic fungicide seed treatments that conventional growers use to control many seedborne and soilborne fungi [USDA National Organic Program (NOP) 2018]. In field trials conducted in the Columbia Basin of Washington over more than 10 years, the effectiveness of diverse organic seed treatments evaluated has been mixed as the various organic treatments did not improve seed germination or stand counts consistently or significantly compared to that of non-treated control plots (Wohleb 2013). In other trials, some organic seed treatments performed similarly to the non-treated control seed or slightly better (Wohleb 2012). As a result of the lack of highly efficacious organic seed treatments, organic sweet corn growers in Washington overseed by ≤30% when planting in order to obtain satisfactory sweet corn stands (C. Burt and T. Bruketta, Twin City Foods, *personal communication*).

In conventional cropping systems, the extensive use of site-specific fungicide seed treatments has resulted in evidence that populations of some soilborne fungal pathogens have developed resistance to these site-specific fungicides. The main example is the fungicide metalaxyl which is a common component of seed treatment combinations used for the control of

plant pathogenic oomycetes such as *Pythium* spp. [United States Environmental Protection Agency (EPA) 1994]. The widespread use of metalaxyl, or the enantiomer mefenoxam, has led to populations of some plant pathogenic *Pythium* spp. developing tolerance or insensitivity to metalaxyl (e.g., Brantner and Windels 1998; Gimmer et al. 2014). Metalaxyl resistant *Pythium* spp. have been found in many regions of the world, including fields of central Washington where potato crops commonly are rotated with other species such as bean, carrot, onion, pea, and sweet corn (Davis and Nunez 1999; Kraft and Burke 1971; Porter et al. 2009; Sumner et al. 1997). In some of these situations, this is related to extensive use of metalaxyl to control other diseases, caused by oomycetes, such as late blight on potato caused by *Phytophthora infestans*, and Pythium leak of potato caused by *P. ultimum*, thus exposing these populations to metalaxyl for extended periods of time (Johnson et al. 2004; Porter et al. 2009). Potato, being a major crop in the Columbia Basin of Washington State, often is grown in rotation with sweet corn (Francovich 2017). Metalaxyl is used in many commercial seed treatments used to control oomycete pathogens that cause seedling, foliar, and other diseases of various crops (Hwang et al. 2001; US EPA 1994).

Many diseases caused by *Pythium* spp. are managed using fungicide seed treatments, including the active ingredient metalaxyl or mefenoxam (Porter et al. 2009; US EPA 1994). *Fusarium* and *Rhizoctonia* species sometimes can be controlled effectively with various fungicides as seed treatments (Glynn et al. 2007). Fungicides such as benomyl, captan, fludioxonil, and thiram were partially effective as seed treatments for control of *Fusarium* spp. in crops such as wheat and pine (Allen et al. 2004; Glynn et al. 2007). Similarly, carbendazim, fludioxonil, iprodione, myclobutanil, pentachloronitrobenzene, and thiram have been effective for control of *Rhizoctonia* spp. when applied as seed treatments on various crops (Davis et al.

1997; Pereira da Silva et al. 2013). In addition to chemical fungicide seed treatments, the treatment of seed with various microbes (fungi, bacteria, and actinomycetes), such as *T. hamatum*, has been shown to be effective and sometimes nearly as effective as conventional fungicide treatments when used as seed treatments to help prevent damping-off from *Pythium* spp. and *R. solani* (Harman et al. 1980). However, these biological fungicides have not performed well or consistently, particularly under field conditions (Cummings et al. 2009; Wohleb 2013). It is for this reason that organic sweet corn growers in the Columbia Basin of Washington routinely overseed by ≤30%.

Conventional fumigants such as sodium *N*-methyldithiocarbamate (metam sodium), 1,3 dichloropropene and chloropicrin have been shown to be effective for control of some soilborne pathogens (Collins et al. 2006; Xie et al. 2015; Yuen et al. 1991). Soil fumigation, before sowing, with various broad-spectrum fumigants has also been effective at controlling populations of some pathogens such as some *Fusarium*, *Pythium*, and *Rhizoctonia* species and others in field soils (Collins et al. 2006; Cook et al. 1987; Yuen et al. 1991). While fumigation is commonly used in potato and carrot production in the Columbia Basin, it is not cost effective for other crops such as sweet corn due to the high cost (Collins et al. 2006; Hutchinson et al. 1999; Sorensen 2000). Soil fumigants may not provide complete control of these soilborne pathogens due to the wide host range of many of these species as well as their ability to persist as saprophytes and in the form of resting structures in the soil, even following fumigation (Domsch et al. 1980a; Munkvold and white 2016). Soil fumigation can also be limited by factors such as soil texture, moisture, temperature, and depth of application of the fumigant (Lembright 1990). For example, fine-textured soils, which have relatively small pore spaces, can limit the diffusion of fumigant into the soil profile. Similarly, if a fumigant is applied too shallow, pathogens found deeper in

the soil may not be controlled effectively due to the mostly upward volatilization of fumigants (Lembright 1990; Yates et al. 2015).

1.6.2 Physical seed treatments. Some seedling blight and damping-off caused by seedborne pathogens can be managed using certain physical seed treatments. Physical seed treatments such as steam and hot water have proven effective for some crops such as carrot, lobelia (*Lobelia erinus*), pumpkin (*Cucurbita pepo*), and spinach for the control of certain seedborne pathogens (e.g., Babadoost and Zhang 2020; du Toit et al. 2018; Hall and Taylor 1983; Temple et al. 2013). Steam and hot water treatments can reduce the levels of inoculum of seedborne pathogens on seed compared to non-treated seeds (du Toit et al. 2018; Hall and Taylor 1983), depending on the thermotolerance of the target pathogens and tolerance of the embryo of the host plant to the temperature duration of the heat treatment. For some crops, the use of hot water treatment of seed has become standard practice to control particular pathogens e.g., carrot seed treatment for *Xanthomonas hortorum* pv. *carotae* (Temple et al. 2013; University of Massachusetts Extension 2020). Seed disinfestation with chemicals such as sodium hypochlorite have proven to be effective for some seedborne pathogens but less effective for others, particularly those that can infect seed internally. Studies on sweet corn have shown that bleach seed treatments significantly reduced fungal infection on seed lots, while other studies indicated that bleach seed treatments were ineffective at improving plant stand (Hartz and Caprile 1995; Parera and Cantliffe 1991). Seed priming or soaking seed in water until the lag phase of germination prior to planting, has been shown to improve early growth and vigor of corn (Subedi and Ma 2005). When corn seed disinfestation is coupled with solid matrix priming, or priming seeds using a soil material to restrict water uptake of seeds, seed germination rate and seedling emergence can be improved, even when seeds are planted under stressful conditions (Hartz and

Caprile 1995; Parera and Cantliffe 1991; Parera and Cantliffe 1994). Solid matrix priming, however, did not decrease the levels of seedborne inoculum or help protect against soilborne pathogens, rather this process increased the speed of emergence which reduced the duration of susceptibility of corn seedlings to damping-off pathogens (Hartz and Caprile 1995; Hotchkiss et al. 1997). There are limitations to solid matrix priming though, as it is expensive and bulky for handling large volumes of sweet corn compared to the application of fungicides to seed, which limits the viability of seed priming of sweet corn in large-scale agriculture, especially when more cost effective seed treatments exist (Hartz and Caprile 1995; Parera and Cantliffe 1991; Parera and Cantliffe 1994).

1.6.3 Cultural practices. Seedling blights can also be managed to some degree through the use of various cultural practices. For example, planting certain *Brassica* species with high levels of isothiocyanates as green manure crops for soil amendment and as biofumigant crops has been effective at suppressing species of *Fusarium* and *Rhizoctonia* causing seedling diseases in some circumstances (Dhingra et al. 2004). While not as effective as synthetic chemical fumigants, soil solarization and burning of residual crop straw from the crop before sowing decreased the levels of *Pythium* inoculum near the soil surface in wheat production (Cook et al. 1987). However, in areas such as the Columbia Basin, it is not economical to have a field out of crop production during the main growing season to allow for soil solarization and there is a limited amount of time in the season with hot enough conditions for soil solarization. However, approximately 20,000 ha of mustard green manure crops are planted in the Columbia Basin annually to improve soil health for soilborne disease management (McGuire 2003; McGuire 2012).

One practice that can help reduce losses to seedling blights in sweet corn is selection of vigorous, high quality seed lots for planting (Callan et al. 1996; Marcos-Filho 2015; Yates et al. 1997). Planting seed lots of sweet corn with higher vigor ratings and percentage germination can result in more uniform emergence and greater yields, particularly during cool, moist soil conditions, compared to planting poorer quality seed lots (Waters and Blanchette 1983). This is described in greater detail in section 1.6.5.

Similarly, the selection of cultivars suited to a particular locations can be useful for managing seedling blights and damping-off. Many damping-off pathogens are active during the cool soil conditions in spring. Planting seed lots of sweet corn cultivars that can emerge rapidly under cool conditions can reduce losses to seedling blights by reducing the duration that seedlings remain in a highly susceptible stage of growth to seedling blight and damping-off pathogens, i.e., from planting to the V3 stage when the plants rely entirely on the seed for energy (Hotchkiss et al. 1997). For example, cultivars with the *su* sweet corn genotype tend to have better cold tolerance compared to cultivars of other sweet corn genotypes (Hassell et al. 2003). In contrast, the *sh2* cultivars typically have poorer seed germination and seedling vigor compared to other sweet corn genotypes (Styler and Cantliffe 1984a). As a result, under cool conditions, it is better to select sweet corn cultivars of the *su* genotype. If *sh2* or other less cold tolerant genotypes are to be grown, the crops could be planted after soil temperatures have warmed, if feasible (University of Illinois Extension 2020; Mock and McNeill 1979).

Along with cultivar selection, growers can time planting with conditions that favor sweet corn germination and seedling development (Garcia et al. 2009). However, this is not always a viable option. For example, sweet corn crops grown for processing, are produced under contract, with the processor determining various crop management decisions such as the cultivars planted,

planting dates, and harvest dates to facilitate having to process thousands of hectares of sweet corn in a season for a crop that has a very narrow window of harvest for optimal quality (Williams 2014).

In areas where soil temperatures are cool and the duration of the growing season is limited, the use of sweet corn transplants and black plastic mulch to increase soil temperature canincrease the rate of plant growth and reduce the time to harvest (Kwabiah 2004). This also reduces the duration seedlings are in the highly susceptible stage of growth to damping-off pathogens (Hotchkiss et al. 1997). However, these strategies are not feasible in large-scale sweet corn production due to the costs of transplanting, for making the planting beds, and covering the beds with plastic mulch (Kwabiah 2004).

1.6.4 Genetic tolerance of cold conditions and resistance to seedling blights

While seed treatments and cultural practices can improve sweet corn germination and stand establishment, these management practices have limited efficacy because of persistence of the pathogens in soil, the broad host range of some pathogens, development of resistance to fungicides, and the large acreage that has to be planted in a season. When growing sweet corn in cold, wet field conditions, the genetic capacity of the plants to tolerate low temperatures is an important factor influencing the establishment of an adequate crop stand (Stewart et al. 1990). Variation in tolerance of cool soil conditions and the capacity for vigorous seedling growth exists in diverse corn lineages that is controlled by several additive and dominate alleles (Li et al. 2018; McConnell and Gardner 1979). However, the genetic base for commercial sweet corn in most breeding programs is relatively narrow due to the need to maintain optimal market eating qualities (Tracy 1990). As a result, many breeding programs have used field corn germplasm, which typically has better performance under cool soil conditions compared to sweet corn

germplasm, to integrate cold tolerance genes into sweet corn breeding material (Rodríguez et al. 2010; Tracy 1990). Rapid seedling emergence and resistance to damping-off and seedling diseases are relatively heritable characteristics in corn (Munkvold and White 2016).

When sweet corn is crossed with field corn, undesirable traits are carried over with the desired traits, that usually affect sweetness, texture, and other traits needed in sweet corn (Allam et al. 2016; Revilla et al. 2000; Tracy 1990). Nonetheless, differences among corn cultivars with respect to cold tolerance suggest that improvements in emergence and vigor in sweet corn grown at low temperatures can be made (Herner 1986). Among the three major sweet corn mutations, cultivars with *su1* lineage tend to have better vigor and emergence under cold conditions compared to cultivars of the *sh2* type (Hassell et al 2003; Styer and Cantliffe 1984a). Selecting breeding lines for increased seedling height, less seed rot in the soil, and improved seed germination using recurrent selection has been successful at improving populations of *sh2* sweet corn for cold tolerance (Viesselmann et al. 2014). However, efforts at breeding for rapid emergence and improved tolerance of cold conditions and resistance to damping-off has been hampered often by the many environmental factors influencing the traits under selection and, in some cases, the presence of both seedborne and soilborne pathogens that can confound selection for genetic tolerance or resistance (Munkvold and White 2016).

As stated before, low soil temperatures reduce the rates of emergence of sweet corn plants and increase the window of susceptibility of sweet corn to seed rots and seedling diseases (Mock and McNeill 1979). Cold tolerant seedlings, grow more vigorously at suboptimal soil temperatures, thus decreasing the amount of time a seed or seedling is in the highly susceptible stage of growth for infection by damping-off pathogens (Broders et al. 2007; Hotchkiss et al. 1997; Hope et al. 1992; Miedema 1982; Mock and McNeill 1979). For many sweet corn

cultivars grown in northern states, the shift to earlier planting to meet market needs or to gain advantage of higher prices for earlier harvests has often resulted in seed being planted in cooler soil than optimal conditions.

1.6.5 Sweet corn seed quality and vigor testing

Seed vigor and quality are two key factors in the establishment of crops and have a profound influence on crop growth and development (Marcos-Filho 2015). Under most soil conditions, planting vigorous seed lots results in more uniform emergence and greater yields than when poorer quality seed lots are planted under the same conditions (Waters and Blanchette 1983). The high moisture and sugar concentrations in sweet corn kernels result in slow drying of the kernels when the corn is grown to produce seed for planting purposes (Tracy 1997). This can result in a high incidence of infection of the drying seed by pathogens such as *F. verticillioides* which in turn, can reduce seed germination and seedling vigor when the seed is planted (Headrick and Pataky 1989; Tracy 1997). Seed can also be infected by other *Fusarium* spp. as well as species of *Penicillium* and *Rhizopus* (Mathre et al. 1995; Parera and Cantliffe 1994; Styer and Cantliffe 1984a). Seeds infected with these fungi can rot and/or develop seedling blights, especially when planted in suboptimal conditions (Halfon-Meiri and Solel 1990). As a result, planting high quality seed is particularly important in sweet corn production (Callan et al. 1996; Marcos-Filho 2015; Yates et al. 1997).

Due to the importance of planting high-quality seed, various tests have been developed to help quantify accurately the vigor and quality of seed lots for a diversity of crops. This includes cold germination tests, conductivity tests, saturated cold tests, and standard germination tests (Baalbaki et al. 2009). Standard seed germination tests typically evaluate seed germination under optimal conditions, whereas stress tests, such as cold germination tests, assess the performance

potential of seed lots under stressful conditions that a grower might encounter. Growers can use results of these tests to assess seed lot quality for planting in a variety of locations and conditions (Baalbaki et al. 2009). For example, it has been shown that in pea the measurement of electrical conductivity can be used to determine the vigor of pea seed lots and predict field emergence (Castillo et al. 1993; Ladone 1989; and Pandey 1992). When peas were grown in the present of *P. ultimum*, pea seed lots with lower electrical conductivity, and thus lower electrolyte leakage, improved emergence compared to seed lots with higher electrical conductivity ratings (Alcala 2013). As a result, electrical conductivity of pea seed lots is routinely used for the selection of vigorous seed lots for planting processing pea crops in the Columbia Basin.

Three primary tests are used to gauge the quality and vigor of sweet corn seed lots: 1) the cold test, 2) the seed conductivity test, and 3) the saturated cold soil test (Baalbaki et al. 2009). The cold test is the standard and most popular vigor test for corn and sweet corn seed lots in North America. This test can be used to assess a variety of qualities of a seed lot but is used most commonly to assess the potential field performance of seed lots under suboptimal temperatures. The saturated cold test is a variation on the cold test that adds the extra conditions of excess water stress and associated oxygen stress to evaluate seed quality under cold, saturated soil conditions (Baalbaki et al. 2009). The conductivity test measures electrolyte leakage from seed lots as an indirect assessment of the potential vigor of a seed lot. The conductivity of electrolytes that leach from imbibing seeds into water is greater for seed lots in which seeds are cracked, old, or damaged, and is used as a measure of a quality of the seed lot since electrical conductivity is negatively correlated with emergence and vigor of corn seed under field conditions (Tracy and Juvik 1988). Seed lots with greater electrolyte leakage (greater electrical conductivity) typically have lower quality and vigor (Baalbaki et al. 2009; Tracy and Juvik 1988).

In corn electrolyte leakage has been used as a tool to predict the shelf life or storability of a seed lot (Marks and Stroshine 1998; Wann 1986). In crops like pea, this data is used to help assess the vigor of a seed lot and predict field emergence (Alcala 2013). However, the electrical conductivity data of sweet corn lots is not routinely used in most sweet corn production regions, including the Columbia Basin, to assess the vigor of a sweet corn lot or to predict field performance. With the successful use of electrical conductivity data to predict vigor in pea (Alcala 2013) there is potential for this data to be used as a decision making tool in sweet corn production, especially in organic crops where growers do not have access to efficacious seed treatments to help improve stand.

1.7 Conclusion and Research Needs

The USDA Specialty Crops Research Initiative (SCRI) is funding the Sweet CAPS project (No. 2018-51181-28419) that is focused on developing technologies and resources to improve sweet corn production and marketability. The Sweet CAPS team is comprised of eight co-investigators, four senior scientists, technical support staff, postdoctoral research associates, and graduate students. This project has five primary objectives: 1) to improve sweet corn breeding technologies, 2) improve sweet corn disease and insect resistance, 3) improve early season cold tolerance in sweet corn, 4) improve sweet corn eating quality, and 5) conduct sweet corn economic assessment and outreach in the United States.

Sweet corn producers in the Columbia Basin face many problems when planting crops in early spring as a result of cool, wet soil conditions that increase the risks of losses to seedborne and soilborne damping-off pathogens. While many pathogens of corn have been well studied, there is little public information on seedling blight pathogens affecting sweet corn in the irrigated agricultural regions of the Pacific Northwest United States, such as the Columbia Basin of

Washington. The Columbia Basin has become a major region of sweet corn production for the United States. Growers within this region have expressed increasing concerns about poor stands and damping-off, particularly for corn sown in the early spring. Thus, there is a need to: 1) assess the prevalence of seedling blights in this region, 2) identify the predominant seedling blight pathogens affecting sweet corn in the Columbia Basin, 3) assess management options for growers to reduce losses to seedling blights, and 4) screen the Sweet CAPS sweet corn germplasm diversity panel for entries that display tolerance of cool soil conditions and resistance to seedling blight pathogens.

This research project was conducted as a part of the Sweet CAPS project to address aspects of two of the Sweet CAPS five main objectives, 2) improving disease and insect resistance (with a focus on seedling blights), and 3) improving sweet corn germplasm for early season cold tolerance. In consideration of these research needs, the specific objectives of this MS thesis project were to:

(1) Survey conventional and organic sweet corn crops in the semi-arid, irrigated Columbia Basin of central Washington to assess the severity of losses to seedling blights;

(2) Identify the predominant *Fusarium, Pythium,* and *Rhizoctonia* species associated with sweet corn seedling blights in the surveyed sweet corn fields;

(3) Assess the virulence to sweet corn of the *Fusarium, Pythium*, and *Rhizoctonia* species identified, under cool and moist soil conditions typical of spring planting in the Columbia Basin;

(4) Initiate the screening of the Sweet CAPS diversity panel of sweet corn breeding lines and germplasm for resistance to the most predominant *Fusarium, Pythium,* and *Rhizoctonia* species identified in the survey;

(5) Evaluate the Sweet CAPS diversity panel for cold tolerance in field trials in the Columbia Basin; and

(6) Evaluate steam treatments of sweet corn seed for efficacy at controlling seedborne fungal pathogens of sweet corn, particularly as an organic seed treatment.

The ultimate goal of this project is to assist sweet corn growers in the Columbia Basin by reducing their losses to seedling blights and advancing the progress of sweet corn breeders at developing cultivars with greater cold tolerance than those currently available.

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CHAPTER TWO

SURVEY OF *FUSARIUM*, *PYTHIUM*, AND *RHIZOCTONIA* SPECIES ASSOCIATED WITH SEEDLING BLIGHTS IN SWEET CORN FIELDS IN THE COLUMBIA BASIN OF WASHINGTON

2.1 Introduction

Sweet corn (*Zea mays*) is one of the most important and popular vegetable crops grown in the United States (Grecu et al. 2018; Revilla and Tracy 1995). It is due, in part, to this demand that sweet corn is grown in every state in the United States (Lizaso et al. 2007). Fresh market sweet corn is produced primarily in southern states such as California, Florida, and Georgia, where warmer climatic conditions allow for early planting, and a long growing season enables multiple crops through the year (Lizaso et al. 2007; United States Department of Agriculture National Agricultural Statistics Survey 2012). Processing sweet corn, however, is produced primarily in northern states, such as Minnesota, Washington, and Wisconsin (USDA NASS 2012). In Washington State, one of the states with the largest acreage of sweet corn production, an average of 36,400 ha of sweet corn is planted annually, of which approximately 31,900 ha are for processing (USDA NASS 2017). Washington also has the largest acreage of organic sweet corn in the United States, with approximately 4,000 ha planted annually (USDA NASS 2018). Most sweet corn production in this area occurs in the semi-arid Columbia Basin of central Washington where sweet corn is planted from late March through early July, and often double-cropped with pea (*Pisum sativum*).

In Washington and many other states, sweet corn crops can suffer from significant losses to seedborne and soilborne pathogenic fungi and oomycetes (Munkvold and White 2016). These

losses are most profound under cool, wet conditions, such as those that occur in the early spring in many of the major corn and sweet corn growing regions (Bakker et al. 2016; Miedema 1982). This is exacerbated by the increasing trend of planting corn crops earlier in the spring in many of these regions to facilitate increased acreage of production. This can result in slow germination and poor vigor of sweet corn seedlings under the cool early spring conditions since sweet corn seed typically grows poorly at soil temperatures <15°C (Hendrix and Campbell 1973; Kucharik 2006; Miedema 1982). Sweet corn varieties of the *shrunken-2* (*sh2*) genotype, which currently dominate the sweet corn industry in the United States, typically have poorer vigor and germination, even under ideal planting conditions, compared to *sugary* (*su*) and *sugary enhancer* (*se*) sweet corn genotypes, which can compound this issue further (Hartz and Caprile 1995; Styer and Cantliffe 1984).

Of the fungi and oomycetes that can cause damping-off and seedling blights, three genera typically account for most of the losses in corn, i.e., *Fusarium*, *Pythium*, and *Rhizoctonia* (Munkvold and White 2016). Unfortunately, many species of these genera are cosmopolitan, abundant within agricultural soils, and active under conditions that occur around the time of planting (Bakker et al. 2016; Hendrix and Cambell 1973; Miedema 1982; Munkvold and White 2016). In regions like the Midwestern United States, *Pythium* spp. have been well documented to be prevalent seedling pathogens in corn production (Broders et al 2007a; Dorrance et al. 2004; Zhang and Yang 2000). Similarly, *Rhizoctonia* spp. such as *R. solani* and *R. zeae* have been documented in many agricultural areas in the United States (e.g., Ohkura et al. 2009; Sumner and Bell 1982; Voorhees 1934). *Fusarium* spp. pathogenic to sweet corn, such as *F. graminearum* and *F. verticillioides*, are found in nearly every region where corn is grown (Bacon et al. 1994; Broders et al. 2007b; Murillo-Williams and Munkvold 2008). Many of these corn pathogens are

also pathogens of other field crops such as wheat (*Triticum aestivum*), onion (*Allium cepa*), pea, and potato (*Solanum tuberosum*) (Alcala et al. 2016; Chang et al. 2013; Glynn and Edwards 2009; Ocamb et al. 2007; Patzek et al. 2013; Porter et al. 2009), which makes management of these pathogens more difficult. This is true, also for sweet corn production in the Columbia Basin of central Washington.

Unfortunately, little can be done to avoid the presence of these pathogen(s) or to avoid conditions conducive to development of seedling blights when other factors are involved such as premium prices for early sweet corn crops, planting dates dictated by the processors, volatility of weather conditions, and cosmopolitan distribution of seedling blight pathogens (Bakker et al. 2016; Mock and McNeill 1979; Styer and Cantliffe 1984; Williams 2014). As a result, management of these pathogens in conventional corn and sweet corn crops has depended primarily on the use of fungicide seed treatments (Berger and Wolf 1974; Hartz and Caprile 1995; Lamichhane et al. 2020; Matthiesen et al. 2016; Rodriguez-Brlijevich et al. 2010). The fungicide seed treatments used commonly include metalaxyl or the isomer mefenoxam to protect seeds and seedlings from pathogenic species of *Pythium* (Baird et al. 1994; Lamichhane et al. 2020; McGee 1992). To help control species of *Fusarium* and *Rhizoctonia*, fungicides such as benomyl, captan, iprodione, pentachloronitrobenzene, and thiram have been used effectively to control some of these pathogens on diverse plant species, though benomyl, iprodione, and pentachloronitrobenzene are not registered for use on sweet corn (Allen et al. 2004; Baird et al. 1994; Glynn et al. 2007). Difenoconazole, fludioxonil, carboxin, and azoxystrobin are widely used to control various fungi like *Fusarium* and *Rhizoctonia* [United States Environmental Protection Agency(EPA) 1999; Wohleb 2013]. However, growers of certified organic sweet corn cannot apply most synthetic fungicides products as they are often not permitted for use in

certified organic production (USDA National Organic Program 2018). Although a rapidly growing number of organic seed treatments is available commercially, organic sweet corn growers do not have access to highly efficacious seed treatments as a large majority of these organic treatments have not proven to be efficacious or to provide consistent efficacy to justify the expense. As a result, in Washington State, organic sweet corn growers routinely over-seed sweet corn crops by ~30% in anticipation of losses to seedling blights (C. Burt and T. Bruketta, Twin City Foods, Pasco, WA, *personal communication*).

Seed and seedling pathogens of corn and sweet corn have been well studied in some regions of the United States, such as the Midwest and South (Bacon et al. 1994; Broders et al. 2007a; Dorrance et al. 2004; Sumner and Bell 1982; Voorhees 1934; Zhang and Yang 2000). However, little public research has been done on seedling pathogens of sweet corn in the semi-arid Columbia Basin of central Washington, which only became a major region of sweet corn production in the past ~30 years. Sweet corn growers in this region have indicated that they regularly encounter damping-off and seedling diseases following spring planting, to the degree that they routinely over-seed at planting to achieve sufficient stands. This is problematic enough for organic sweet corn crops, that planting of organic processing sweet corn crops is initiated at least a month later than planting of the first conventional sweet corn crops (C. Burt, *personal communication*). Thus, the goals of this study were to: (1) survey the prevalence of seedling blights and identify the predominant *Fusarium, Pythium,* and *Rhizoctonia* species in conventional and organic sweet corn crops in the Columbia Basin of Washington; (2) assess the prevalence of *Pythium* spp. with resistance to mefenoxam to understand the degree to which this might contribute to losses in sweet corn production; and (3) determine which of the predominant

Fusarium, *Pythium*, and *Rhizoctonia* species detected in these crops are pathogenic to sweet corn under cool and moist soil conditions typical of early spring planting in the Columbia Basin.

2.2 Materials and Methods

2.2.1. Fields surveyed. In the spring and early summer of 2018, 47 sweet corn fields, including 31 conventional and 16 certified organic fields, were surveyed in the Columbia Basin for seedling blights (Table 2.1). Fields were selected based on reports by processing company field representatives of suspected issues with poor stand counts or damping-off; to represent both certified organic and conventional production; and to represent the north (n = 11 fields), central (n = 15), and south (n = 22) regions of the Columbia Basin (Fig. 2.1). Pertinent information about each field (e.g., recent crop rotation history, sweet corn cultivar, etc.) was obtained from processing company representatives and the growers or managers of the farms (Table 2.1). All of the fields surveyed were irrigated using center pivots.

Stand counts and the incidences of stunted seedlings were estimated within three to six weeks after planting each crop. At the same time, stunted seedlings were sampled from each field. Assessments were done along four parallel transects in each field, with a preference for areas of the field with suspect symptoms of seedling blight or areas which might favor seedling blights, such as low-lying areas where water might collect. For each transect, 200 plants were counted, and the stand loss was estimated based on the original seeding rate. The incidence (%) of stunted seedlings was estimated by counting the number of seedlings in each transect that were ≥25% shorter than the surrounding plants, expressed as a percentage of total emerged plants. From each transect, up to 10 stunted seedlings were collected by gently digging up each seedling to maintain as complete a root system as possible. Each seedling was placed in a labeled

plastic bag in a cooler with ice and transferred to a cold storage facility (4 ± 2°C) at the Washington State University (WSU) Mount Vernon Northwestern Washington Research and Extension Center (NWREC). The estimated stand counts and incidences of stunted seedlings for each field were correlated with planting dates using Pearson's correlation coefficient (Fig. 2.2). Daily mean soil temperature (5-cm depth) recordings from the WSU AgWeatherNet system (weather.wsu.edu) for the Columbia Basin were also examined in relation to planting date, stand counts, and incidence of stunted plants (Fig. 2.2).

***2.2.1.1. Isolation of* Fusarium, Pythium*, and* Rhizoctonia *species*.** *Fusarium, Pythium,* and *Rhizoctonia* species were isolated from the stunted sweet corn seedlings collected in each field. Each seedling was rinsed under running tap water for at least 5 minutes, photographed, and dried in a laminar flow hood on sterilized paper towels for at least 20 minutes. Each seedling was then cut into hypocotyl/mesocotyl, roots, and seed, and each section was divided further into three smaller sections. The three pieces of each section where plated onto *Pythium* selective agar medium (PSM) (Mircetich and Kraft 1973), 1.5% water agar medium (WA), and Nash-Snyder agar medium (NS) (Nash and Snyder 1962). The plates were incubated in the dark at room temperature (21 ± 2°C) for 24 to 36 h, after which each section of tissue was transferred to half-strength potato dextrose agar medium amended with 100 mg/L chloramphenicol (½ cPDA), except for those originally plated on PSM, which were transferred onto non-amended, half-strength PDA medium as chloramphenicol is inhibitory to some *Pythium* species. Hyphal growth of each isolate was observed microscopically to select *Fusarium, Pythium,* and *Rhizoctonia* species.

Single-spore isolates were generated for the *Fusarium* isolates. A pure culture of each isolate was stored. *Fusarium* isolates were grown on 1.5-cm-diameter sterilized filter disks

(VWR Scientific Products, West Chester, PA) on PDA, which were then dried in a laminar flow hood after complete colonization by the isolates, and placed into sterilized coin envelopes (57 cm x 8.9 cm) (Westvaco Envelope Division, Springfield, MA). For each isolate, the dried colonized filter disks in the coin envelopes were stored at -20°C and a second set of disks for the isolates was stored at room temperature, with both sets in air-tight containers with desiccant. Pure cultures of each *Pythium* isolate were maintained on cornmeal agar medium (CMA) in a test tube that was stored at room temperature in the dark. For long-term storage, a 1-cm^3 block of CMA colonized by the *Pythium* isolate was placed in a glass vial containing sterilized water and two sterilized hemp seeds (HBD International, Inc., Brentwood, TN), and stored at room temperature. Pure cultures of *Rhizoctonia* isolates were maintained on ½ cPDA slants and stored at 4°C. A 1-cm^3 block of ½ cPDA colonized by each *Rhizoctonia* isolate was placed in a glass vial (25 ml) containing 5.5 g of sterilized rye seeds, and stored at room temperature for three weeks for colonization of the rye seeds, followed by long-term storage at 4°C. The sterilized rye seeds were prepared by imbibing the seed for 24 h in deionized water, after which the rye seed was aliquoted into 25 ml glass vials, each loosely capped with a autoclavable plastic cap, and autoclaved for 60 min at 121°C and 100 kPa. Each glass vial was autoclaved again 24 h later for 90 min.

***2.2.1.2. Identification of* Fusarium, Pythium, *and* Rhizoctonia *species*.** Isolates were each identified to genus based on microscopic examination of morphological features characteristic of *Fusarium*, *Pythium*, and *Rhizoctonia* (Domsch and Gams 1993; Seifert et al. 2011; Watanabe 2002). To verify the species of each isolate, the internal transcribed spacer (ITS) region of the ribosomal DNA (rDNA) was sequenced for each *Pythium* and *Rhizoctonia* isolate using a modified version of the method described by Paulitz and Adams (2003), and the translation elongation factor 1-α (*EF 1-α*) region was sequenced for the *Fusarium* isolates

following the method described by (Rehner and Buckley 2005). Each isolate was grown in 40 ml of potato dextrose broth (PDB) in a 125 ml Nalgene flask for 5 to 7 days (depending on whether the isolate was slow- or fast-growing). The mycelium was then decanted from the PDB, and excess liquid removed by filtering the mycelium through a 70 mm-diameter filter disk using a vacuum pump. The harvested mycelium was washed twice with sterilized deionized water, drained, and placed in a 1.7 ml Eppendorf tube. Harvested mycelia were kept at -20°C until used for DNA extraction.

DNA extraction was done using the FastDNA Kit (MP Biomedicals LLC., Solon, OH) following a modified version of the manufacturer's protocol. Polymerase chain reaction (PCR) amplification of the ITS rDNA was done as described by Schroeder et al. (2006), using the primers UNUP18S42 (5'-CGTAACAAGGTTTCCGTAGGTGAAC-3') and UNLO28S576B (UN-LO28S22) (5'-GTTTCTTTTCCTCCGCTTATTAATATG-3') (Bakkeren et al. 2000). The reaction mixture contained: 2.00 µl DNA template, 3.00 µl of 10 x buffer, 1.80 µl of 25 mM $MgCl_2$, 0.60 µl of a 10 mM mixture of dNTPs, 0.12 µl of each of the primers, 22.06 µl of molecular grade water, and 0.30 µl of Ampli-Taq polymerase (Invitrogen Life Technologies, Grand Island, NY) stock at 5 U/µl, for a total volume of 30 µl per reaction. Amplification of DNA was conducted using a Thermo Hybaid PCR Express (Thermo Hybaid, Middlesex, United Kingdom) with the following program: initial denaturation at 94°C for 3 min; followed by 31 cycles of 92°C for 45 s, 45 s at the annealing temperature of 60°C, and 60 s at 72°C; and a final extension step for 10 min at 72°C.

PCR amplification of the *EF-1α* gene was done as described by (Rehner and Buckley 2005) using the primers EF1-526F (5'-GTCGTYGTYATYGGHCAYGT-3'), EF1-1567R (5'-ACHGTRCCRATACCACCRATCTT-3') and EF1-1567Ra (5'-ACHGTRCCRATACCA-3').

EF1-1567a was only used during the sequencing reaction. The reaction mixture contained: 2.00 µl DNA template, 2.50 µl of 10 x buffer, 1.50 µl of 25 mM $MgCl_2$, 0.50 µl of a 10 mM mixture of dNTPs, 0.06 µl of each of the primers, 18.08 µl of molecular grade water, and 0.20 µl of Ampli-Taq polymerase stock at 5 U/µl for a total volume of 25 µl per reaction. Amplification of DNA was completed with the thermal cycler, using the following program: initial denaturation at 94°C for 2 min; followed by 9 cycles (with a reduction of annealing temperature by 1°C each cycle) of 94°C for 30 s, 66°C for the first cycle of 30 s for annealing, and 72° for 90 s; this was followed by 28 cycles of 94°C for 30 s, 30 s of annealing at 56°C, and 72°C for 90 s; and a final extension step for 10 min at 72°C.

PCR products were separated on a 1.5% agarose gel with a 100 bp DNA ladder (Invitrogen Life Technologies) to verify the sample template before sequencing. The amount of DNA was quantified using a Quant-iT dsDNA assay kit (Invitrogen Life Technologies) for Qubit fluorometric quantification. DNA products were treated with Exo SAP-IT or Exo SAP-IT Express (Thermo Fisher Scientific Baltics UAB, Vilnius, Lithuania) using 2 µl for every 5 µl of PCR product to remove remaining dNTPs and primers. For DNA sequencing, each pre-mixed sample consisting of 10 to 15 ng template, 8 pmole forward or reverse primer (for the *EF-1α* sequencing, the alternative reverse primer, EF1-1567Ra, was used for reverse sequencing), and molecular grade water was added for a total volume of 15 µl, which was sent to Elim Biopharmaceuticals, Inc. (Hayward, CA). The sequences were edited manually using Chromas (Technelusium Pty. Ltd., South Brisbane, Australia) and MEGA 7 (Kumar et al. 2016), and compared with available sequences in the GenBank database using the National Center for Biotechnology Information (NCBI) online Basic Local Alignment Search Tool (BLAST) tool.

Isolates with 99 to 100% homology to ITS rDNA sequences or to *EF1-α* sequences in GenBank were considered the same species.

2.2.2. Screening *Pythium* isolates for mefenoxam resistance. Mefenoxam-amended corn meal agar (mCMA) medium was used to assess sensitivity of the *Pythium* isolates to mefenoxam because of prior evidence of resistance to this fungicide in *Pythium* populations in the Columbia Basin (Porter et al. 2009) and widespread use of this fungicide as a seed treatment for sweet corn production. The base medium contained 17 g corn meal agar (Becton, Dickinson and Co., Sparks, MD) and 10 g Bacto agar (Becton, Dickinson and Co.) per liter of deionized water. Technical grade mefenoxam (Syngenta Crop Protection LLC, Greensboro, NC) was added once the autoclaved medium had cooled to 50°C, using a 0.2 µm filter-sterilized stock suspension at 10,000 µg mefenoxam/ml in deionized water. The medium was amended at 0, 10, and 100 µg/ml of mefenoxam. A 5-mm-diameter colonized agar plug taken from the leading edge of a 24-h-old colony of each isolate was transferred to the center of each mCMA plate. Three replicate plates were set up for each mefenoxam concentration for each isolate. Inoculated plates were incubated at 20°C in the dark, and colony growth was assessed 36 h after inoculation for a majority of the isolates or 48 h after plating for the few slow growing isolates (Pym089 = *P. irregulare* and Pym094 = *P. rostratifingens*). Growth was assessed by measuring the colony diameter in each of two perpendicular directions per plate. The measurements were averaged for the three replicates at each mefenoxam concentration. The growth rate of each isolate was calculated as a percentage of the growth of the same isolate on non-amended mCMA. Known mefenoxam sensitive and resistant isolates of *P. ultimum*, Metalaxyl Res 406 (resistant) and Pu-014-272-5 (sensitive), obtained from Dr. Lyndon Porter, USDA ARS Grain Legume Research Unit, Prosser, WA, were used as control isolates. The mefenoxam screening was completed

twice. In each trial, the same 62 isolates were tested with the same protocol. The first trial was completed by Mike Derie (Scientific Assistant Sr., WSU Vegetable Seed Pathology program) and the second trial by Ryan Solemslie.

For each of the two mefenoxam concentrations tested, *Pythium* isolates were grouped into five resistance categories based on the percentage growth on the mefenoxam-amended plates compared to the non-amended control plates for the same isolate. Isolates with no growth were classified as sensitive (S), isolates with 1 to 25% of the growth of the control plates were classified as moderately sensitive (MS), those with 26 to 50% growth were classified as moderately resistant (MR), those with 51 to 75% growth as resistant (R), and those with >75% growth as highly resistant (HR).

2.2.3. Pathogenicity tests. Pathogenicity tests on the sweet corn cv. SuperSweet Jubilee Plus were completed with representative isolates of each species of *Fusarium, Pythium,* and *Rhizoctonia* obtained from the sweet corn survey, using cool and moist conditions typical of the soil conditions during spring planting in the Columbia Basin. Isolates of each genus were tested in separate trials, and the trials were all repeated. The numbers of isolates tested for each species within a genus were selected to represent both the diversity and prevalence of the species in the survey. Since *Fusarium* isolates were the most prevalent of the three genera, 40 isolates of *Fusarium* were tested, and 10 isolates of each of *Pythium* and *Rhizoctonia* were tested, with isolates selected to represent the diversity of species, and regions of the Columbia Basin surveyed (Table 2.2).

Isolates of each of 14 *Fusarium* species were tested: *F. acuminatum* (1 isolate), *F. avenaceum* (1), *F. commune* (1), *F. concolor* (1), *F. equiseti* (4), *F. fujikuroi* (2), *F. graminearum* (2), *F. lacertarum* (1), *F. oxysporum* (8), *F. proliferatum* (5), *F. redolens* (1), *F.*

solani (4), *F. torulosum* (1), and *F. verticillioides* (8). Isolates of each of four species of *Pythium* were tested: *P. irregulare* (1 isolate), *P. rostratifingens* (1), *P. sulcatum* (1), and *P. ultimum* (7) (Table 2.2). Isolates of each of five anastomosis groups (AGs) of binucleate and multinucleate *Ceratobasidium* and *Rhizoctonia*, respectively, were tested: *Ceratobasidium* sp. AG A (1), *Ceratobasidium* sp. AG K (1), *R. solani* AG 2-1 (2), *R. solani* AG 3 (2), and *R. solani* AG 4 (4) (Table 2.2).

2.2.3.1 Preparation of inocula. Inoculum was produced for each isolate of the *Fusarium* spp. and *Pythium* spp. using a sterilized oat-soil mixture. Non-sterile silt loam soil collected from a field at the WSU Mount Vernon NWREC was air-dried for 1 week on tarps (Klungland and McArthur 1989). The dried soil was crushed using a marble rolling pin and sieved (1 mm diameter size mesh). Ground oatmeal (Quaker Oats Brand, Chicago, IL) was added (1% by weight) to the dried, sieved soil and mixed for 10 min in a PK Blendmaster soil blender (Paterson-Kelly Co. Division of Harsco Corp., East Stroudsburg, PA). During the final 5 minutes of mixing, deionized water was added at 25% (wt/wt) to the soil/oatmeal mix. A 400 g sample of this mixture was then added to a 1 liter Mason jar and capped with a metal Mason jar ring lid and 70-mm-diameter synthetic filter disk used for mushroom spawning (Fungi Perfecti, Olympia, WA). Each was covered with 2 layers of aluminum foil, and the soil/oatmeal in the jars was autoclaved for 60 min at 121°C and 100 kPa. Each jar was then autoclaved again 24 h later for 60 min. The soil/oatmeal mixture was stored at room temperature in the dark until used to produce inoculum.

To produce inoculum for the *Rhizoctonia* isolates, 320 ml of whole oats (Skagit Farmers Supply, Mount Vernon, WA) were placed into each 1-liter Mason jar, and 320 ml of deionized water was added to each jar. Each jar was then capped with a metal mason jar ring lid and 70-

mm-filter disk, and incubated at room temperature for 24 h for the oats to imbibe. Excess water was then drained from the oats, and a double foil cap was placed over the Mason jar lid in preparation for autoclaving. The jars were then autoclaved for 90 min at 121°C and 100 kPa. Each jar was autoclaved again 24 h later for 90 min. Jars of the autoclaved oats were stored in the dark at room temperature until used for inoculum production.

For isolates of all three genera, 10 5-mm-diameter agar plugs taken from the edge of actively growing cultures were added to each jar of substrate relevant for the genus. The isolates were grown for 28 days in the dark at room temperature. Jars with *Pythium* isolates were shaken every 3 days to ensure even colonization of the soil/oat mixture, while jars with *Fusarium* and *Rhizoctonia* isolates were shaken every 7 days. After 28 days, the *Pythium* and *Fusarium* cultures were moved to 4°C to arrest further growth, where the inoculum was stored. The *Rhizoctonia* inoculum was dried on 25 cm × 45 cm × 5 cm deep nursery flats in a fume hood for 7 days. The inoculum was turned every 2 days to ensure complete drying. The dried inoculum was ground for 30 s using a coffee grinder, and then sieved. Particles between 250 and 1,000 μm were stored in resealable, wax lined bags at 4°C.

Inoculum for each isolate was quantified on WA using soil-dilution plating. Each jar of inoculum was shaken vigorously to mix the inoculum, and a 10 g subsample was added to a 250 ml French square bottle containing 100 ml of sloppy agar (0.1% WA). The French square bottle was then shaken at 250 rpm for 10 minutes on a rotary shaker (Innova 2100; New Brunswick Scientific, Enfield, CT). Five-fold dilutions were then prepared using 10 ml aliquots transferred serially to 100 ml-capacity French square bottles, each containing 40 ml of sloppy agar. Three 0.5 ml aliquots of each dilution were then spread onto plates of 1.5% WA using a flame-sterilized, bent glass rod. Plates were incubated in the dark at 22 ± 1°C. Colonies of *Pythium*

isolates were counted 12, 24, and 36 h after plating. Colonies of *Fusarium* isolates and *Rhizoctonia* isolates were counted 24 and 48 h after plating. The number of colony forming units (CFU)/g soil was determined for inoculum of each isolate using the average number of colonies counted from the three replicate plates of each dilution.

2.2.3.2. Soil pasteurization. Field soil obtained from the WSU Mount Vernon NWREC was moistened with tap water, pasteurized for 45 min at 65°C, and pasteurized again after 24 h for the same duration and temperature using a custom-built steam pasteurizer (Siebring Model SG10, Siebring MFG Inc., George, IA). The cooled soil was placed onto tarps sterilized with 70% isopropanol, and dried for 2 to 3 days. The soil was then crushed using a marble rolling pin and sieved using a 1 mm-diameter mesh sieve. The sieved, pasteurized soil was stored at 15°C in 20-liter buckets sterilized with 70% isopropanol, and each bucket was covered with a lid to minimize the risk of contamination.

2.2.3.3. Seed surface-disinfestation. Sweet corn seeds of the cv. SuperSweet Jubilee Plus were surface-disinfested using a sodium hypochlorite treatment derived from the method described by Hartz and Caprile (1995), to minimize potentially confounding effects of seedborne fungi on this seed lot with the soilborne inoculum of the isolates tested for pathogenicity. Each sample of 550 seeds was enclosed in a 1-liter mesh bag and soaked in 0.5% NaOCl (v/v) amended with one drop of Tween-20 (Sigma-Aldrich, Inc., St. Louis, MO) per 100 ml of NaOCl solution for 10 min. The seeds were then triple-rinsed with deionized water, and dried overnight on sterilized paper towels in a laminar flow hood.

2.2.3.4. Preparation of inoculated soil and planting. A different concentration of inoculum was used for isolates of each of the three genera based on previous research published on pathogenicity tests with these genera on various plant species (Alcala 2013; Bacon et al.

1994; Patzek et al. 2013). For each *Fusarium* isolate tested for pathogenicity on sweet corn, 2.5 kg of pasteurized soil was mixed with soil-oatmeal inoculum at a final inoculum density of 1,000 CFU/g soil. Similarly, for each *Pythium* and *Rhizoctonia* isolate tested, 2.5 kg of pasteurized soil was mixed with the soil-oatmeal inoculum (for *Pythium*) or the ground, autoclaved oats (for *Rhizoctonia*), for a final inoculum density of 1,000 and 500 CFU/g soil for *Pythium* and *Rhizoctonia,* respectively. The soil-inoculum mix for each isolate was then mixed for 10 minutes using a PK Blendmaster Laboratory mixer. After 5 min of mixing, 450 ml of deionized water was added slowly to the soil-inoculum mixture. A sample of 650 g of infested soil was then placed into each of four 10-cm wide by 10-cm tall plastic pots (Anderson Die and Manufacturing, Portland, OR). Seeds of the sweet corn cv. SuperSweet Jubilee Plus (n = 12, for a seed lot that had 88% normal germination) were planted in each pot in three rows of four seeds. This was repeated for each isolate and the non-inoculated control soil. The mixer was rinsed with deionized water, sterilized with 70% isopropanol, and wiped dry with paper towels between isolates.

After planting four replicate pots per isolate, the pots of soil for each trial were arranged in a randomized completed block design (RCBD) in a PGC Controlled Environment Chamber (Percival Scientific Inc., Perry, IA) set at 15°C during the day and 13°C at night with a 12 h photoperiod/day to mimic cool spring planting conditions. Each pot was placed in a small plastic bag to prevent excess water from draining out of the pots and contaminating surrounding pots. Plants in the *Pythium* trial were watered every day with 10 ml of water, to ensure adequate soil moisture to favor growth of the inoculum. Plants in pots for the *Fusarium* and *Rhizoctonia* trial were watered with 10 ml of water approximately every 2 days to avoid saturated conditions. The water used to irrigate the pots in each trial was kept at room temperature.

2.2.3.5. *Data collection*. The number of seedlings that emerged in each pot was counted every 7 days for 4 weeks, starting 7 days after planting (dap). After 28 days, the height of each plant was measured. The seedlings and non-germinated seeds were then removed from the pots and the remaining soil was rinsed gently from the roots and seed. The washed plants were photographed and rated for root rot severity using a 0-to-5 scale, where: 0 = no visible symptoms on the roots; 1 = a few, small, discolored lesions on the roots; 2 = minor discoloration covering most roots and the mesocotyl; 3 = brown discoloration of the mesocotyl and roots, with most of the lateral roots missing; 4 = complete discoloration of mesocotyl and roots, lateral roots missing; 5 = rotten seeds with no root or shoot development (Fig. 2.3). The aboveground parts of each plant, including the mesocotyl, were removed, collated for all plants from the same pot, and dried in an oven at 60°C for 3 to 4 days to measure the total dry weight of plants in each pot. Isolations from representative root pieces were carried out from seedlings in each pot following the protocol described for the original seedlings collected in the survey. Root pieces were plated onto ½ PDA and WA. After 24 to 36 h, fungi and oomycetes growing out of the pieces were transferred to ½ PDA plates and incubated for 3 to 5 days for microscopic identification to genus.

2.2.3.6. *Repeat pathogenicity tests*. The pathogenicity tests of the same 40 *Fusarium* isolates, 10 *Pythium* isolates, and 10 *Rhizoctonia* isolates were each repeated with slight modifications. *Pythium* isolates were each inoculated at 500 CFU/g soil (vs. 1,000 CFU/g soil in the first trial) and *Rhizoctonia* isolates were inoculated at 200 CFU/g soil (vs. 500 CFU/g in the first trial). The inoculum concentration in the repeat *Fusarium* trial remained at 1,000 CFU/g soil. Inoculum concentration was reduced for the *Pythium* and *Rhizoctonia* isolates because of

the severity of root rot and poor plant stand and height in the first trials with some of these isolates.

2.2.3.7. *Statistical analyses*. For each pathogenicity test, data were analyzed as a RCBD with analysis of variance (ANOVA) and Fisher's protected least significant difference (LSD at $P < 0.05$) for treatment means comparisons calculated using SAS Proc MIXED (Version 9.4, SAS Institute, Cary, NC) for each of the dependent variables: sweet corn stand counts measured 28 dap, and root rot severity, plant height, and aboveground plant dry weight measured 28 dap. Isolates were considered fixed effects and replications random effects in the model. Dependent variables that did not meet the parametric analysis assumptions of normality of the data and equal variances were subjected to logarithmic, square root, or arcsine transformation; or Friedman's non-parametric rank test if the transformations failed to meet these assumptions.

2.3 Results

2.3.1. Field survey. Of the 47 fields surveyed in the Columbia Basin in 2018, 11 fields were in the north, 15 were in the central region, and 22 were in the south (Fig. 2.1 and Table 2.1). The planting dates ranged from 27 March to 14 June, 27 March to 4 July, and 4 April to 5 July, respectively, for the three regions. For conventional fields, planting dates ranged from 27 March to 4 July, and planting dates for organic fields ranged from 13 June to 6 July. Eleven fields were planted with *su* sweet corn cultivars and 36 fields were planted with *sh2* sweet corn cultivars. In total there were 17 sweet corn cultivars planted across the 47 fields surveyed: 3879 XR (*sh2*, 1 field), Basin (*sh2*, 4), Chase (*su*, 3), Devotion (*sh2*, 4), GH 4927 (*su*, 2), Glacial (*sh2*, 1), GSS 1477 (*sh2*, 2), GSS 1972 (*sh2*, 1), GSS 3071 (*sh2*, 2), GSS 3951 (*sh2*, 6), Klondike (*sh2*,

8), Prelude (*sh2*, 1), Seminis 5808 (*sh2*, 3), SC 1263 (*su*, 1), Sheba (*sh2*, 2), Sockeye (*su*, 3), and SV 7538 (*sh2*, 1).

Plant stands in the 31 conventional sweet corn fields surveyed ranged from 61.9 to 96.7% with a mean of 85.2 ± 2.1% (standard error) (Fig. 2.2A). This equated to stand losses of 3.3 to 38.1% of the seed planted in conventional fields. In addition, the incidence of stunting in these fields ranged from 3.7% to 23.4% of the emerged plants, with a mean of 10.6 ± 1.0% (Fig. 2.2B). In comparison, stands in the 16 organic fields surveyed ranged from 52.5 to 93.6% with a very similar mean of 85.0 ± 2.5% (Fig. 2.2A). This equated to stand losses of 6.4 to 47.5% of the seed planted. The incidence of stunting in these organic fields ranged similarly to the conventional fields, from 4.4 to 20.4%, with a mean of 8.9 ± 1.0% of the emerged seedlings (Fig. 2.2B). Stand counts ranged from 80.8 to 96.7%, 61.9 to 91.6%, and 72 to 96.3% for the north, central, and south regions of the Columbia Basin, respectively, with means of 89.9 ± 1.6, 76.6 ± 3.5, and 88.7 ± 1.5%, respectively. Similarly, stunting ranged from 3.9 to 13.6, 6.2 to 23.4, and 3.7 to 14.9%, respectively, with a mean of 7.5 ± 1.0, 14.1 ± 1.6, and 8.5 ± 0.8%, respectively.

Planting date was positively correlated with sweet corn stand counts ($r = 0.2892$, $P = 0.0486$; Fig. 2.2A) and negatively correlated with incidence of stunting ($r = -0.3639$, $P = 0.0106$; Fig. 2.2B). Stand counts were also positively correlated with soil temperature at a 5-cm depth ($r = 0.3240$, $P = 0.0263$; Fig. 2.2A), whereas the incidence of stunting was negatively correlated with soil temperature at a 5-cm depth ($r = -0.3789$, $P = 0.0086$). For conventional fields, stand counts were positively correlated with planting date ($r = 0.5538$, $P = 0.0012$) and soil temperature ($r = 0.4723$, $P = 0.0073$), whereas incidence of stunting was negatively correlated with planting date ($r = -0.4286$, $P = 0.0161$) and soil temperature ($r = -0.3661$, $P = 0.0428$). For organic fields, there was no significant correlation between stand counts and planting date (r = -

0.0112, *P* = 0.9671) or stand counts and soil temperature (r = 0.2521, *P* = 0.3462). Similarly, there was no significant correlation between the incidence of stunting with planting date (r = -0.1837, *P* = 0.4959) and incidence of stunting and soil temperature (r = -0.3890, *P* = 0.1364).

In some fields, stand losses were attributed to issues other than seedling blights. For example, in four organic fields, approximately 1 to 3% of the stand losses observed were associated with wireworm (*Conoderus rudis*) damage to seed and seedlings. In five fields in the southern Columbia Basin, dieback of an estimated 1 to 5% of seedlings was the result of feeding damage by the webworm *Crambus rickseckerellus* (Klots 1940; Fig. 2.4). Larvae of this pest collected from these fields were sent to Steven Passoa [USDA Animal and Plant Health Inspection Service (APHIS), Ohio State University, Columbus, OH] for identification. This is the first recorded incidence of this pest in central Washington. Corn seed maggot and other production issues (e.g., blocked irrigation nozzles and cloddy field preparation in some early-planted conventional fields) were also contributing factors to stand losses in three of the fields sampled.

In total, 350 *Fusarium* isolates, 63 *Pythium* isolates, and 66 *Rhizoctonia* isolates were collected and stored from stunted sweet corn seedlings sampled from 31 conventional and 16 organic fields in the Columbia Basin of Washington between 1 May and 24 July 2018. Of the 485 isolates, 34.2% (166) were from 10 fields in the northern region, 14.4% (70) from 15 fields in the central region, and 51.3% (249) from 22 fields in the southern region of the Columbia Basin (Table 2.3). This reflects, in part, the number of fields surveyed in each region. Identification of 479 of the 485 isolates to genus and species by sequencing the ITS rDNA for *Pythium* and *Rhizoctonia* isolates or *EF-1α* gene for *Fusarium* isolates revealed the presence of 14 species of *Fusarium*, 4 species of *Pythium*, and 5 species and AGs of *Rhizoctonia* (Table 2.3).

Isolates of nine *Fusarium* species were detected in all 10 fields from the north Columbia Basin, 6 *Fusarium* species were isolated from 5 of the 15 fields in the central Columbia Basin, and 13 *Fusarium* species were identified from 22 fields in the southern Columbia Basin. *F. oxysporum* made up 32.0% of the *Fusarium* isolates (29.1% of all isolates), followed by *F. verticillioides* comprising 26.0% of the *Fusarium* isolates (18.8% of all isolates), *F. solani* at 13.7% (10.1% of all isolates), *F. equiseti* at 10.6% (7.6% of all isolates), *F. proliferatum* at 4.6% (3.3% of all isolates), and *F. fujikuroi* for 4.0% (2.9% of all isolates). Only one isolate was collected of each of *F. acuminatum, F. concolor, F. redolens,* and *F. torulosum,* each from a different field in the southern Columbia Basin, except for the *F. redolens* isolate which was from a field in the north Columbia Basin (Table 2.3). Of the 112 *F. oxysporum* isolates collected, the majority were from conventional fields (67.9%). Similarly, *F. solani* (36/49 isolates = 73.5%), *F. proliferatum* (10/16 isolates = 62.5%), *F. graminearum* (11/11 isolates = 100%), *F. acuminatum* (1/1 isolate = 100%), *F. avenaceum* (2/2 isolates = 100%), and *F. concolor* (1/1 isolate = 100%) isolates predominately originated from conventional fields. In contrast, *F. equiseti* (28/37 isolates = 75.7%), *F. acuminatum* (2/2 isolates = 100%), *F. lacertarum* (8/12 isolates = 66.7%), and *F. verticillioides* (53/91 isolates = 58.2%) predominately originated from organic fields.

Only isolates of *P. ultimum* were obtained from fields in the northern Columbia Basin, isolates of *P. ultimum* and *P. sulcatum* were obtained from fields in the central region, and isolates of *P. ultimum, P. irregulare,* and *P. rostratifingens* were obtained from a total of 16 fields in the southern Columbia Basin. *P. ultimum* made up 95.2% of the *Pythium* isolates (12.4% of all isolates) (Table 2.3). A single isolate of each of *P. irregulare, P. rostratifingens,* and *P. sulcatum* was collected, with the isolates of *P. irregulare* and *P. rostratifingens* collected from two fields in the southern Columbia Basin, and the isolate of *P. sulcatum* collected from a

field in the central region. Of the 60 *P. ultimum* isolates, a majority (60.0%) were from organic fields (Table 2.2.). The *P. irregulare* and *P. rostratifingens* isolates were from conventional fields. However, the 63 *Pythium* isolates represent only a portion of the total *Pythium* isolates collected originally from the 47 fields surveyed. In total, 118 *Pythium* isolates were obtained (*data not shown*) but, for the first 20 fields surveyed, a single isolate of each colony morphotype was maintained in storage. Subsequently, all *Pythium* isolates collected from fields 21 to 47 were maintained in long-term storage and identified to species.

Isolates of five species and AGs of *Rhizoctonia* were collected from the 47 fields surveyed, one from two fields in the north Columbia Basin, one from each of six fields in the central Columbia Basin, and five from a total of eight fields in the southern region (Tables 2.2 and 2.3). *R. solani* AG 4 isolates (46) made up 69.7% of the *Rhizoctonia* isolates and 9.5% of all isolates, followed by *R. solani* AG 2-1 (7) that comprised 10.6% of the isolates of this genus. Isolates of binucleate *Ceratobasidium* species in AG A and AG K accounted for 4.5 and 6.1% of the *Rhizoctonia* isolates, respectively (0.6 and 0.8% of all isolates, respectively). For *R. solani* AG 4, the majority of the 46 isolates (87.0%) were from organic fields. Similarly, two of three *Ceratobasidium* sp. AG A isolates (66.7%) originated from organic fields. However, all seven isolates of *R. solani* AG 2-1, all six isolates of *R. solani* AG 3, and three of four *Ceratobasidium* sp. AG K isolates (75.0%) were from conventional fields.

An additional 387 fungal isolates (44.7% of the total) were collected during the 2018 Columbia Basin sweet corn field survey. The majority of these isolates were in the genera *Penicillium* and *Trichoderma*, with 103 and 243 isolates, respectively. The remaining 41 isolates were genera such as *Mucor* and *Rhizopus*. These isolates were not identified to species or stored. While some species of *Penicillium* are known to be pathogens of sweet corn (Munkvold and

White 2016), the goal of this survey was to investigate the prevalence of damping-off pathogens in the genera *Fusarium*, *Pythium*, and *Rhizoctonia*. Nonetheless, the prevalence of *Penicillium* spp. on the isolation plates illustrated the potential contributions of pathogenic strains of this genus to stand losses and seedling blights in sweet corn.

2.3.2. Mefenoxam resistance screening. Of the 63 *Pythium* isolates obtained from stunted sweet corn seedlings in 25 of the 47 fields surveyed (13 conventional and 12 certified organic crops), 62 were screened for resistance to mefenoxam. One isolate of *P. sulcatum* became contaminated so the isolate was excluded from the resistance screening trials. Of the 62 isolates screened for resistance to mefenoxam, 26 originated from conventional sweet corn crops and 36 from organic sweet corn.

In the first mefenoxam screening trial, the mefenoxam-resistant control isolate of *P. ultimum*, Pym101, had 58.7% (3.4 ± 0.2 cm) and 18.3% (1.1 ± 0.2 cm) growth at 10 and 100 µg/ml concentrations of mefenoxam, respectively, compared to growth on the non-amended control plates (Table 2.4). In contrast, the mefenoxam-sensitive control isolate, Pym102, did not display any measurable growth at both mefenoxam concentrations. Results were very similar in the repeat trial, in which the resistant control isolate grew 59.5% (3.4 ± 0.1 cm) on plates with 10 µg/ml mefenoxam and 19.7% (1.1 ± 0.3 cm) on plates with 100 µg/ml compared to the non-amended control plates (Table 2.4).

In trial 1, 24 (38.7%) of the 62 isolates tested displayed no measurable growth at 10 µg/ml mefenoxam, i.e., they were completely sensitive (S) to the fungicide (Table 2.4). Only three of the 24 S isolates originated from conventional sweet corn crops (each from a different field). Another five isolates (8.1%) were classified as MS. No isolates were classified as MR, but 48.4% were classified as R to mefenoxam, and three (4.8%) as HR. Of the three HR isolates, two

displayed similar growth rates on amended medium as on the control plates (97.3 and 105.8% for Pym107 and Pym106, respectively; Table 2.4).

When tested at 100 µg mefenoxam/ml, 27 isolates (43.6%) displayed no measurable growth, i.e., were completely S to the fungicide (Table 2.4). Only four of these were from conventionally managed fields, and the other 23 isolates originated from 11 organic fields. Of the remaining isolates, 26 (41.9%) were classified as MS, 6 (38.7%) as MR, and 3 (4.84%) as R. No isolate was HR at 100 µg mefenoxam/ml.

Overall, results were similar in trial 2 with slight variation between the trials (Table 2.4). Only 17 (27.4%) of the 62 isolates were completely S to mefenoxam at 10 ug/ml (vs. 38.7% in trial 1). Of these isolates, one was from a conventional field. More isolates were classified as MS at 10 ug/ml in trial 2 (12 = 19.35%) compared to trial 1 (8.1%), with none of the isolates classified as MR (similar to trial 1), 28 (45.3%) classified as R (vs. 48.4% in trial 1), and 5 (8.1%) as HR (vs. 4.8% in trial 1). Similar to trial 1, isolates Pym107 and Pym106 were HR, with 106.3 and 110.1% growth compared to the control plates (Table 2.4). When tested at 100 ug mefenoxam/ml, 21 (33.9%) of the isolates were S (vs. 43.6% in trial 1), of which only 2 (7.7%) were from conventional fields; 26 (41.9%) were classified as MS (vs. 41.9% in trial 1), 11 (17.7%) as MR (vs. 38.7% in trial 1), 4 (6.5%) as R (vs. 4.8% in trial 1), and none as HR (as in trial 1).

2.3.3. Pathogenicity trials. Nineteen isolates representing 8 *Fusarium* species, 9 isolates representing 3 *Pythium* species, and 4 isolates representing 2 *Rhizoctonia* species and AGs were pathogenic on the sweet corn cv. SuperSweet Jubilee Plus in at least one of the repeat growth chamber trials completed with isolates of each genus using cool soil conditions (Suppl. Tables 2.1 to 2.3, and Fig. 2.5 to 2.7, respectively). Pathogenicity was based on the fact that sweet corn

seedlings growing in pots of soil inoculated with isolates had significantly reduced ($P < 0.05$) stand counts, plant height, and/or plant dry weight by 28 dap compared to seedlings in the non-inoculated control soil. In the first pathogenicity trials for *Fusarium, Pythium,* and *Rhizoctonia* isolates, the non-inoculated control plots had mean stand counts of 62.5 ± 5.4, 50.0 ± 15.2, and 52.1 ± 5.2%, respectively, illustrating the poor stands and stunted growth of seedlings from this seed lot of SuperSweet Jubilee Plus, even in the absence of soilborne inoculum, under the cool, moist soil conditions of these trials (Fig. 2.5 to 2.7). The non-inoculated control plots had seedlings with a mean height of 2.4 ± 0.3, 1.8 ± 0.8, and 2.3 ± 0.8 cm for the *Fusarium, Pythium* and *Rhizoctonia* trials, respectively. In the repeat pathogenicity trials, the non-inoculated control plots had mean sweet corn stand counts of 27.1 ± 6.3, 62.5 ± 5.4, and 52.1 ± 5.9%, respectively. Similarly, mean plant height for 12 seedlings in each non-inoculated control plot was 0.6 ± 0.1, 3.3 ± 0.5, and 2.4 ± 1.4 cm, respectively (Fig. 2.5 to 2.7, Suppl. Tables 2.1 to 2.3).

2.3.3.1. **Fusarium *pathogenicity trials*.** For the 40 *Fusarium* isolates tested, only 19 isolates, including of *F. acuminatum* (1 isolate), *F. fujikuroi* (2 isolates), *F. graminearum* (2 isolates), *F. oxysporum* (4 isolates), *F. proliferatum* (4 isolates), *F. redolens* (1 isolate), *F. solani* (2 isolates), and *F. verticillioides* (3 isolates), were pathogenic on sweet corn in the first trial (Fig. 2.5 and Suppl. Table 2.1). The single *F. acuminatum* isolate tested (Fus485) was pathogenic in the first trial, with a mean plant stand of just 6.3%, plant height of 0.1 cm, and plant dry weight of 0.023 g, all of which were significantly less than that of the non-inoculated control plants. (Fig. 2.5A, 2.5C, and 2.5E and Suppl. Table 2.1). However, in the repeat trial, this isolate was not pathogenic as stand count (18.8), root rot severity (3.6), and plant height (0.5 cm) were not significantly different than that of the non-inoculated control plants (Fig. 256B, Fig. 2.5D, Fig 2.5E, and Suppl. Table 2.1).

The single isolates tested for each of *F. avenaceum* (Fus757), *F. commune* (Fus488), and *F. concolor* (Fus566) were not pathogenic on the sweet corn cv. SuperSweet Jubilee Plus compared to the non-inoculated control plants for all variables measured (Fig. 2.5A, 2.5C, and 2.5E, and Suppl. Table 2.1). Similarly, these isolates were not pathogenic in trial 2. All four of the *F. equiseti* isolates tested (Fus706, Fus748, Fus754, and Fus761) were not pathogenic in the first and second trials for any of the variables measured (Suppl. Table 2.1; Fig. 2.5). In contrast, both isolates of *F. fujikuroi* tested (Fus515 and Fus766) were pathogenic on sweet corn in trial 1 compared to the non-inoculated control plants. Mean plant stand was 8.3 and 27.1%, root rot severity averaged 4.21 and 4.33, plant height averaged 0.2 and 0.9 cm, and plant dry weight averaged 0.023 and 0.025 g, respectively (Fig. 2.5B, 2.5D, and 2.5E, and Suppl. Table 2.1). However, these two isolates were not pathogenic in trial 2 (Fig. 2.5 and Suppl. Table 2.1). The two isolates of *F. graminearum* tested (Fus490 and Fus596) also were pathogenic on SuperSweet Jubilee Plus in trial 1, with mean plant stands of 18.8 and 0.0, root rot severity of 4.92 and 4.14, mean plant height of 0.48 and 0.0 cm, and mean plant dry weight of 0.020 and 0.000 g, respectively (Fig. 2.5A, 2.5C, and 2.5E and Suppl. Table 2.1). In the repeat trial, however, only *F. graminearum* isolate Fus596 was pathogenic compared to the non-inoculated control plants (Fig. 2.5B, 2.5D, and 2.5F, and Suppl. Table 2.1). Similar to the first trial, plants grown in soil inoculated with Fus596 had 0.0% emergence by 35 dap. The single isolate of *F. lacertarum* (Fus505) was not pathogenic on SuperSweet Jubilee Plus in either trial (Suppl. Table 2.1).

Soils inoculated with each of the eight *F. oxysporum* isolates in the first pathogenicity trial had mean plant stands ranging from 18.8 to 62.5%, root rot severity of 2.04 to 3.85, mean plant height of 0.4 to 1.9 cm, and total plant dry weights of 0.020 to 0.075 g (Fig. 2.5A, 2.5C, and 2.5E, and Suppl. Table 2.1). Of the eight isolates, four (Fus603, Fus737, Fus805, and

Fus849) were pathogenic as they caused significant reductions in stand compared to the non-inoculated control plants. However, only one isolate (Fus849) was pathogenic in the repeat trial (Fig. 2.5B, 2.5D, and 2.5E, and Suppl. Table 2.1). All but one of the five *F. proliferatum* isolates tested (Fus555, Fus635, Fus695, and Fus782) were pathogenic on sweet corn in the first pathogenicity trial. Sweet corn grown in soil inoculated with these four isolates had mean plant stands ranging from 12.5 to 58.3%, mean root rot severity ratings from 2.73 to 4.06, mean plant heights of 0.4 to 1.9 cm, and plant dry weights of 0.020 to 0.050 g (Fig. 2.5A, 2.5C, and 2.5E and Suppl. Table 2.5). In the repeat trial, only two of these four isolates (Fus635 and Fus782) were pathogenic. In soil inoculated with *F. redolens* isolate Fus645 in the first pathogenicity trial, mean sweet corn stand count was 33.3%, mean root rot severity was 2.96, plant height was 0.8 cm, and total plant dry weight 0.025 g (Fig. 2.5A, 2.5C, and 2.5E and Suppl. Table 2.1), which were all significantly less ($P < 0.05$) than those of the non-inoculated control plants except for root rot severity. However, this isolate was not pathogenic in the repeat trial. For the four *F. solani* isolates (Fus482, Fus743, Fus801, and Fus852), three were pathogenic in trial 1: Fus482, Fus743, and Fus852, based on at least one of the variables measured being significantly less than that of the control treatment (Fig. 2.5A, 2.5C, and 2.5E and Suppl. Table 2.1). However, in the second trial, none of the four isolates of *F. solani* was pathogenic. The single isolate of *F. torulosum* was not pathogenic in either of the pathogenicity trials. In contrast, three of the eight *F. verticillioides* isolates tested (Fus583, Fus627, and Fus744) were pathogenic in the first trial. Sweet corn grown in soils inoculated with these three isolates had mean plant stands ranging from 16.7 to 20.8%, mean root rot severity rating ranging from 3.44 to 4.19, mean plant height ranging from 0.6 to 0.7 cm, and mean plant dry weight ranging from 0.023 to 0.050 g (Fig. 2.5A,

2.5C, and 2.E and Suppl. Table 2.1). However, none of the *F. verticillioides* isolates tested was pathogenic in the repeat trial.

In summary, some isolates of eight *Fusarium* species (*F. acuminatum, F. fujikuroi, F. graminearum, F. oxysporum, F. proliferatum, F. redolens, F. solani,* and *F. verticillioides*) were pathogenic on sweet corn in at least one of the pathogenicity trials. There were differences in the degree of pathogenicity among these isolates within each species.

***2.3.3.2.* Pythium *pathogenicity trials*.** All seven isolates of *P. ultimum* and the one isolate of each of *P. irregulare* and *P. sulcatum* tested were each pathogenic on sweet corn under the conditions of these trials. The single *P. rostratifingens* isolate tested, Pym094, was not pathogenic on SuperSweet Jubilee Plus in either trial. (Fig. 2.6 and Suppl. Table 2.2). In soil inoculated with each of the seven isolates of *P. ultimum* in the first pathogenicity trial, mean sweet corn stand counts ranged from 2.1 to 18.8%, mean root rot severity ranged from 4.3 to 4.5, plant height ranged from 0.1 to 0.7 cm, and plant dry weight ranged from 0.003 to 0.055 g (Fig. 2.6A, 2.6C, and 2.6E, and Suppl. Table 2.2) compared to the non-inoculated control plots, which had a mean stand count of 50.0%, a mean root rot severity rating of 3.67, a mean plant height of 1.8 cm, and plant dry weight of 0.087 g at 28 dap. Similarly, all *P. ultimum* isolates were pathogenic in the repeat trial (Fig. 2.6B, 2.6D, and 2.6F, and Suppl. Table 2.2).

Soil inoculated with isolate Pym089 of *P. irregulare* in the first pathogenicity trial had a mean plant stand of 6.3%, a mean plant height of 1.8 cm, total plant dry weight of 0.008 g, and mean root rot rating of 4.67, which were all significantly different from those of the non-inoculated control plants (Fig. 2.6A, 2.6C, and 2.6E, and Suppl. Table 2.2). In the repeat trial, this isolate of *P. irregulare* was again pathogenic on sweet corn (Fig. 2.7B, 2.7D, and 2.7F, and Table 2.6). The single *P. sulcatum* isolate tested, Pym130, was pathogenic in the first trial with a

mean stand count of 0.0% and, thus, no mean plant height and no plant dry weight (Fig. 2.6A, 2.6C, and 2.6E, and Suppl. Table 2.2). This isolate of *P. sulcatum* was slightly less pathogenic in the repeat trial, with a stand count of 8.3%, mean plant height of 0.2 cm, total plant dry weight of 0.007, and root rot severity of 4.66 (Fig. 2.6B, 2.6D, and 2.6F, and Suppl. Table 2.2).

In summary, isolates of three species of *Pythium* (*P. irregulare, P. sulcatum,* and *P. ultimum*) were pathogenic in both trials. Of these isolates, Pym089 (*P. irregulare*), Pym130 (*P. sulcatum*), Pym092 (*P. ultimum*), Pym096 (*P. ultimum*), Pym116 (*P. ultimum*), Pym142 (*P. ultimum*), and Pym152 (*P. ultimum*) were the most pathogenic.

2.3.3.3. **Rhizoctonia *pathogenicity trials*.** One isolate of *R. solani* AG 2-1 and three isolates of *R. solani* AG 4 were each pathogenic on sweet corn under the cool, moist conditions of these trials. The single isolate of *Ceratobasidium* AG A tested (Rhz073) caused an increase in mean stand count (79.2%), mean plant height (5.0 cm), and total plant dry weight (0.247 g), and a reduction in mean root rot severity rating (2.06) in the first pathogenicity trial, compared to the non-inoculated control plots, i.e., this isolate improved growth of sweet corn (Fig. 2.7A, 2.7C, and 2.7E, and Suppl. Table 2.3). In the repeat trial, however, the beneficial effects of this isolate of *Ceratobasidium* AG A on sweet corn growth were not observed (Fig. 2.7B, 2.7D, and 2.7F, and Suppl. Table 2.3). The single isolate of *Ceratobasidium* AG K tested (Rhz021) was not pathogenic, but increased stand count in the first trial compared to the non-inoculated treatment (Fig. 2.7A), similar to Rhz073 of AG A. However, this isolate caused more severe root rot in trial 2 compared to the non-inoculated control treatment, but did not affect stand or plant height significantly (Fig. 2.7B, 2.7D, and 2.7F, and Suppl. Table 2.3).

Of the two *R. solani* AG 2-1 isolates tested (Rhz022 and Rhz028), only one was pathogenic on sweet corn in both trials (Rhz028) (Fig. 2.7 and Suppl. Table 2.3). Inoculation of

soil with this isolate in trial 1 resulted in sweet corn plants with a mean stand of 33.3%, mean plant height of 1.7 cm, total plant dry weight of 0.094 g, and mean root rot severity rating of 1.97 (Fig. 2.7A, 2.7C, and 2.7E, and Suppl. Table 2.3) compared to the non-inoculated soil in which there was a mean stand of 52.1%, plant height of 2.3 cm, plant dry weight of 0.193 g, and mean root rot severity of 3.22. Similarly, *R. solani* AG 2-1 isolate Rhz028 was pathogenic on sweet corn in the repeat trial (Fig. 2.7B, 2.7D, and 2.7F, and Suppl. Table 2.3).

The two isolates of *R. solani* AG 3 (Rhz016 and Rhz020) caused significant increases in plant stand compared to the non-inoculated control soil in one or both trials. Rhz020 reduced root rot severity and increased plant height in trial 1 compared to the control treatment, but not in trial 2 (Fig. 2.7 and Suppl. Table 2.3) (Fig. 2.8B, 2.8D, and 2.8F, and Table 2.7).

All but one of the four *R. solani* AG 4 isolates tested (Rhz035, Rhz036, Rhz058, and Rhz068) were pathogenic on sweet corn in the two trials (Fig. 2.7 and Suppl. Table 2.3). Isolate Rhz036 was not virulent on sweet corn in either trial. For soil inoculated with the three virulent isolates, sweet corn stand counts ranged from 2.1 to 10.4%, plant height ranged from 0.1 to 0.6 cm, plant dry weight ranged from 0.001 to 0.030 g, and root rot severity ranged from 3.50 to 4.60 (Fig. 2.7A, 2.7C, and 2.7E, and Suppl. Table 2.3). In comparison, sweet corn planted in the non-inoculated soil had a mean stand count of 52.1%, plant height of 2.3 cm, plant dry weight of 0.193 g, and root rot severity of 3.19. In the repeat trial, results were similar for stand count and plant height effects of the three virulent isolates, but only Rhz035 increased root rot severity compared to that of the control plots, not Rhz058 and Rhz068.

2.4 Discussion

For this study, as part of the USDA SCRI Sweet CAPS project aimed at improving sweet corn production nationally, 47 sweet corn fields across the Columbia Basin were surveyed in 2018 to identify the predominant genera and species of fungi and oomycetes associated with seedling blights of sweet corn in this semi-arid, irrigated region of central Washington that has become a primary region of sweet corn production for the United States. The survey revealed the extent to which sweet corn production in the Columbia Basin of Washington is affected by stand losses and stunting, and can be attributed to various causes, including seedling blight pathogens. Stand losses of ≤38.1% in conventional fields and ≤47.5% in organic fields were documented, in addition to potential losses from stunting of plants at incidences of ≤23.4% in conventional fields and ≤20.4% in organic fields. Severely stunted plants may not develop marketable ears (Berger and Wolf 1974). Furthermore, the survey revealed a significant correlation between planting date and plant stand, confirming the greater risk of poorer stands the earlier sweet corn crops are planted in spring. These results illustrate why growers in the Columbia Basin typically do not plant organic sweet corn crops until mid-May or June and overseed organic sweet corn crops by as much as 30% to achieve adequate stands. Even for the 31 conventional crops surveyed, stand losses ranged from 3.3 to 38.1%, with a mean of 14.8 ± 2.1%, illustrating the capacity for significant improvements in sweet corn production if the factors that contribute to poor stands and stunting can be addressed (Stewart et al. 1990).

Not all stand losses and stunting observed in the Columbia Basin sweet corn crops in this survey were associated with damping-off or seedling blight pathogens. In five fields in the south Columbia Basin, 1 to 5% of seedlings were wilting as a result of feeding damage immediately beneath the soil surface by a webworm, identified as *C. rickseckerellus* (Klots 1940). This pest has not been reported previously in central Washington. A specimen of this pest from the Kitsap

Peninsula in western Washington had been deposited in the British Museum of Natural History in 1955 by Don Frechin, but otherwise this insect has been reported to be a pest in the United States primarily in California (Butterflies and Moths of North America 2020; Powell and Opler 2009). It is not known how long this pest has been present in central Washington, or if this pest is an emerging pest for sweet corn growers in this region. Further sampling and investigation are needed. Three other sweet corn fields surveyed had stand losses that were attributed to malfunctioning irrigation equipment or cloddy soil as a result of working the ground when the soil was too wet in early spring.

From a total of 479 fungi and oomycetes obtained from stunted seedlings sampled from the 47 sweet corn fields, 15 *Fusarium* species, 4 *Pythium* species, and 5 *Rhizoctonia* species and AGs were identified. *F. oxysporum, F. verticillioides, F. solani,* and *F. equiseti* were the most prevalent *Fusarium* species collected. *F. acuminatum, F. avenaceum, F. commune, F. concolor, F. fujikuroi, F. graminearum, F. lacertarum, F. proliferatum, F. redolens,* and *F. torulosum* were less prevalent. This is similar to other corn seedling blight studies. Broders et al. (2007b) found *F. equiseti, F. graminearum, F. oxysporum,* and *F. verticillioides* to be prevalent in corn fields in Ohio. However, they also found *F. semitectum,* and *F. subglutinans* associated with corn seedling diseases, which were not found in this survey in Washington. A study by McKeen (1957) also found *F. graminearum* and *F. verticillioides* commonly associated with corn seedling diseases in southern Ontario, Canada, similar to this study.

The most prevalent *Pythium* species identified was *P. ultimum,* with isolates of *P. irregulare, P. rostratifingens,* and *P. sulcatum* found in individual fields in the Columbia Basin. However, this may not reflect accurately the prevalence, distribution, and diversity of *Pythium* species associated with seedling blights in sweet corn fields in the Columbia Basin. The isolation

medium and method used in this study favored faster-growing species such as *P. ultimum,* as has been demonstrated in other studies (Burr and Stanghellini 1973; Jeffers and Martin 1986; Morita and Tojo 2007). A previous study investigating the prevalence of *Pythium* species in pea crops in the Columbia Basin identified 16 species (Alcala et al. 2016). Similarly, a study investigating metalaxyl resistance of *Pythium* species sampled from soils in potato crops in the same region found eight *Pythium* species (Porter et al. 2009). Dorrance et al. (2004) baited *P. catenulatum, P. irregulare, P. paroecandrum, P. splendens,* and *P. torulosum* from corn and soybean fields in Ohio that previously had stand establishment issues. The results of these studies however, differed from the *Pythium* isolates found in this study, with the exception of *P. irregulare*. *P. ultimum,* was commonly found in corn-soybean rotation fields in Iowa (Zhang and Yang 2000), similar to results of this study. The agar medium used in this survey for isolating *Pythium* species, PSM, may have influenced the number and diversity of species recovered from the stunted sweet corn seedlings (Mircetich and Kraft 1973). A large number of isolates obtained from the first 27 fields sampled earlier in the season were discarded accidentally, so a majority of the isolates (53.3%) identified to species originated from fields sampled later in the season, which likely influenced the species identified (Schroeder et al. 2013).

R. solani AG 4 was the most common *Rhizoctonia* species and AG collected (69.7%). *Ceratobasidium* AG A, *Ceratobasidium* AG K, *R. solani* AG 2-1, and *R. solani* AG 3 were also collected but were less prevalent compared to *R. solani* AG 4. Previous studies on stunting of onion seedlings in the Columbia Basin of Washington and Oregon found isolates of *R. solani* AG 2-1, 3, 4, 5, 8, and 9; *Ceratobasidium* AG A, E, and I, as well as *Waitea circinata* var. *circinata* and *W. circinata* var. *zeae* (Patzek et al. 2013). Similar to this study, Patzek et al. (2013) found *R. solani* AG 4 to be one of the most prevalent identified. A study in New York also found

similar *Rhizoctonia* AGs in vegetable crops, including *R. solani* AG 1, AG 2-1, AG 5, AG 11, *Ceratobasidium* AG 2 (CAG), *Ceratobasidium* CAG 6, and *W. circinata* var. *zeae*, with *R. solani* AG 4 and *R. solani* AG 2-2 being the most prevalent (Ohkura et al. 2009).

Fusarium, Pythium, and *Rhizoctonia* species were likely not the only fungi and oomycetes causing damping-off and seedling blights on sweet corn seedlings in the Columbia Basin. For example, many *Penicillium* species are known to cause damping-off on sweet corn seedlings, and isolates of this genus were very abundant on the stunted sweet corn seedlings sampled in this survey (Halfon-Meriere and Solel 1990; Munkvold and White 2016). However, the isolates of *Penicillium* were not identified to species and were not stored as the focus of this study was on *Fusarium, Pythium* and *Rhizoctonia* species. An investigation into *Penicillium* species causing seedling blights on sweet corn seedlings in the Columbia Basin is warranted as *Penicillium* species can be major pathogens of sweet corn and were abundant on the seedlings plated onto various agar media. The prevalence of other fungi should also be investigated as potential pathogens of sweet corn seedlings in the Columbia Basin, as species of *Alternaria, Aspergillus, Nigrospora*, and *Rhizopus* have been reported as pathogens of sweet corn seedlings (Munkvold and White 2016; Robertson and Munkvold 2009), and observed on many of the isolation plates in this survey. In addition, this survey only examined isolates of fungi and oomycetes affecting stunted sweet corn seedlings, not sweet corn seeds and non-emerged seedlings (i.e., those with pre-emergence damping-off). Matthiesen et al. (2016), collected symptomatic corn seedlings from fields with pre-emergence damping-off and post-emergence seedling blight, from which they identified nine *Pythium* species, with *P. torulosum* the most prevalent. However, that study focused on the isolation and identification of *Pythium* species only, not other potential pathogenic fungi. Broders et al. (2007a) similarly focused on *Pythium*

species associated with diseased corn and soybean seed and seedlings in the Midwestern United States.

Mefenoxam is one of the most effective fungicides for control of diseases caused by *Pythium* species (Davidse et al. 1983; Porter et al. 2009). However, resistance to this fungicide is increasingly common in many agricultural systems where this fungicide has been used for extended periods and/or is used intensively. In this survey, a majority of the 62 *Pythium* isolates obtained from stunted sweet corn seedlings had some level of resistance to mefenoxam when tested at both 10 and 100 µg/ml, i.e., 38 of the isolates (61.3%) in the first trial and 45 of the isolates (72.6%) in the repeat trial. These isolates would not be controlled effectively with mefenoxam seed treatment in sweet corn production. Thirty-three of the isolates had >60% growth compared to the control plates when cultured on medium with 10 mg mefenoxam/ml, i.e., they were classified as R to HR to mefenoxam. Similar results were observed at 100 µg mefenoxam/ml, with (56.5 to 66.1%) of the isolates classified as R to HR to mefenoxam.

A majority of the *Pythium* isolates had similar responses to the two concentrations of mefenoxam tested in each trial, but there was slight variation in results between the two trials. For example, Pym095, Pym110, Pym128, Pym132, Pym134, Pym137, and Pym138 were characterized as S in trial 1 but MS in trial 2. Minor differences in colony diameters between the two trials probably reflect natural variation displayed by most isolates, and/or minor differences associated with the individual who completed each trial. There was a trend of greater colony diameters for most *Pythium* isolates when measured in trial 2 compared with trial 1.

In this survey, a majority of isolates S to mefenoxam originated from the organic sweet corn fields sampled. When tested with 10 µg mefenoxam/ml, 21 (58.3%) and 16 (44.4%) isolates that originated from organic fields were S to mefenoxam in trials 1 and 2, respectively. Similarly,

23 (63.9%) and 20 (55.6%) of the 62 isolates characterized as S at 100 μg/ml were from organic fields in trials 1 and 2, respectively. In contrast, only three isolates (11.5%) in trial 1 and one isolate (3.8%) isolate in trial 2 that originated from conventional fields were rated as S to mefenoxam at 10 μg/ml, and 4 (15.4%) and 2 (7.7%) isolates from conventional fields were S to 100 mg mefenoxam/ml in trials 1 and 2, respectively. This difference in prevalence of sensitive isolates to mefenoxam between organic and conventional fields probably reflects the lack of use of mefenoxam in certified organic fields, with limited exposure of *Pythium* species in these fields to the fungicide. However, some of the MR isolates originated from organic fields, i.e., 15 (41.7%) and 20 (55.6%) isolates were characterized as MR in trials 1 and 2, respectively, when tested at 10 μg mefenoxam/ml, and 13 (36.1%) and 16 (44.4%) of the isolates originating from organic fields were characterized as MR to 100 μg/ml mefenoxam in trials 1 and 2, respectively. This probably reflects the fact that some of the certified organic fields surveyed had been transitioned from conventional to organic production within 5 to 10 years of the 2018 survey.

The prevalence of mefenoxam resistance among the *Pythium* isolates obtained from stunted sweet corn seedlings sampled in the Columbia Basin indicates widespread exposure of these oomycetes to the fungicide, resulting in widespread selection for resistance. These results are similar to observations by Porter et al. (2009) who investigated metalaxyl resistant *Pythium* species in potato production in the Pacific Northwest. Similarly, a study investigating metalaxyl resistance of *Pythium* species in wheat crops in the Pacific Northwest showed that *Pythium* species resistant to metalaxyl comprised 25 to 75% of the isolates. In the Columbia Basin, sweet corn is often grown in rotation with potato and wheat, so the prevalence of isolates with mefenoxam resistance in this survey was not surprising. Conventional sweet corn growers should consider alternatives to mefenoxam for control of damping-off caused by *Pythium* spp., such as

ethaboxam and captan (Broders et al. 2007a; Kim et al. 2004). Resistance to mefenoxam has also been reported in *Pythium* isolates collected from potato, corn, and soybean crops in regions such as Minnesota (Radmer et al. 2017; Taylor et al. 2002). Similarly, Lookabaugh et al. (2015) found that 52% of the *Pythium* isolates tested from floriculture crops in North Carolina were resistant to mefenoxam.

Results of the pathogenicity tests under cool conditions within a growth chamber showed that, of the isolates of 14 *Fusarium* species, 4 *Pythium* species, and 5 *Rhizoctonia* species and AGs tested, 8, 3, and 2, respectively, were pathogenic on sweet corn seedlings. There were differences in virulence of isolates among the species within each genus, and among isolates within species, based on the mean stand counts, plant height, dry plant weight, and root rot severity of sweet corn seedlings.

For the 14 *Fusarium* species tested, isolates of *F. fujikuroi, F. graminearum, F. proliferatum,* and *F. verticillioides* consistently were the most pathogenic on SuperSweet Jubilee Plus. For each of these species, at least one isolate was pathogenic. An isolate of *F. graminearum* was the most virulent of the *Fusarium* isolates tested. *F. graminearum* is known to cause both seedling rots as well as stalk and ear rot of corn (Broders et al. 2007b). Similarly, *F. proliferatum* has been known to cause disease on corn seedlings, but this species typically is considered less virulent compared to isolates of *F. graminearum* and *F. verticillioides* (Gai et al. 2018; Munkvold and White 2016). Some isolates of each of *F. acuminatum, F. oxysporum, F. redolens, F. solani,* and *F. verticillioides* were pathogenic on sweet corn in this study. *F. verticillioides* has been well documented as a pathogen of corn, causing diseases ranging from seedling rots to corn ear rots (Bacon et al. 1994; Gai et al. 2018; Murillo-Williams and Munkvold 2008). Isolates of *F. avenaceum, F. commune, F. concolor, F. equiseti, F. lacertarum,*

and *F. torulosum* tested in this study were not pathogenic on SuperSweet Jubilee Plus. In the repeat *Fusarium* pathogenicity trial in this study, poor seed germination and relatively severe root rot in the non-inoculated control plots made it difficult to differentiate levels of virulence among the species and isolates tested compared to the first pathogenicity trial.

Among the *Rhizoctonia* species and AGs tested in this study, *R. solani* AG 4 consistently was the most virulent on SuperSweet Jubilee Plus, with three of the four isolates tested causing significant decreases in stand counts, more severe root rot, reduced plant height, and/or reduced plant dry weight compared to the control plants. One of two isolates of *R. solani* AG 2-1 was also pathogenic. In contrast, isolates of *R. solani* AG 3, and isolates of each of *Ceratobasidium* AG A and *Ceratobasidium* AG K were not pathogenic. Other studies investigating the pathogenicity of *Rhizoctonia* isolates on vegetable crops, including corn, also showed isolates of *R. solani* AG 2 and AG 4 to be pathogenic on corn (e.g., Ohkura et al. 2009). However, *R. solani* AG 2 isolates were more pathogenic on corn than the *R. solani* AG 4 isolates in the New York study Ohkura et al. (2009), in contrast to this study.

Of the four *Pythium* species tested in this survey, *P. irregulare*, *P. sulcatum*, and *P. ultimum* isolates were all pathogenic on sweet corn in the cool, moist soil conditions of the growth chamber trials. Isolates of *P. ultimum* and *P. sulcatum* were the most virulent species tested. Similar results were shown by Zhang and Yang (2000), who tested the pathogenicity of *Pythium* species on soybean and corn, and found that most of the *P. ultimum* isolates were highly virulent on corn seedlings. *P. ultimum* and *P. irregulare* have been reported commonly in association with damping-off of many crops, including wheat, pea, corn, and barley (Dorrance et al. 2004; Ingram and Cook 1990). Broders et al. (2007a) demonstrated that isolates of both *P. irregulare* and *P. ultimum* were pathogenic on corn in the Midwestern United States. The single

isolate of *P. rostratifingens* evaluated in this survey in the Columbia Basin was not pathogenic on sweet corn.

Variability in results were observed when the pathogenicity trials were repeated, particularly for the 40 isolates of *Fusarium* tested, as almost none of these isolates was recorded as pathogenic on sweet corn in the repeat trial. This could be due, partially, to the age of the inoculum of the isolates at the time the repeat trial was done. Inoculum was prepared several months before the first pathogenicity trials. Although inoculum for each isolate was quantified by dilution plating one week prior to initiation of each trial, the inoculum had been placed in cold storage (4 ± 1°C) for several months by the time it was used in the repeat trials. It is possible the level of virulence of each *Fusarium* isolate had reduced due to age of the inoculum. It is also possible that the seed lot of the sweet corn cv. SuperSweet Jubilee Plus could have influenced results of the pathogenicity trials. The particular seed lot used for all of the pathogenicity trials was severely infested with seedborne inoculum of *Fusarium* spp. and *Penicillium* spp., based on warm and cold germination assays, which could have affected the vigor of the seed lot over the duration the seed was stored for this study (*data not shown*). This seed lot was still used as the infection of sweet corn seed can be common (Mathre et al. 1995). In an attempt to limit the level of fungal inoculum on the seed during the trials, the seed to be planted was treated with 0.5% NaOCl for 10 minutes, rinsed with deionized water, and dried overnight the day prior to setting up each trial to reduce the impact of seedborne inoculum on the ability to differentiate pathogenic from non-pathogenic isolates tested.

This study showed that seedling blights caused by *Fusarium, Pythium,* and *Rhizoctonia* were prevalent in both conventional and organic sweet corn fields throughout the Columbia Basin of Washington with substantial opportunity to reduce losses caused by these pathogens.

Some species tested from each of the three genera caused significant reductions in emergence of the sweet corn cultivar tested, showing that *Fusarium*, *Pythium*, and *Rhizoctonia* can be causal agents of seedling blights in the Columbia Basin. This information can be used to help sweet corn growers develop strategies to help manage these pathogens better in both conventional and organic sweet corn production. Over 40% of the *Pythium* isolates showed moderate resistance to mefenoxam, complementing the results of other studies that investigated metalaxyl and mefenoxam resistance of *Pythium* species in crops grown in the Columbia Basin. This indicates that growers using conventional fungicidal seed treatments to control *Pythium* on sweet corn should consider fungicides other than mefenoxam and metalaxyl, such as ethaboxam. Future research should evaluate the prevalence of other pathogenic genera of fungi such as *Penicillium*, which are also important pathogens of sweet corn seedlings.

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Table 2.1. Field, survey date, general location, and cropping history of sweet corn fields surveyed for seedling diseases in the Columbia Basin of Washington in 2018

Field code	Survey date[a]	Location[b]	Production	Crop(s) grown in 2017
1	1 May	Central	Conventional	Sweet Corn
2	1 May	Central	Conventional	Carrot with wheat cover crop
3	1 May	Central	Conventional	Onion
4	1 May	Central	Conventional	Corn
5	1 May	Central	Conventional	Wheat
6	1 May	Central	Conventional	Wheat
7	1 May	Central	Conventional	Corn
8	15 May	Central	Conventional	Winter wheat followed by buckwheat
9	15 May	North	Conventional	Winter wheat followed by buckwheat
10	15 May	South	Conventional	Wheat
11	15 May	South	Conventional	Wheat
12	15 May	South	Conventional	Wheat
13	15 May	South	Conventional	Wheat
14	15 May	South	Conventional	Onion with wheat cover crop
15	16 May	South	Conventional	Wheat
16	16 May	South	Conventional	Wheat
17	16 May	South	Conventional	Wheat
18	16 May	South	Conventional	Wheat
19	16 May	South	Conventional	Wheat
20	16 May	South	Conventional	Wheat
21	16 May	South	Conventional	Wheat
22	16 May	South	Conventional	Wheat
23[a]	24 May	North	Conventional	Potato followed by wheat cover crop
24	20 June	North	Conventional	Wheat
25	20 June	North	Conventional	Wheat
26	20 June	North	Conventional	Wheat
27	20 June	North	Conventional	Wheat
28	20 June	North	Conventional	Potato
29	20 June	North	Conventional	Wheat
30	20 June	North	Conventional	Wheat
31	3 July	South	Organic	Alfalfa
32	3 July	South	Organic	Alfalfa
33	3 July	South	Organic	
34	3 July	South	Organic	
35	3 July	South	Organic	
36	3 July	Central	Organic	Pea
37	3 July	Central	Conventional	Timothy hay
38	3 July	Central	Organic	Pea
39	3 July	Central	Organic	Pea
40	3 July	Central	Organic	Wheat and fall mustard
41	5 July	North	Organic	Wheat and fall mustard
42	5 July	North	Organic	Barley, pea, and then sweet corn
43	17 July	Central	Organic	
44	24 July	Central	Conventional	Bluegrass
45	24 July	South	Organic	Wheat
46	24 July	South	Organic	Pea
47	24 July	South	Organic	
48	24 July	South	Organic	Corn

[a] Refer to the main text for details on how each crop was surveyed.

[b] Fields were located in the north, central, or south region of the Columbia Basin (see Fig. 2.1).

[c] F23 (Field 23) was not included in the overall survey results as the area sampled in that field was planted with a seed treatment trial for the International Sweet Corn Development Association (ISCDA), by Dr. Carrie Wohleb, Washington State University Grant County Extension, Moses Lake, WA. The trial was located within a sweet corn field and, thus, did not represent the cultivar and seed treatment of the surrounding crop.

Table 2.2. Isolates of *Fusarium*, *Pythium*, and *Rhizoctonia* obtained from stunted seedlings sampled from each of 47 sweet corn fields in the Columbia Basin of Washington in spring and summer of 2018, and tested for pathogenicity on the sweet corn cv. SuperSweet Jubilee Plus

				Pathogenicity test[c]	
***Fusarium, Pythium,* and *Rhizoctonia* species[a]**	**Isolate**	**Field code[b]**	**Farm type**	**Trial 1**	**Trial 2**
Fusarium					
F. acuminatum	Fus485	F4	Conventional	+	
F. avenaceum	Fus757	F31	Organic		
F. commune	Fus488	F5	Conventional		
F. concolor	Fus566	F22	Conventional		
F. equiseti	Fus706	F42	Organic		
	Fus748	F36	Organic		
	Fus754	F31	Organic		
	Fus761	F47	Organic		
F. fujikuroi	Fus515	F9	Conventional	+	
	Fus766	F43	Organic	+	
F. graminearum	Fus490	F1	Conventional	+	
	Fus596	F26	Conventional	+	+
F. lacertarum	Fus505	F7	Conventional		
F. oxysporum	Fus487	F5	Conventional		
	Fus527	F11	Conventional		
	Fus603	F25	Conventional	+	
	Fus721	F43	Organic		
	Fus737	F43	Organic	+	
	Fus805	F29	Conventional	+	
	Fus849	F44	Conventional	+	+
	Fus859	F47	Organic		
F. proliferatum	Fus555	F20	Conventional	+	
	Fus635	F37	Conventional	+	+
	Fus694	F43	Organic		
	Fus695	F37	Conventional	+	
	Fus782	F45	Organic	+	+
F. redolens	Fus645	F27	Conventional	+	
F. solani	Fus482	F1	Conventional		
	Fus743	F43	Organic	+	
	Fus801	F45	Organic		
	Fus852	F44	Conventional	+	
F. torulosum	Fus562	F5	Conventional		
F. verticillioides	Fus519	F10	Conventional		
	Fus583	F23	Conventional	+	
	Fus627	F42	Organic	+	
	Fus735	F37	Conventional		

Fusarium, Pythium, and *Rhizoctonia* species[a]	Isolate	Field code[b]	Farm type	Pathogenicity test[c] Trial 1	Trial 2
	Fus741	F39	Organic		
	Fus744	F23	Conventional	+	
	Fus833	F47	Organic		
Pythium					
P. irregulare	Pym089	F4	Conventional	+	+
P. rostratifingens	Pym094	F10	Conventional		
P. sulcatum	Pym130	F39	Organic	+	+
P. ultimum	Pym092	F7	Conventional	+	+
	Pym096	F14	Conventional	+	+
	Pym110	F23	Conventional	+	+
	Pym116	F29	Conventional	+	+
	Pym118	F31	Organic	+	+
	Pym142	F41	Organic	+	+
	Pym152	F42	Organic	+	+
Rhizoctonia					
Ceratobasidium sp. AG A	Rhz073	F46	Organic		
Ceratobasidium sp. AG K	Rhz021	F4	Conventional		
R. solani AG 2-1	Rhz022	F4	Conventional		
	Rhz028	F5	Conventional	+	+
R. solani AG 3	Rhz016	F7	Conventional		
	Rhz020	F4	Conventional		
R. solani AG 4	Rhz035	F23	Conventional	+	+
	Rhz036	F31	Organic		
	Rhz058	F43	Organic	+	+
	Rhz068	F45	Organic	+	+

[a] Species were identified by sequencing the translation elongation factor 1-alpha (*EF-1α*) gene for *Fusarium* isolates, and the internal transcribed spacer (ITS) region of ribosomal DNA (rDNA) for *Pythium* and *Rhizoctonia* isolates, following the protocols described by Bakkeren et al. (2000), and Paulitz and Adams (2003), respectively.

[b] Details of the 47 fields sweet corn fields surveyed are described in Table 2.1.

[c] Pathogenicity trials were done in a growth chamber set at 15°C by day and 13°C by night with a 12 h photoperiod/day to mimic spring planting conditions in the Columbia Basin of Washington. '+' indicates the isolate was classified as pathogenic based on results of that pathogenicity trial.

Table 2.3. Prevalence of *Fusarium*, *Pythium*, and *Rhizoctonia* species obtained from stunted plants sampled from 47 sweet corn fields in the Columbia Basin of Washington in 2018[a]

	No. of isolates collected/species for each region of the Columbia Basin				
Genus and species[b]	**North**	**Central**	**South**	**Total**	**Percentage of all isolates**
Fusarium					
F. acuminatum	0	0	1	1	0.3
F. avenaceum	0	0	2	2	0.6
F. commune	0	0	2	2	0.6
F. concolor	0	0	1	1	0.3
F. equiseti	10	12	15	37	10.6
F. fujikuroi	6	0	8	14	4.0
F. graminearum	5	0	6	11	3.1
F. lacertarum	3	2	7	12	3.4
F. oxysporum	36	12	64	112	32.0
F. proliferatum	7	2	7	16	4.6
F. redolens	1	0	0	1	0.3
F. solani	15	7	27	49	13.7
F. torulosum	0	0	1	1	0.3
F. verticillioides	36	12	43	91	26.0
Total (% of 350 isolates)	119 (34.0)	47 (13.4)	184 (52.6)	350	
Pythium					
P. irregulare	0	0	1	1	1.6
P. rostratifingens	0	0	1	1	1.6
P. sulcatum	0	1	0	1	1.6
P. ultimum	30	9	21	60	95.2
Total (% of 63 isolates)	30 (47.6)	10 (15.9)	23 (36.5)	63	
Rhizoctonia					
Ceratobasidium sp. AG-A	0	0	3	3	4.5
Ceratobasidium sp. AG-K	0	0	4	4	6.1
R. solani AG-2-1	0	0	7	7	10.6
R. solani AG-3	0	0	6	6	9.1
R. solani AG-4	14	12	20	46	69.7
Total (% of 66 isolates)	14 (21.2)	12 (18.2)	40 (60.6)	66	

[a] Refer to details of the 47 fields, 3 regions of the Columbia Basin, and sampling protocol described in Tables 2.1 and 2.3, Fig. 2.1, and the main text.

[b] *Fusarium* isolates were identified to species by sequencing the translation elongation factor 1-alpha (*EF-1α*) gene, and *Pythium* and *Rhizoctonia* isolates were identified by sequencing the internal transcribed spacer (ITS) region of the ribosomal DNA (rDNA), as described by Bakkeren et al. (2000), and Paulitz and Adams (2003), respectively.

[c] Percentage of isolates of each of the 14 *Fusarium* species, 4 *Pythium* species, and 5 *Rhizoctonia* anastomosis groups out of a total of 350, 63, and 66 isolates examined per genus, respectively.

Table 2.4. Isolate, species, field of origin, and mefenoxam sensitivity of *Pythium* isolates obtained from stunted seedlings sampled from sweet corn fields in the Columbia Basin of Washington in 2018[a]

			Trial 1				Trial 2			
			Mefenoxam concentration (µg/ml)				Mefenoxam concentration (µg/ml)			
			10		100		10		100	
Isolate	*Pythium* sp.	Field number - Organic or conventional production	Colony growth (cm)[b]	Percentage of control plate	Colony growth (cm)	Percentage of control plate	Colony growth (cm)	Percentage of control plate	Colony growth (cm)	Percentage of control plate
Pym094	*P. rostratifingens*	F10-Conventional	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0
Pym118	*P. ultimum*	F31-Organic	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0
Pym122	*P. ultimum*	F33-Organic	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0
Pym125	*P. ultimum*	F34-Organic	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0
Pym126	*P. ultimum*	F34-Organic	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0
Pym127	*P. ultimum*	F35-Organic	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0
Pym129	*P. ultimum*	F38-Organic	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0
Pym140	*P. ultimum*	F41-Organic	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0
Pym141	*P. ultimum*	F41-Organic	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0
Pym146	*P. ultimum*	F41-Organic	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0
Pym148	*P. ultimum*	F42-Organic	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0
Pym149	*P. ultimum*	F42-Organic	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0
Pym150	*P. ultimum*	F42-Organic	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0
Pym151	*P. ultimum*	F42-Organic	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0
Pym152	*P. ultimum*	F42-Organic	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0
Pym153	*P. ultimum*	F48-Organic	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0
Pym156	*P. ultimum*	F42-Organic	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0
Pym110	*P. ultimum*	F23-Conventional	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.1 ± 0.1	1.1	0.2 ± 0.2	3.1
Pym134	*P. ultimum*	F40-Organic	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.1± 0.1	1.5	0.1 ± 0.1	1.9
Pym128	*P. ultimum*	F36-Organic	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.1 ± 0.1	1.9	0.0 ± 0.0	0.0
Pym138	*P. ultimum*	F40-Organic	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.2 ± 0.1	3.6	0.0 ± 0.0	0.0
Pym137	*P. ultimum*	F40-Organic	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.2± 0.1	3.6	0.0 ± 0.0	0.0
Pym132	*P. ultimum*	F39-Organic	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.3± 0.2	5.1	0.2 ± 0.1	3.2
Pym095	*P. ultimum*	F11-Conventional	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.4 ± 0.1	6.9	0.0 ± 0.0	0.0
Pym089	*P. irregulare*	F4-Conventional	0.3 ± 0.1	6.9	0.0 ± 0.0	0.0	0.1 ± 0.1	2.8	0.1 ± 0.1	1.8
Pym091	*P. ultimum*	F6-Conventional	0.6 ± 0.1	9.7	0.2 ± 0.1	3.8	1.0 ± 0.2	15.6	0.6 ± 0.4	9.3
Pym123	*P. ultimum*	F33-Organic	0.6 ± 0.3	9.7	0.0 ± 0.0	0.0	0.8 ± 0.1	14.1	0.3 ± 0.1	5.4
Pym154	*P. ultimum*	F32-Organic	0.6 ± 0.2	11.7	0.5 ± 0.1	10.7	0.6 ± 0.2	11.2	0.7 ± 0.2	14.9
Pym139	*P. ultimum*	F40-Organic	0.8 ± 0.2	14.2	0.0 ± 0.0	0.0	1.3 ± 0.1	22.3	0.5 ± 0.1	7.5
Pym116	*P. ultimum*	F29-Conventional	3.1 ± 0.1	56.5	0.6 ± 0.2	10.6	3.7 ± 0.2	61.2	1.1 ± 0.0	18.6
Pym155	*P. ultimum*	F33-Organic	3.2 ± 0.3	56.7	1.1 ± 0.3	19.7	3.8 ± 0.4	66.9	1.5 ± 0.1	26.3
Pym135	*P. ultimum*	F40-Organic	3.2 ± 0.1	56.8	1.3 ± 0.0	23.4	3.7 ± 0.1	64.0	1.5 ± 0.3	25.1

Isolate	*Pythium* sp.	Field number - Organic or conventional production	Trial 1				Trial 2			
			Mefenoxam concentration (µg/ml)				Mefenoxam concentration (µg/ml)			
			10		100		10		100	
			Colony growth (cm)[b]	Percentage of control plate	Colony growth (cm)	Percentage of control plate	Colony growth (cm)	Percentage of control plate	Colony growth (cm)	Percentage of control plate
Pym105	*P. ultimum*	F23-Conventional	3.1 ± 0.2	56.8	1.4 ± 0.3	25.1	4.2 ± 0.3	71.0	1.5 ± 0.1	24.3
Pym097	*P. ultimum*	F15-Conventional	3.2 ± 0.1	56.9	1.1 ± 0.2	18.5	3.9 ± 0.1	62.6	0.8 ± 0.4	13.4
Pym088	*P. ultimum*	F2-Conventional	3.3 ± 0.2	58.3	1.1 ± 0.2	18.8	3.9 ± 0.2	64.5	1.2 ± 0.2	19.8
Pym133	*P. ultimum*	F40-Organic	3.2 ± 0.1	58.7	1.0 ± 0.1	17.6	3.8 ± 0.2	68.1	1.4 ± 0.1	24.0
Pym120	*P. ultimum*	F32-Organic	3.4 ± 0.2	59.4	1.2 ± 0.3	20.3	4.4 ± 0.2	71.6	1.8 ± 0.6	28.7
Pym144	*P. ultimum*	F41-Orgnaic	3.4 ± 0.2	60.4	1.4 ± 0.1	23.8	3.6 ± 0.4	63.4	1.6 ± 0.4	27.7
Pym136	*P. ultimum*	F40-Organic	3.5 ± 0.2	60.5	1.3 ± 0.1	21.6	4.0 ± 0.1	70.1	1.7 ± 0.2	30.2
Pym121	*P. ultimum*	F35-Organic	3.4 ± 0.2	60.6	1.1 ± 0.4	19.4	3.7 ± 0.2	61.6	1.0 ± 0.3	16.5
Pym092	*P. ultimum*	F7-Conventional	3.4 ± 0.2	60.8	1.1 ± 0.4	19.3	4.0 ± 0.2	64.7	1.3 ± 0.2	20.5
Pym147	*P. ultimum*	F41-Organic	3.5 ± 0.2	61.0	1.0 ± 0.0	17.1	3.7 ± 0.2	65.2	1.3 ± 0.3	22.2
Pym099	*P. ultimum*	F20-Conventional	3.3 ± 0.3	61.2	1.1 ± 0.2	19.4	4.6 ± 0.1	77.4	1.4 ± 0.5	23.7
Pym096	*P. ultimum*	F14-Conventional	3.3 ± 0.2	62.1	3.0 ± 0.2	56.4	3.8 ± 0.2	67.1	3.3 ± 0.2	56.9
Pym113	*P. ultimum*	F28-Conventional	3.6 ± 0.1	62.3	1.3 ± 0.6	21.6	4.2 ± 0.1	67.2	0.9 ± 0.1	13.8
Pym124	*P. ultimum*	F33-Organic	3.6 ± 0.3	62.7	1.5 ± 0.3	25.9	3.6 ± 0.1	66.4	1.3 ± 0.0	24.7
Pym145	*P. ultimum*	F41-Organic	3.6 ± 0.2	62.8	1.2 ± 0.2	21.8	3.7 ± 0.2	66.8	1.7 ± 0.4	31.4
Pym143	*P. ultimum*	F41-Organic	3.5 ± 0.1	63.1	1.0 ± 0.0	18.0	3.5 ± 0.3	72.2	1.0± 0.1	20.1
Pym115	*P. ultimum*	F29-Conventional	3.5 ± 0.2	65.2	0.8 ± 0.1	14.7	4.0 ± 0.2	69.3	0.9 ± 0.2	15.9
Pym114	*P. ultimum*	F29-Conventional	3.7 ± 0.1	65.4	1.1 ± 0.3	18.9	4.1 ± 0.1	69.5	1.1 ± 0.3	17.9
Pym112	*P. ultimum*	F28-Conventional	3.8 ± 0.1	65.4	1.4 ± 0.2	23.8	4.2 ± 0.1	68.8	1.8 ± 0.1	29.4
Pym142	*P. ultimum*	F41-Organic	3.8 ± 0.2	65.9	1.1 ± 0.1	18.7	3.8 ± 0.2	67.3	1.3 ± 0.4	22.2
Pym117	*P. ultimum*	F29-Conventional	3.0 ± 0.2	65.5	0.9 ± 0.1	18.5	3.6 ± 0.2	65.2	1.0 ± 0.2	18.6
Pym104	*P. ultimum*	F23-Conventional	3.6 ± 0.1	66.2	1.6 ± 0.3	29.2	4.2 ± 0.3	72.7	1.8 ± 0.2	31.7
Pym098	*P. ultimum*	F7-Conventional	3.8 ± 0.1	66.2	1.5 ± 0.2	26.2	4.1 ± 0.2	68.7	1.5 ± 0.1	25.4
Pym087	*P. ultimum*	F1-Conventional	3.7 ± 0.1	66.3	2.6 ± 0.3	46.6	4.2 ± 0.1	67.7	3.2 ± 0.2	52.2
Pym108	*P. ultimum*	F23-Conventional	3.4 ± 0.1	67.5	1.2 ± 0.1	24.3	4.5 ± 0.1	75.5	2.0 ± 0.2	33.0
Pym109	*P. ultimum*	F23-Conventional	3.4 ± 0.2	69.5	1.4 ± 0.4	27.8	4.3 ± 0.3	78.2	2.0 ± 0.3	35.8
Pym111	*P. ultimum*	F23-Conventional	3.6 ± 0.0	69.6	1.5 ± 0.2	28.9	4.2 ± 0.0	74.3	2.1 ± 0.2	36.4
Pym103	*P. ultimum*	F23-Conventional	3.8 ± 0.1	75.3	1.4 ± 0.5	28.8	4.2 ± 0.1	75.8	1.8 ± 0.4	31.6
Pym107	*P. ultimum*	F23-Conventional	2.5 ± 0.4	97.3	1.8 ± 0.1	71.0	2.8 ± 0.4	106.3	1.9 ± 0.4	72.3
Pym106	*P. ultimum*	F23-Conventional	2.4 ± 0.1	105.8	1.4 ± 0.4	60.1	3.1 ± 0.1	110.1	1.5 ± 0.5	54.2
Pym101	*P. ultimum*	N/A[c]	3.4 ± 0.2	58.7	1.1 ± 0.2	18.6	3.4 ± 0.1	59.5	1.1 ± 0.3	19.7
Pym102	*P. ultimum*	N/A[c]	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0	0.0 ± 0.0	0.0

[a] Highlighted cells indicate the mefenoxam resistance category of the isolates for each trial at each concentration of mefenoxam tested. Dark green = sensitive (isolate displayed no measurable hyphal growth on the amended agar plates), light green = moderately sensitive (1 to 25% of the growth of the isolate on the

non-amended control plates), yellow = moderately resistant (26 to 50% growth), orange = resistant (51 to 75% growth), and brown = highly resistant (>76% growth). Isolates are listed in order of slowest to fastest growth in trial 1 on plates amended with 10 ug mefenoxam/ml.

[b] Colony diameter (mean ± standard deviation) for each isolate was averaged for three replicate plates for each mefenoxam concentration.

[c] NA = not applicable as these were control isolates known to be resistant or sensitive to mefenoxam, courtesy of Dr. Lyndon Porter (United States Department of Agriculture Agricultural Research Service Grain Legume Research Unit, Prosser, WA).

Supplementary Table 2.1. Pathogenicity of 40 *Fusarium* isolates on the sweet corn cv. SuperSweet Jubilee Plus in a growth chamber set at 13°C by night and 15°C by day with a 12 h photoperiod per day

		Trial 1				Trial 2			
***Fusarium* species**	**Isolate**	**Emergence (%) 35 dap**	**Root rot severity (0-5)**	**Plant height (cm)**	**Plant dry weight (g)**	**Emergence (%) 35 dap**	**Root rot severity (0-5)**	**Plant height (cm)**	**Plant dry weight (g)**
Non-inoculated control	-	62.5 ab[a]	2.77 l-r	2.39 ab	0.100 a	27.1 a-g	3.66 c-j	0.61 b-h	0.025
F. acuminatum	Fus485	6.3 no	4.58 ab	0.13 jk	0.023 abc	18.8 d-j	3.61 c-k	0.50 f-i	0.030
F. avenaceum	Fus757	37.5 b-l	2.75 m-r	1.67 a-h	0.075 abc	41.7 a	2.47 n	2.64 ab	0.108
F. commune	Fus488	45.8 a-g	2.58 o-s	2.21 a-d	0.125 a	12.5 f-k	3.91 a-f	0.72 c-h	0.035
F. concolor	Fus566	47.9 a-f	3.67 c-i	1.48 a-g	0.025 abc	10.4 g-k	4.04 abc	0.28 f-i	0.020
F. equiseti	Fus706	60.4 abc	2.35 p-t	1.44 a-g	0.075 ab	10.4 g-k	3.23 j-n	0.52 c-h	0.015
	Fus748	56.3 a-e	2.40 p-t	2.34 a-c	0.050 abc	27.1 a-g	2.75 mn	2.01 a-d	0.100
	Fus754	52.1 a-f	2.58 o-s	1.25 a-h	0.025 abc	35.4 a-d	2.64 k-n	1.22 a-f	0.068
	Fus761	43.8 a-i	2.79 l-r	1.35 a-h	0.075 ab	27.1 a-g	3.25 i-n	1.34 a-h	0.060
F. fujikuroi	Fsu515	8.3 m-o	4.21 b-d	0.17 j-k	0.023 abc	8.3 h-k	3.79 b-h	0.49 e-i	0.020
	Fus766	27.1 f-n	4.33 a-c	0.93 d-j	0.025 abc	16.7 e-k	3.81 b-h	0.85 d-i	0.035
F. graminearum	Fus490	18.8 h-o	4.14 b-e	0.48 f-j	0.020 abc	18.8 d-j	4.10 a-d	0.94 c-h	0.040
	Fus596	0.0 o	4.92 ab	0.00 k	0.000 c	0.0 k	4.63 a	0.00 i	0.000
F. lacertarum	Fus505	70.8 a-g	1.73 t	2.67 a	0.125 a	29.2 a-f	3.68 c-j	1.18 a-g	0.045
F. oxysporum	Fus487	45.8 a-g	2.85 k-r	1.64 a-g	0.075 ab	20.8 c-j	3.45 f-l	1.17 a-h	0.055
	Fus527	39.6 b-j	2.57 o-s	1.57 a-h	0.050 abc	25.0 a-h	3.54 e-l	1.50 a-g	0.045
	Fus603	31.3 d-m	3.29 g-n	0.68 f-j	0.020 abc	22.9 b-i	3.97 a-e	0.56 c-h	0.023
	Fus721	62.5 abc	2.04 st	1.88 a-e	0.075 ab	20.8 c-j	3.10 j-n	0.97 a-h	0.048
	Fus737	20.8 g-o	3.85 c-h	0.48 h-k	0.025 abc	27.1 a-g	3.10 lmn	0.95 b-h	0.040
	Fus805	18.8 j-o	3.79 c-h	0.43 h-k	0.025 abc	25.0 a-h	3.04 lmn	1.92 a-e	0.095
	Fus849	35.4 c-l	3.48 e-l	1.24 a-h	0.025 abc	4.2 j-k	3.56 d-l	0.19 hi	0.023
	Fus859	39.6 b-j	3.56 d-j	1.45 a-h	0.050 abc	14.6 e-k	3.91 a-f	0.66 c-i	0.020
F. proliferatum	Fus555	31.3 e-m	3.29 e-m	0.96 c-i	0.040 ab	39.6 ab	3.13 k-n	1.94 abc	0.075
	Fus635	16.7 j-o	3.31 g-n	0.42 h-k	0.020 abc	8.3 h-k	3.96 a-f	0.19 g-i	0.005
	Fus694	58.3 a-d	2.73 n-s	2.01 a-d	0.050 abc	29.2 a-f	3.29 j-n	1.05 a-h	0.030
	Fus695	14.6 k-o	4.06 b-f	0.49 i-k	0.025 abc	25.0 a-h	3.63 c-j	1.06 a-h	0.043
	Fus782	12.5 l-o	3.94 b-g	0.60 g-j	0.028 abc	6.3 i-k	3.27 j-n	0.28 g-i	0.015
F. redolens	Fus645	33.3 c-l	2.96 j-p	0.80 d-j	0.025 abc	18.8 d-j	3.79 b-h	0.47 c-h	0.020
F. solani	Fus482	39.6 b-j	3.61 d-j	0.81 e-j	0.025 abc	14.6 e-k	4.00 a-e	0.86 b-h	0.038
	Fus743	18.8 i-o	3.38 f-n	0.64 e-j	0.030 abc	22.9 b-i	3.33 h-n	1.17 a-g	0.045
	Fus801	39.6 b-k	3.44 f-m	1.49 b-i	0.100 a	27.1 a-g	3.56 d-l	2.78 a	0.145

Fusarium species	Isolate	Trial 1				Trial 2			
		Emergence (%) 35 dap	Root rot severity (0-5)	Plant height (cm)	Plant dry weight (g)	Emergence (%) 35 dap	Root rot severity (0-5)	Plant height (cm)	Plant dry weight (g)
	Fus852	20.8 h-o	4.04 b-f	0.45 h-k	0.020 abc	14.6 e-k	3.66 c-j	0.79 b-h	0.033
F. torulosum	Fus562	68.8 a	2.26 q-t	2.55 ab	0.100 a	20.8 c-j	3.89 a-f	0.75 a-h	0.028
F. verticillioides	Fus519	39.6 b-j	2.94 j-q	0.89 d-i	0.025 abc	14.6 e-k	3.85 b-g	0.79 c-h	0.028
	Fus583	16.7 j-o	3.44 f-l	0.56 g-j	0.023 bc	14.6 e-k	4.27 ab	0.26 e-i	0.010
	Fus627	20.8 h-o	4.02 b-f	0.72 e-j	0.050 abc	31.3 a-e	3.64 c-j	1.34 a-g	0.050
	Fus631	54.2 a-e	2.17 r-t	1.67 a-f	0.100 a	37.5 a-c	3.06 k-n	0.83 b-h	0.043
	Fus735	45.8 a-h	3.10 i-o	2.08 a-d	0.075 abc	18.8 d-j	3.27 g-m	1.84 a-g	0.093
	Fus741	47.9 a-f	3.25 h-o	0.85 d-j	0.025 abc	29.2 a-f	3.75 b-h	1.19 a-h	0.055
	Fus744	16.7 j-o	4.19 b-d	0.58 g-j	0.025 abc	12.5 f-k	3.81 b-h	0.65 d-i	0.030
	Fus833	47.9 a-f	3.21 h-o	1.44 a-g	0.050 abc	25.0 a-h	3.35 g-m	1.39 a-h	0.073
	LSD[a] (P < 0.05)	Log[b]	0.9957	Square root[b]	Rank[b]	0.6124	Rank	Square root	Log
	P value	<0.0001	<0.0001	<0.0001	0.0065	0.0006	< 0.0001	0.0282	0.1574

[a] For each of the variables measured, means followed by the same letter within a column are not significantly different based on Fisher's protected least significant difference (LSD) at $P = 0.05$ (Steele and Torrie 1980). "dap" = days after planting. Each trial was a randomized complete block design with four replications.

[b] Data were transformed as needed to meet assumptions for parametric analyses. Log = logarithmic transformation. Square root = square root transformation. Rank = Friedman's non-parametric rank test because of heterogeneous variances. The original means are shown but the means separation based on the transformed data analyses.

Supplementary Table 2.2. Pathogenicity of 10 *Pythium* isolates on the sweet corn cultivar SuperSweet Jubilee Plus in a growth chamber set at 13°C by night and 15°C by day with a 12 h photoperiod per day

		Trial 1				Trial 2			
Pythium species	**Isolate**	**Stand count (%) 35 dap**	**Root rot severity (0-5)**	**Plant height (cm)**	**Plant dry weight (g)**	**Stand count (%) 35 dap**	**Root rot severity (0-5)**	**Plant height (cm)**	**Plant dry weight (g)**
Non-inoculated control	-	50.0 a[a]	3.67 c	1.75 a	0.087 a	62.5 a	2.43 f	2.43 a	0.100 a
P. irregulare	Pym089	6.3 cd	4.67 ab	0.16 cd	0.008 bc	4.2 cd	4.63 bcd	0.15 bc	0.012 ab
P. rostratifingens	Pym094	45.8 a	3.38 c	2.08 a	0.098 a	43.8 ab	3.04 e	1.49 a	0.075 a
P. sulcatum	Pym130	0.0 d	5.00 a	0.00 d	0.000 c	8.3 d	4.66 abc	0.22 bc	0.007 a-d
P. ultimum	Pym092	2.1 d	4.88 ab	0.16 cd	0.008 bc	4.2 d	4.81 ab	0.06 cd	0.005 bcd
	Pym096	2.1 cd	4.96 a	0.10 cd	0.003 bc	0.0 d	4.96 a	0.00 d	0.000 d
	Pym110	18.8 b	4.33 b	0.72 ab	0.055 a	6.3 cd	4.46 cd	0.19 bc	0.010 abc
	Pym116	6.3 cd	4.73 ab	0.21 cd	0.010 bc	4.2 d	4.60 bcd	0.08 cd	0.003 cd
	Pym118	10.4 bc	4.66 ab	0.19 bcd	0.010 b	10.4 bc	4.33 d	0.49 b	0.028 a
	Pym142	6.3 cd	4.81 ab	0.13 cd	0.003 bc	0.0 d	4.87 ab	0.06 cd	0.005 bcd
	Pym152	8.3 bcd	4.81 ab	0.34 bc	0.010 bc	0.0 d	4.90 ab	0.02 cd	0.003 cd
	LSD[a] ($P < 0.05$)	Square root[b]	Square root[b]	Rank[b]	Rank[b]	Rank	0.8982	Square root	Rank
	P value	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	0.0079

[a] For each of the variables measured, means followed by the same letter within a column are not significantly different based on Fisher's protected least significant difference (LSD) at $P = 0.05$ (Steele and Torrie 1980). "dap" = days after planting. Each trial was a randomized complete block design with four replications.

[b] Data were transformed as needed to meet assumptions for parametric analyses. Log = logarithmic transformation. Square root = square root transformation. Rank = Friedman's non-parametric rank test because of heterogeneous variances. The original means are shown but the means separation is based on the transformed data analyses.

Supplementary Table 2.3. Pathogenicity of 10 *Rhizoctonia* isolates on the sweet corn cv. SuperSweet Jubilee Plus in a growth chamber set at 13°C by night and 15°C by day with a 12 h photoperiod per day.

		Trial 1				+	Trial 2			
Rhizoctonia or *Ceratobasidium* species	Isolate	Stand count (%) 35 dap	Root rot severity (0-5)	Plant height (cm)	Plant dry weight (g)		Stand count (%) 35 dap	Root rot severity (0-5)	Plant height (cm)	Plant dry weight (g)
Non-inoculated control	-	52.1 c[a]	3.19 bc	2.34 cd	0.193 ab		45.8 bc	2.54 cd	3.29 ab	0.200 ab
Ceratobasidium sp. AG A	Rhz073	79.2 ab	2.06 d	4.96 a	0.247 a		43.8 bc	2.67 cd	2.31 ab	0.125 ab
Ceratobasidium sp. AG K	Rhz021	85.4 a	1.97 bc	3.37 abc	0.165 ab		37.5 cd	3.62 b	1.30 ab	0.097 ab
R. solani AG 2-1	Rhz022	44.4 cd	1.97 d	3.85 abc	0.246 a		29.2 cde	2.63 cd	1.24 bc	0.050 abc
	Rhz028	33.3 d	2.95 c	1.74 de	0.094 bc		14.6 def	3.13 bc	0.63 cde	0.012 bc
R. solani AG 3	Rhz016	68.8 b	2.71 c	3.85 abc	0.220 a		70.8 a	2.21 d	2.39 a	0.125 a
	Rhz020	68.8 b	2.13 d	4.14 ab	0.270 a		64.6 ab	1.98 d	3.03 ab	0.150 a
R. solani AG 4	Rhz035	2.1 e	4.60 a	0.11 e	0.001 e		0.0 f	4.52 a	0.00 f	0.000 c
	Rhz036	45.8 cd	3.25 bc	2.58 bcd	0.170 ab		37.5cd	2.75 cd	1.20 bcd	0.025 bc
	Rhz058	4.2 e	4.33 a	0.16 e	0.013 de		8.3 ef	3.23 bc	0.20 ef	0.012 bc
	Rhz068	10.4 e	3.50 b	0.59 e	0.030 cd		16.7 def	3.38 bc	0.51 de	0.030 abc
	LSD[a] (P < 0.05)	Rank[b]	Square root[b]	0.6013	Square root[b]		Rank	0.9208	Rank	Rank
	P value	<0.0001	<0.0001	<0.0001	<0.0001		<0.0001	0.0001	<0.0001	0.0277

[a] For each of the variables measured, means followed by the same letter within a column are not significantly different based on Fisher's protected least significant difference (LSD) at $P = 0.05$ (Steele and Torrie 1980). "dap" = days after planting. Each trial was a randomized complete block design with four replications.

[b] Data were transformed as needed to meet assumptions for parametric analyses. Log = logarithmic transformation. Square root = square root transformation. Rank = Friedman's non-parametric rank test because of heterogeneous variances. The original means are shown but the means separation is based on the transformed data analyses.

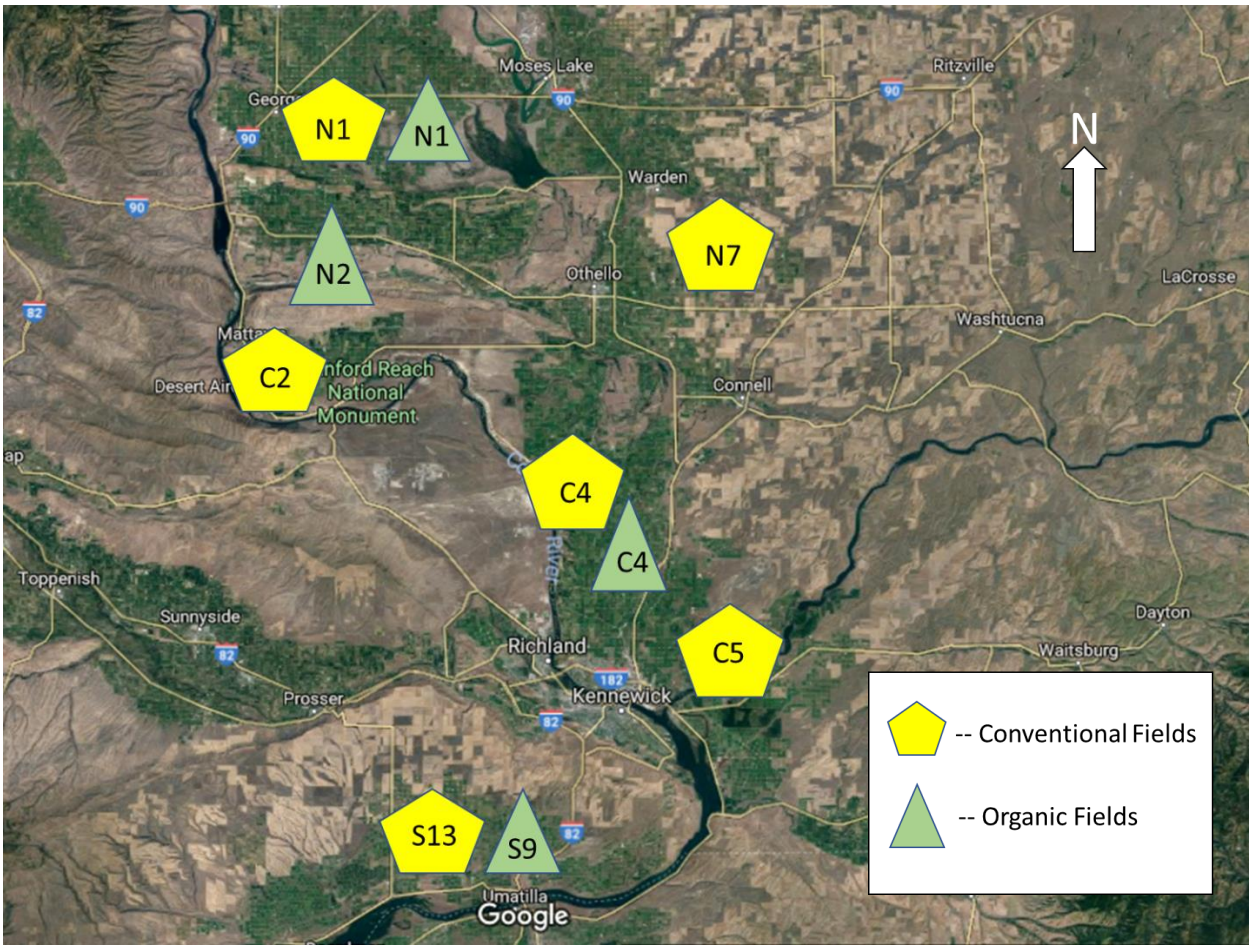

Fig. 2.1. Approximate locations of conventional and certified organic sweet corn crops in the Columbia Basin of central Washington that were surveyed for seedling blights in spring and early summer of 2018. The letter and number indicate the region (N = north, C = central, S= south) and the number of fields surveyed in that location. Map source: http://maps.google.com/ (accessed November 2018).

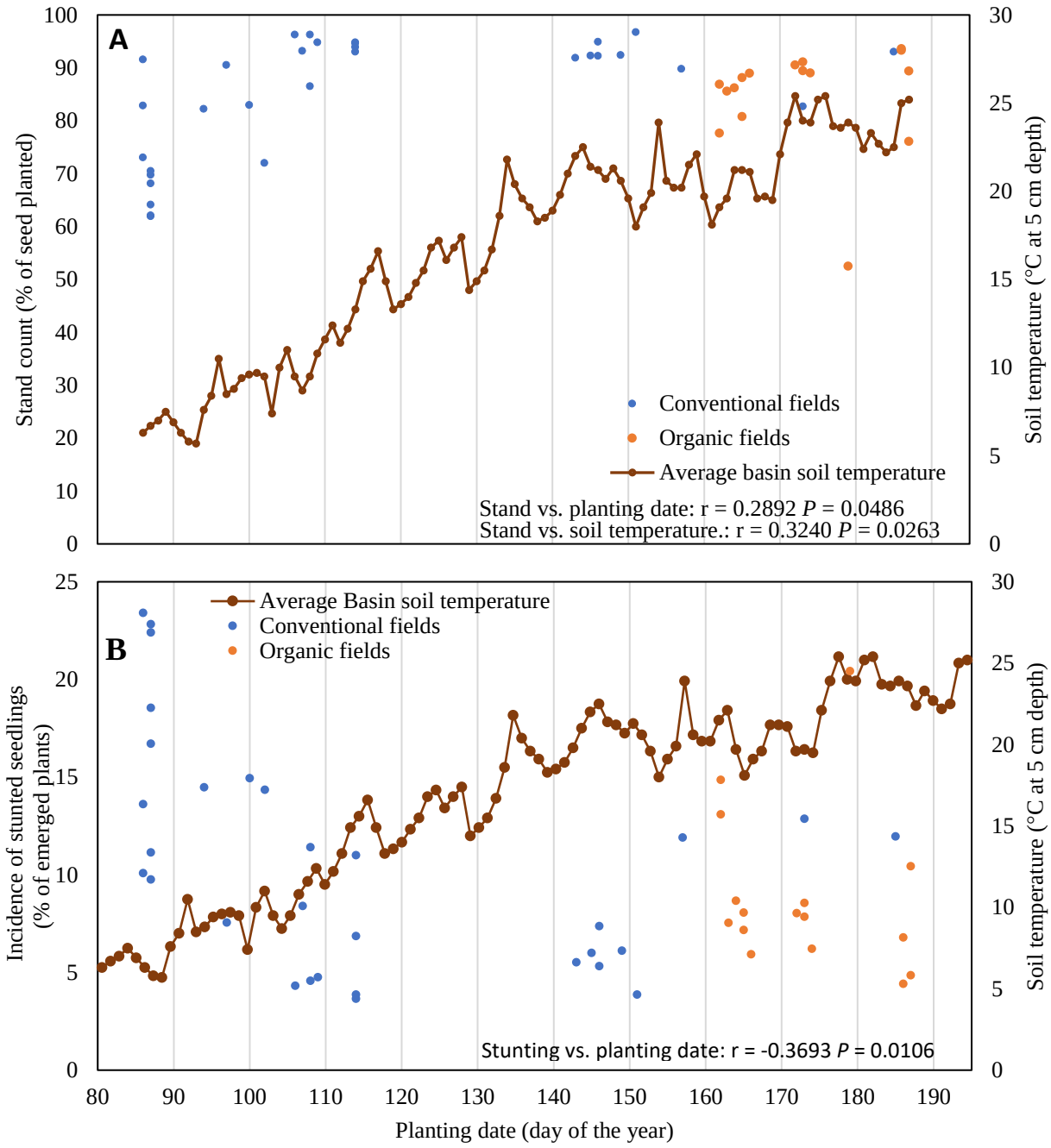

Fig. 2.2. Stand count (% of planted seed) (**A**) and incidence of stunting (%) (**B**) in relationship to planting date and average daily soil temperature (at a 5-cm depth) for 47 sweet crops surveyed in the Columbia Basin of Washington in 2018. Refer to the main text for details on how each field was surveyed. The 86th day of the year = 27 March, and 187th day = 6 July, which represent the range in planting dates for the fields sampled.

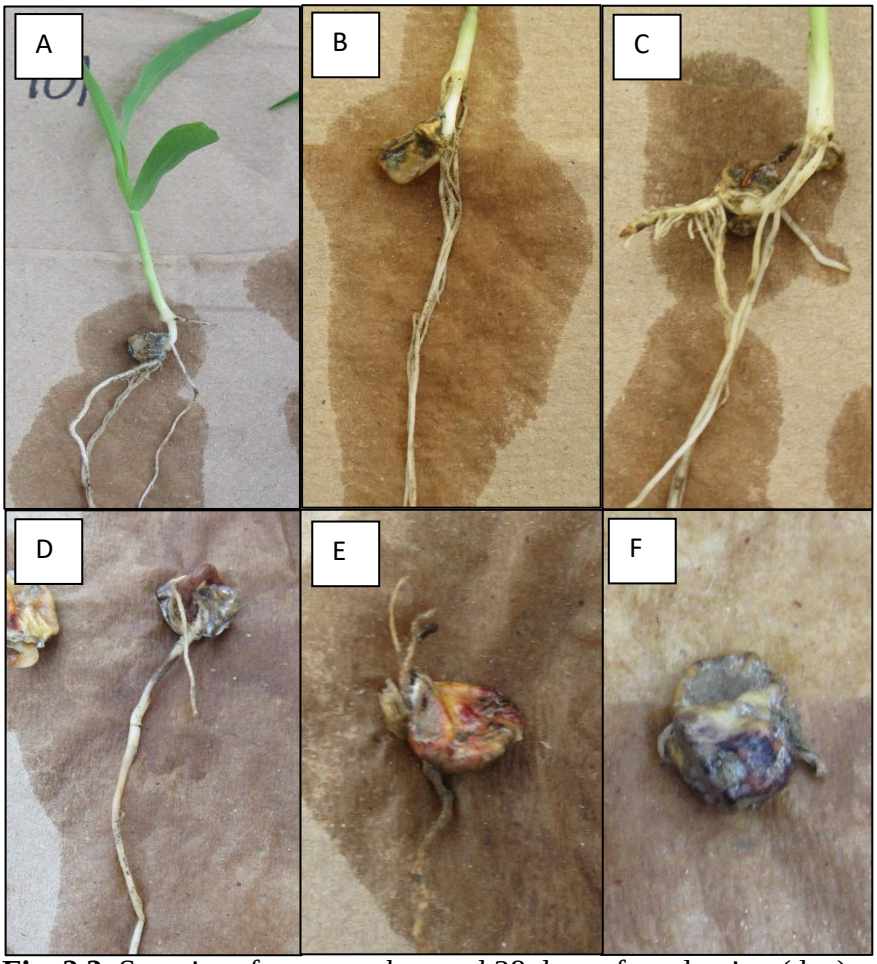

Fig. 2.3. Severity of root rot observed 28 days after planting (dap) seed of the sweet corn cv. SuperSweet Jubilee Plus into pasteurized soil inoculated with isolates of *Pythium* obtained from stunted plants in sweet corn fields in the Columbia Basin of Washington. Rating scale: 0 = no symptoms on the roots (**A**); 1 = a few, small, discolored root lesions (**B**); 2 = light brown discoloration covering most of the roots and the mesocotyl (**C**); 3 = darker brown discoloration of the mesocotyl and roots, with most of the lateral roots missing (**D**); 4 = complete discoloration of the mesocotyl and roots, and the lateral roots missing (**E**); and 5 = seed rotten with no roots or shoot (**F**).

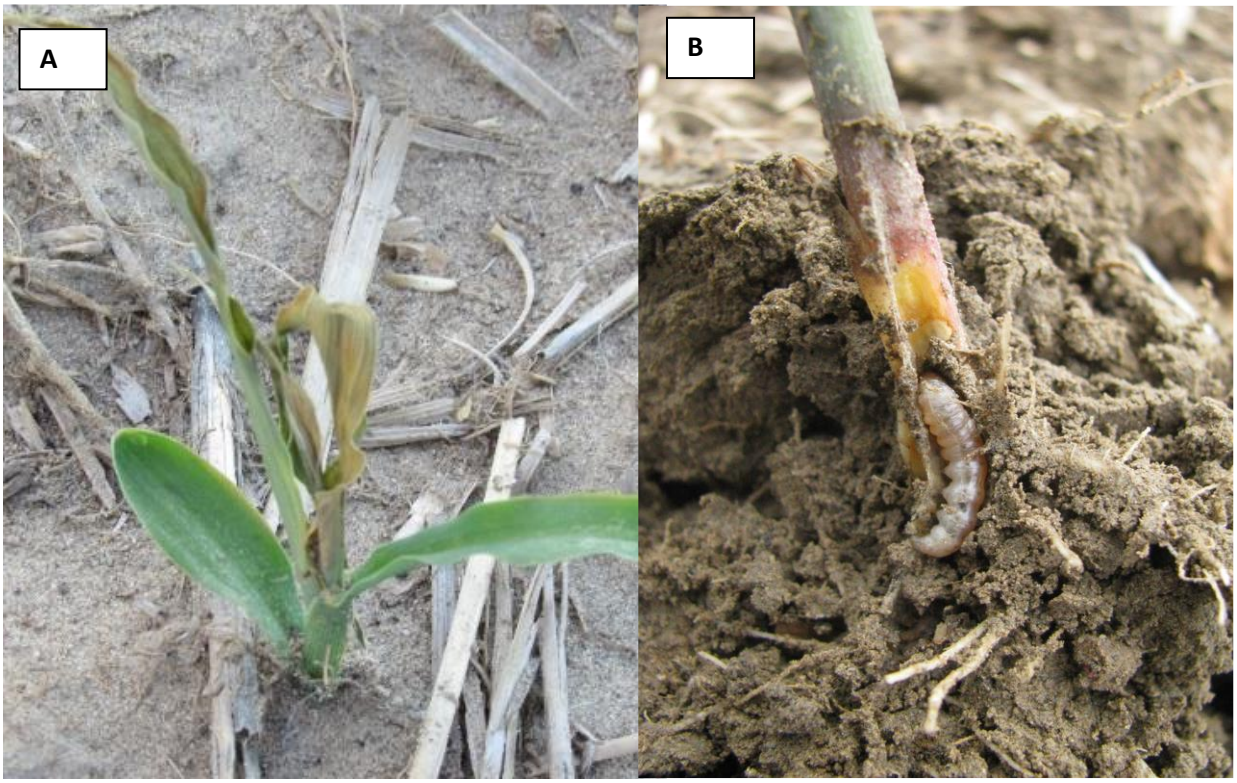

Fig. 2.4. Dieback of a sweet corn seedling affected by a larva of the sod webworm, *Crambus rickseckerellus* (Klots 1940) (**A**), which was found at 1 to 5% incidence in sweet corn fields sampled in the Columbia Basin of Washington in 2018. Larva of *C. rickseckerellus* feeding on a sweet corn seedling (**B**). Photos courtesy of Lindsey du Toit.

Trial 1
Trial 2
A
B
D
Stand count (%)
Root rot severity (0-5)
Shoot length (cm)
Non-inoculated

Fig. 2.5. Virulence of 40 isolates of *Fusarium* as measured by stand count 28 days after planting (dap) (**A** and **B**), root rot severity (**C** and **D**), and plant height (**E** and **F**) 28 dap the sweet corn cv. SuperSweet Jubilee Plus in two pathogenicity trials carried out in a growth chamber set at 13°C by night and 15°C by day with a 12 h photoperiod/day. Each data point is the mean 12 seeds planted in each of 4 replicate pots with soil inoculated with that isolate. Non-inoculated = the non-inoculated control soil treatment. Within each subfigure, white bars represent isolates for which that variable measured did not differ significantly from that of the non-inoculated control treatment, and black bars represent isolates for which the variable differed significantly from the non-inoculated control treatment. Isolates are listed in order of the least to most impact on stand count in Trial 1, and are presented in the same order for all variables in both trials. Within each subfigure, bars with a common means separation letter are not significantly different based on Fisher's protected least significant difference at $P = 0.05$. Fus485 = *F. acuminatum*; Fus757 = *F. avenaceum*; Fus488 = *F. commune*; Fus566 = *F. concolor*; Fus706, Fus748, Fus754, and Fus761 = *F. equiseti*; Fus515 and Fus766 = *F. fujikuroi*; Fus490 and Fus596 = *F. graminearum*; Fus505 = *F. lacertarum*; Fus487, Fus527, Fus603, Fus721, Fus737, Fus805, Fus849, and Fus859 = *F. oxysporum*; Fus555, Fus635, Fus694, Fus695, and Fus782 = *F. proliferatum*; Fus645 = *F. redolens*; Fus482, Fus743, Fus801, and Fus852 = *F. solani*; Fus562 = *F. torulosum*; Fus519, Fus583, Fus627, Fus631, Fus735, Fus741, and Fus833 = *F. verticillioides*.

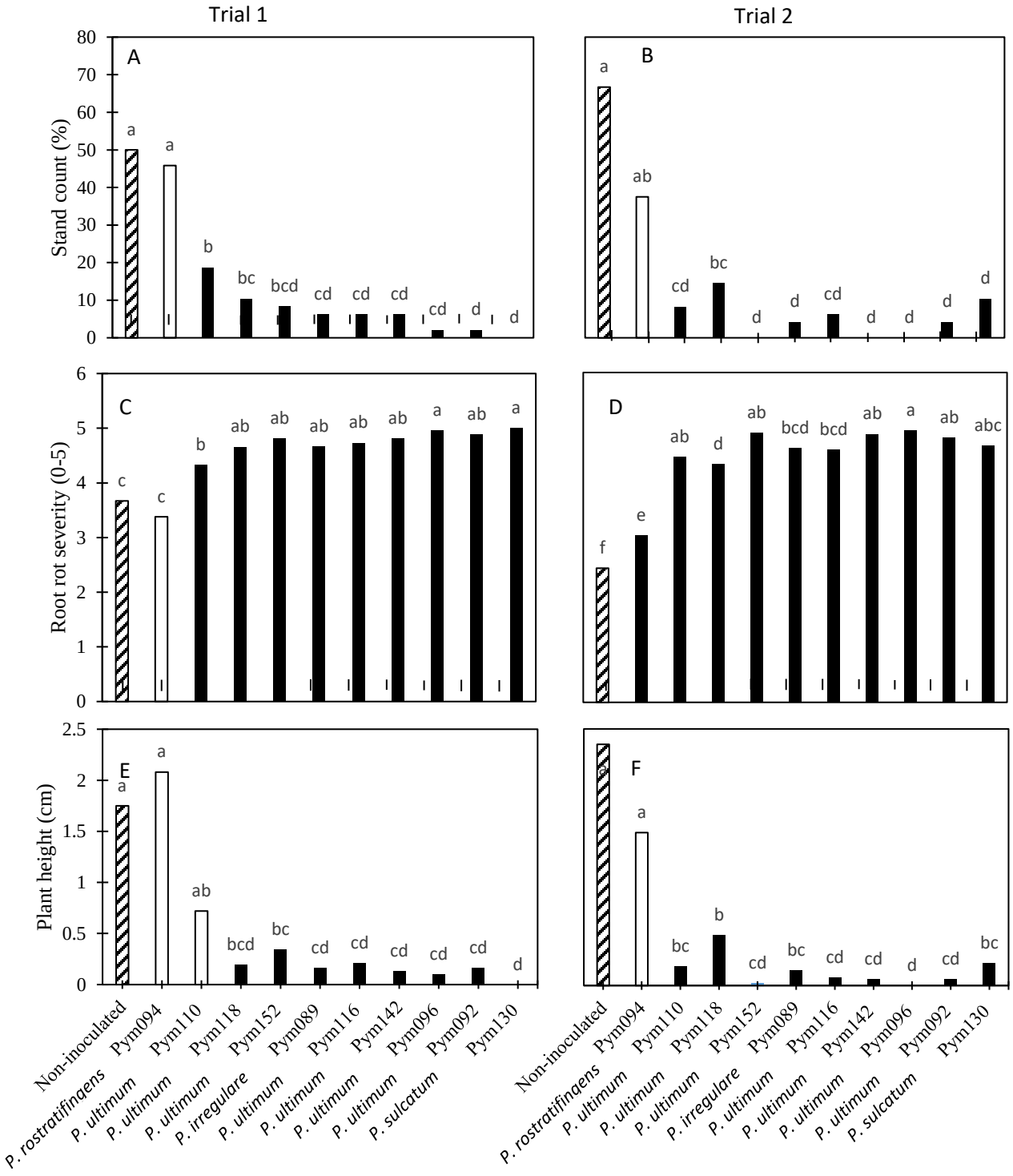

Fig. 2.6. Effect of 10 isolates of *Pythium* on stand counts (**A** and **B**), root rot severity ratings (**C** and **D**), and plant height (**E** and **F**) 28 days after planting (dap) the sweet corn cv. SuperSweet Jubilee Plus in pots of pasteurized soil that was inoculated with each of these isolates, and

incubated in a growth chamber set at 13°C by night and 15°C by day with a 12 h photoperiod/day. Each data point is the mean for 12 seedlings in each of 4 replicate pots. Non-inoculated = the non-inoculated control soil treatment. Within each subfigure, white bars represent isolates for which that variable measured did not differ significantly from that of the non-inoculated control treatment, and black bars represent isolates for which the variable differed significantly from that of the non-inoculated control treatment. Isolates are listed in order of least to greatest reduction in stand count in Trial 1, and in the same order for all variables in both trials. Within each subfigure, bars with a common letter are not significantly different based on Fisher's protected least significant difference at $P = 0.05$. Pym089 = *P. irregulare*; Pym094 = *P. rostratifingens*; Pym130 = *P. sulcatum*; and all other isolates = *P. ultimum.*

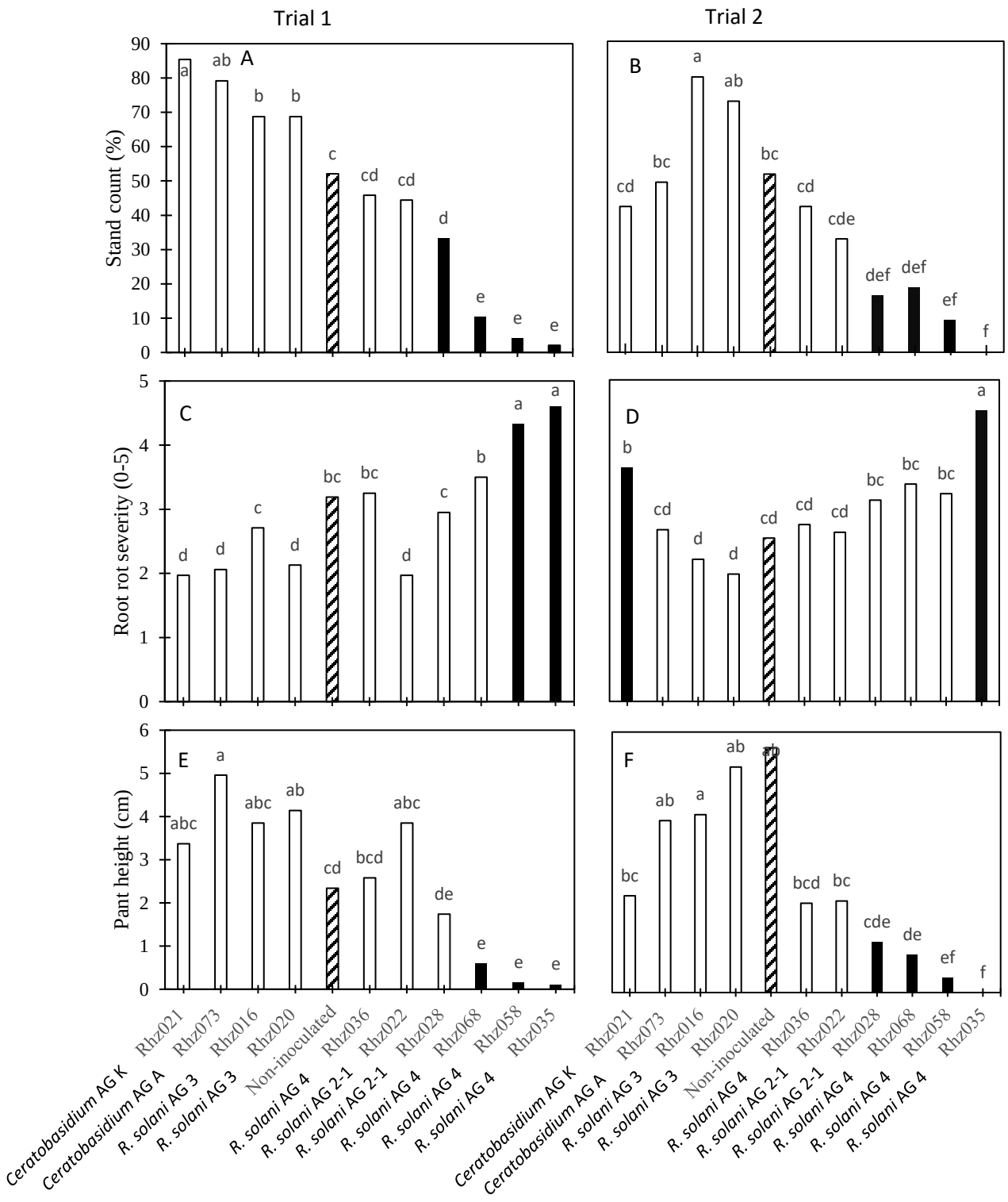

Fig. 2.7. Effect of 10 isolates of *Rhizoctonia* on stand count (**A** and **B**), root rot severity (**C** and **D**), and plant height (**E** and **F**) 28 days after planting (dap) the sweet corn cv. Super Sweet

Jubilee Plus in pasteurized soil that was inoculated with those isolates and incubated in a growth chamber set at 13°C by night and 15°C by day with a 12 h photoperiod/day. Each data point is the mean for 12 seedlings in each of 4 replicate pots/isolate. Non-inoculated represents the non-inoculated control treatment. Within each subfigure, white bars represent isolates for which that variable did not differ significantly ($P < 0.05$) from that of the non-inoculated control treatment, and black bars represent isolates for which that variable differed significantly from that of the non-inoculated control treatment for that variable. For all subfigures, the isolates are listed in order of the least to greatest negative impact on stand count in Trial 1. Rhz073 = *Ceratobasidium* sp. AG A; Rhz021 = *Ceratobasidium* sp. AG K; Rhz022 and Rhz028 = *R. solani* AG 2-1; Rhz016 and Rhz020 = *R. solani* AG 3; and Rhz035, Rhz036, Rhz058, and Rhz068 = *R. solani* AG 4.

CHAPTER THREE

SCRI SWEET CAPS GERMPLASM COLD TOLERANCE SCREENING FIELD TRIALS IN THE COLUMBIA BASIN OF WASHINGTON

3.1 Introduction

Sweet corn, *Zea mays* var. *rugosa*, is a subtropical, annual, monocotyledon in the family Poaceae that grows best at average air temperatures of 20 to 22°C during the seedling stage, followed by 25 to 33°C by day and 17 to 23°C by night during subsequent vegetative and reproductive growth stages (Hassell et al. 2003; Pothour et al. 2002). When grown under suboptimal conditions, particularly at air and soil temperatures <15°C, seed germination and development can be slow (Hassell et al. 2003). As a result, sweet corn should only be planted after the top 10 to 15 cm of soil have warmed to ≥15°C (Grecu et al. 2018; Hassell et al. 2003; Huelsman 2000). Poor emergence and vigor can be a limiting factor in sweet corn production areas with cool springs, like the northern United States (Allam et al. 2016). However, early harvested sweet corn crops produced by early planting often command a greater price in fresh markets and facilitate spreading out harvest for large acreage of processing crops (Revilla et al. 2000; Revilla et al. 2003). Early planting of sweet corn is also advantageous in dryland production regions as it can provide the potential benefits of avoiding high temperatures, drought, and late season diseases and pests (Mock and McNeill 1979; Wijewardana et al. 2015).

The poor germination and vigor associated with early planting of sweet corn cultivars can affect all sweet corn types, i.e., *shrunken-2* (*sh2*), *sugary-1* (*su*), and *sugar enhanced* (*se*) (Stewart et al. 1990; Styer and Cantliffe 1984). However, some sweet corn cultivars are able to germinate, emerge, and grow better than others under low temperatures (Hotchkiss et al. 1997;

Mock and McNeil 1979). Typically, cultivars with the *su* genotype have greater cold tolerance compared to *sh2* sweet corn genotypes (Hassell et al. 2003). Furthermore, some cultivars within the *sh2* group germinate and establish more poorly than others, even under optimal field conditions, which can be influenced significantly by the quality of seed lots as well as genetics of the cultivars (Styer and Cantliffe 1984).

Germination of sweet corn seed and growth of seedlings can be affected greatly by the presence of seedborne and/or soilborne fungi that are pathogenic on corn, which can be a major contributing factor to reduced emergence and seedling vigor (Miedema 1982). Four genera of fungi and oomycetes, *Fusarium*, *Pythium*, *Penicillium,* and *Rhizoctonia* are attributed most commonly as the causal agents of damping-off and seedling blights under the conditions that typically occur at planting (Bakker et al. 2016; Miedema 1982; Munkvold and White 2016; Styer and Cantliffe 1984). In conventional agronomic systems, these pathogens can be managed to some degree with the use of disinfectants and/or site-specific and broad-spectrum fungicide seed treatments (Hartz and Caprile 1995; Matthiesen et al. 2016; Rodriguez-Brlievich et al. 2010). However, seed treatments may only provide control for a short period after planting, after which pathogens can infect the seedlings (Cook et al. 2002; Jaaffar et al. 2016). In contrast, organic growers cannot use these highly effective, synthetic fungicide seed treatments to control many seedborne and soilborne fungi [United States Department of Agriculture (USDA) National Organic Program (NOP) 2018]. There is also a lack of highly or consistently efficacious organic seed treatments available for use in organic sweet corn crops (C. Burt and T. Bruketta, Twin City Foods, *personal communication*; Wohleb 2013).

Emergence and vigor of sweet corn under low soil temperatures can be improved with some agronomic practices. For example, the selection of vigorous, high quality seed lots for

planting can result in more uniform emergence and greater yields (Callan et al. 1996; Marcos-Filho 2015; Waters and Blanchette 1983; Yates et al. 1997). Planting seed lots of sweet corn cultivars that can emerge rapidly under cool soil conditions reduces the time to emergence and the duration that seedlings remain in the highly susceptible stage of growth to seedling blights and damping-off pathogens (Hotchkiss et al. 1997). In areas where soil temperatures at planting are cool and the duration of the growing season is limited, sweet corn transplants and black plastic mulch have been used to increase soil temperature and the rate of growth of sweet corn crops, thereby reducing the time to harvest (Kwabiah 2004).

Tolerance to cool conditions during emergence and seedling development in corn is controlled by additive and dominant alleles (Li et al. 2018; McConnell and Gardner 1979). It has been shown that selecting for increased seedling height, fewer dead kernels, and improved germination using recurrent selection can improve sweet corn germplasm for cold tolerance (Viesselmann et al. 2014). Cold tolerance improvements have also been made through the introgression of this trait from field corn cultivars, which typically have better performance under cool soil conditions compared to sweet corn (Rodríguez et al. 2010; Tracy 1990). However, the risk of introgression of undesirable traits that negatively affect required traits such as sweetness and texture, can occur when sweet corn is crossed with field corn (Allam et al. 2016; Revilla et al. 2000; Tracy 1990). Further improvements in cold tolerance should be possible in sweet corn with additional selection and screening for this trait (Herner 1986).

In northern growing regions of the United States, such as Minnesota, Wisconsin, Idaho, and the Columbia Basin of Washington, cool spring conditions that are suboptimal for sweet corn emergence and growth occur almost annually. Sweet corn growers in these regions incur stand losses to damping-off and seedling blight pathogens that are exacerbated by poor seedling

vigor under cool soil conditions. This is particularly problematic for organic sweet corn crops, for which there is a lack of highly efficacious seed treatments to help combat seedling blight and damping-off pathogens. The purpose of this research was to contribute to the development of sweet corn germplasm with greater tolerance of cool soil conditions, by screening a diversity panel of >600 sweet corn germplasm lines as part of the USDA National Institute of Food and Agriculture (NIFA) Specialty Crop Research Initiative Sweet (SCRI) CAPS Project No. 2018-51181-28419 that is focused on improving sweet corn germplasm for production and marketability. This study was completed with field trials in each of 2019 and 2020 in the northern region of the semi-arid Columbia Basin of central Washington.

3.2 Materials and Methods

3.2.1. Seed preparation. In 2019, seed of sweet corn germplasm comprising 182 USDA plant introductions (PIs), inbred lines, and crosses were received from the University of Florida as part of the USDA NIFA SCRI Sweet CAPS project to plant in a cold tolerance screening field trial in the Columbia Basin. The 182 entries evaluated in this trial included 163 of the *su* genotype, 2 *se*, 5 *sh2*, 8 *sh2su*, and 4 wild type entries (field corn type). In 2020, 580 USDA PIs, inbred lines, crosses, and other entries were received from the University of Florida and University of Wisconsin (25 to 30 seed per line) to plant in a similar field trial in the Columbia Basin. In this trial, 340 entries were of the *su* genotype, 186 of *sh2*, 32 of *se*, 1 of *suse* (a hybrid between *su* and *se* genotypes), 7 were heterozygous for *su* (Het-*su*), 8 *sh2su*, 5 *sh2se*, 5 *sh2suse*, 4 *sh2* heterozygous for *su* (Het-*su*), and 24 wild type entries. For each trial, the seeds (25 seeds per line) were treated with the PNW Blend 127 pesticide mix used by (Syngenta Crop Protection LLC., Greensboro, NC) at the rate of 1.96 ml of blended product/100 kg seed. This treatment

comprised the insecticide Cruiser 5FS (active ingredient thiamethoxam, Syngenta Crop Protection LLC) and the fungicides Captan 4 (captan, Drexel Chemical, Memphis, TN), Dividend Extreme (difenoconazole + mefenoxam, Syngenta Crop Protection LLC), Thiram 480 DP (thiram, MacDermid Agricultural Solutions Inc., Waterbury, CT), Vitavax-34 (carboxin, MacDermid Agricultural Solutions Inc.), and Apron XL (mefenoxam, Syngenta Crop Protection LLC), which were blended together by Syngenta staff at the highest recommended label rate for sweet corn. Seeds for each entry received were treated at the Washington State University (WSU) Mount Vernon Northwestern Washington Research and Extension Center (NWREC) by adding the recommended volume of PNW Blend 127 to a 50 ml flask, based on the weight of seeds for each line. The seeds were then added to the flask, which was capped with a silicone plug, and the flask was shaken for 2 minutes to ensure the seeds were covered thoroughly with the fungicide mix and there was minimal fungicide remaining on the inner sides of the flask. The treated seeds of each entry were then placed into a plastic weigh boat in a fume hood to dry overnight. Flasks were washed with soap and water between seed samples.

The treated seeds for each entry were divided into two coin envelopes, each containing 12 seeds. For each trial the experiment consisted of two complete blocks of all entries, planted as a randomized complete block design (RCBD). For the 2019 trial, seed of the supersweet hybrid, GSS 3071 (Syngenta Crop Protection LLC) was included to represent a standard *sh2* hybrid grown in the Columbia Basin, which was planted at regular intervals throughout the trial for a total of 56 plots of GSS 3071 across the two complete blocks (28 per block). GSS 3071 is a moderately vigorous, processing sweet corn hybrid planted widely in the Columbia Basin. In 2020, due to the lack of available seed of GSS 3071, the supersweet hybrid GSS 3951 (Syngenta Crop Protection LLC) was planted as the control hybrid at regular intervals in the trial for a total

of 88 plots of GSS 3951 across the two complete blocks (44 per block). GSS 3951 is a moderately vigorous, processing *sh2* sweet corn hybrid that is also grown widely in the Columbia Basin.

3.2.2. 2019 Trial planting. The 2019 trial was planted south of Road 5 and west of Road K, in a field at Weber Farms LLC between Quincy and George, WA, in collaboration with Kevin Moe (Syngenta Crop Protection LLC, PNW Vegetable Seed Sales Representative), on 10 April. The trial covered 91 m x 24 m, and included two replicate blocks. Each plot was 4.5 m long with a 76 cm spacing between rows. Seeds were planted 18 cm apart within the row, to a depth of 2.5 cm, using an ALMACO two-row, 30-cell cone planter (ALMACO, Nevada, IA) mounted on a John Deere 71 planter (Deere and Company, Moline, IL), and operated using 14- and 20-sprockets for the front and back gears, respectively. A New Holland Workmaster 45 tractor (CNH Industrial N.V., London, United Kingdom) was used to operate the planter. The trial was planted in 15 passes, starting at the northeast corner of the field, and progressing to the southwest, with rows planted in a north-south direction. For the first 12 passes, seeds were planted in each plot using an electronic tripper on the planter. However, for passes 13 through 15, the cones had to be tripped manually because of a mechanical failure with the electronic trip system.

3.2.3. 2019 Trial ratings. The 2019 trial was rated for emergence (stand count) in each plot starting 14 days after planting (dap), as the first seedlings were observed 10 dap, and continuing at a 7-day interval until 49 dap. Individuals doing the rating were blocked by replication. Photographs of plants in the trial and the surrounding commercial sweet corn crop were taken weekly to document some of the variation in emergence and growth stage. Starting 28 dap, the number of stunted seedlings, and seedling vigor in each plot were also rated.

Seedlings were considered stunted if they were ≤75% the height of the rest of the seedlings in that plot. Vigor was scored on a 0 to 9 scale based on the scale used by sweet corn specialists at Syngenta Crop Protection, LLC, i.e., the vigor rating for each plot was made in comparison to the nearest plot of GSS 3071, with each plot of GSS 3071 rated as a 5. A vigor rating of 9 was assigned to plots with the most vigorous growth possible at that maturity, and 0 was assigned to plots with no plants emerged. At the 28 dap rating, it became evident that plots planted in one direction, north-to-south, had been staked incorrectly on the north end, i.e., approximately 0.6 m too far into the plot. The placement of the stakes was corrected. However, stand counts and height ratings for these plots at 14 and 21 dap had to be treated as missing data (about 50% of all plots). The same variables of stand, number of stunted seedlings, and vigor, as well as the average number of leaves per plant were rated 35, 42, and 49 dap.

On 20 May 2019, 40 dap, the grower applied Laudis (tembotrione, Bayer Crop Science, Whippany, NJ), Atrazine 4L (atrazine, Drexel Chemical), Conform DP (polyoxyethylene sorbitan fatty acid ester, soybean oil ethoxylate, copolymer of alpha- and beta-pinene, The McGregor Company, Colfax, WA), and McGregor Fluid Grade (ammonium sulfate, The McGregor Company) to control weeds in the sweet corn crop and the trial. About 20% of the plots had extensive weed pressure by this time. At 42 and 49 dap, those plots with ≥50% of the plants producing tillers was also recorded.

3.2.4. 2020 Trial planting. The 2020 trial was planted south of Road 5 and east of Road K, between Quincy and George, WA, in a different field at Weber Farms LLC than the 2019 trial, on 3 April 2020. The trial covered 119 m x 37 m, and included two replicate blocks. Each plot was a single row 4.6 m long with a 76 cm spacing between rows. Seeds were planted 18 cm apart within the row, to a depth of 2.5 cm, using the same planter and tractor described for the

2019 trial. The trial was planted in 24 passes beginning at the southwestern corner of the field and progressing to the northeast, with rows planted in a north-south direction. Seeds were planted in each plot using an electronic tripper on the planter.

3.2.5. 2020 Trial ratings. The 2020 trial was rated for emergence (stand count) in each plot starting 11 (dap), when the first emerged seedlings were observed, and continuing twice a week until 28 dap, after which emergence was rated once more at 35 dap. Stand counts were conducted twice weekly in the 2020 trial to differentiate the small differences in emergence among the entries during the first couple of weeks after planting. During the 2019 trial, these early differences in stand were not detected because ratings were done only weekly. At 28 and 35 dap, the number of stunted seedlings, plant vigor, and average number of leaves per plant were also rated for each plot as described for the 2019 trial. The vigor rating for each plot was made in comparison to the nearest plot of GSS 3951, with each plot of GSS 3951 rated as a 5. Photographs of select plants in the trial were taken at every rating to document variation in emergence and growth stage. On 14 May 2020, 41 dap, the grower applied the herbicide Outlook (dimethenamid-P, BASF Corp., Triangle Park, NC) to control weeds in the surrounding sweet corn crop and the trial, by which time about 40% of the plots had extensive weed pressure. At 49 dap, data were collected on the plots with ≥50% of the plants producing tillers.

3.2.6. Data analyses. For each trial, the area under the emergence progress curve (AUEPC) was calculated for each entry, following the method of Sun et al. (2015), based on weekly stand counts in 2019 from 14 to 49 dap, and twice-weekly stand counts in 2020 from 11 to 28 dap and one week later at 35 dap. Mean emergence time (MET) in days was calculated for each line as described by Demir and Mathews (2010). For all variables measured, the mean ± standard error was calculated for each line using SAS Version 9.4 (SAS Institute, Cary, NC).

3.3 Results

3.3.1. 2019 Trial. Over the 49 days of the 2019 trial, minimum daily temperature ranged from -1.2 to 14.8°C, and maximum daily temperature ranged from 12.6 to 29.2°C (Fig. 3.1A, Table 3.1). The average daily temperature over this duration was 14.3°C and ranged from 6.8°C on 14 April to 20.5°C on 29 May. Soil and air temperatures generally increased over the duration of the trial and remained >15°C after 5 May (125 day of the year) (Fig. 3.1A). However, there were two nights during which the air temperature dropped below freezing (15 and 29 April = 5 and 19 dap, respectively). The minimum air and soil temperatures dropped <15°C on 49 and 8 of the 49 days of the trial, respectively (Fig. 3.1A). A soil temperature of 15°C is considered a minimum threshold for planting sweet corn seed (Hassell et al. 2003; Parera et al. 1995; Styer and Cantliffe 1984). Therefore, this trial provided relevant conditions for assessing cold tolerance of the 182 sweet corn entries evaluated in 2019.

There was little precipitation over the 49 days of the trial, with rainfall recorded on 8 days for a total of 28 mm (Fig. 3.1A, Table 3.1). The field was irrigated by the grower, using a center pivot, on 20 of the 49 days of the trial (Fig. 3.1A, Table 3.1). A total of 127 mm of water was applied by irrigation, with an average of 7 mm per irrigation (Table 3.1).

Given the cold conditions at the start of the trial, almost no seedlings had emerged by 7 dap, so stand counts were first recorded 14 dap (Table 3.2). Seed of two of the 182 sweet corn entries, MSR_su and GSSS_sh2, did not germinate in either of the replicate plots over the duration of the trial (Tables 3.2 and 3.3). All other entries produced at least one seedling in at least one plot. Stand counts averaged only 1.1 ± 0.2 seedlings out of the 12 seed planted/plot at

the first rating (14 dap), and increased to 7.1 ± 0.1 seedlings/plot by 21 dap, and remained at an average of 7.8 ± 0.2 seedlings/plot from 28 to 49 dap (Table 3.3).

Based on the AUEPC ratings, the greatest mean emergence was recorded for lines IL451b (mean AUEPC of 390.25), IaCG4189 (386.75), IL44b (381.50), A15 (374.50), and C90 (374.50) (Fig. 3.3, Table 3.3). In comparison, the standard hybrid GSS 3071 had a mean AUEPC rating of 245.94. Of the 182 entries screened in this trial, 90 had AUEPC ratings greater than that of GSS 3071. Of these 90 entries, 88 were of the *su* genotype and 2 were of the *sh2su* genotype. As noted above, MSR_su and GSSS_sh2 had no plants emerge over the duration of the trial (Table 3.3). ARZM_19_051 (12.25), Red_NCLB (12.25), and 34f (12.25) had the next lowest AUEPC ratings, with no seedlings observed until 28 dap. AUEPC and stand count were positively correlated r = 0.9722, $P < 0.0001$.

Mean emergence time (MET) for the 182 entries tested ranged from 18.2 ± 4.2 days for IL279xRpld to 28.7 ± 0.7 days for Ranniya_Zoltaya_401, with an average MET of 24.6 ± 0.3 days, illustrating the slow emergence of most accessions under the cool conditions of this 2019 trial. The lowest MET (fastest emergence) was recorded for IL279xRpld (18.2 ± 4.2 days), Strain 465A-421-68B (18.5 ± 2.6 days), Il451b (18.7 ± 1.8 days), A15 (18.9 ± 1.4 days), and A7 (19.0 ± 0.6 days) (Table 3.3). GSS 3071, the standard hybrid, had a MET of 23.2 ± 0.6 days. Compared to GSS 3071, 59 of the 182 entries had a lower MET than that of GSS 3071. Of the 59 entries that had faster emergence (lower MET) than GSS 3071, 56 were of the *su* genotype, 1 of *sh2* (Glancaster_sh2), and 2 were *sh2su* genotypes. The entries with the highest MET values (slowest emergence) were IL777a with 28.3 ± 1.5 days, I97A-381-68A with 28.6 ± 0.6 days, and Ranniaya_Zoltaya_401 with 28.7 ± 0.7 days (Table 3.3). MET and AUEPC were significantly negatively correlated (r = -0.3299, $P < 0.0001$), as expected.

The number of seedlings stunted by ≥25% in each plot ranged from 0 to 9 out of 12, and was greatest when measured 28 dap, with an average of 2.8 ± 0.1 stunted seedlings/plot for the 182 accessions, compared to 3.1 ± 0.2 stunted seedlings/plots of GSS 3071. The number of stunted seedlings/plot for the whole trial decreased slightly after 28 dap, to 2.6 ± 0.1 at 35 dap, 2.5 ± 0.1 at 42 dap, and 2.1 ± 0.1 at 49 dap. By 35 dap, the five entries with the most severe stunting had an average of ≥5 stunted plants/plot: IL21f (6.5), C90 (6.0), IL773a (6.0), IL798c (6.0), and IL279xRpld (5.0) (Table 3.3). A total of 118 entries of the 182 averaged the same or fewer stunted seedlings than GSS 3071 (fewer than 3.0 ± 0.2 stunted seedlings/plot). For these 118 entries, 101 were *su*, 1 was *se*, 4 were *sh2*, 8 were *sh2su*, and 4 were wild types (field corn genotypes [WT]). The top five entries with the lowest average number of stunted seedlings/plot and the highest plant stand were: P39M94 (1.0 ± 1.0 stunted seedlings/plot), P39xRpld (1.5 ± 0.5), 21-396-68B (1.0 ± 0.0), Strain T33-399-68B (1.5 ± 0.5), and IL303b (1.5 ± 0.5) (Table 3.3). Stunting was positively correlated with stand count ($r = 0.6579$, $P < 0.0001$).

Vigor ratings ranged from 0 to 7 out of a maximum of 9 in comparison to a vigor rating of 5 assigned to the nearest plot of GSS 3071 (Fig. 3.2). Weekly plant vigor ratings averaged 3.8 ± 0.1, 3.9 ± 0.1, 3.8 ± 0.1, and 3.8 ± 0.1 at 28, 35, 42, and 49 dap, respectively (Table 3.2). The Sweet CAPS diversity panel entry with the greatest vigor rating was Andjar bekaa, which had an average vigor of 7.0 ± 0.0 at 35 dap. At this rating, 26 of the 182 diversity panel entries had vigor ratings at least as good as that of GSS 3071 (≥5.0): Andjar bekaa (7.0), Cuzco_suse (6.0), NJ159 (6.0), IL104g (6.0), 21-396-68B (6.0), Cubano (5.5); Strain T35-388-68A (5.5), Strain 465A-421-68B (5.5), C7e (5.5), Me135 (5.5), IL788a (5.5), NJ112 (5.5), IL689a (5.5), ARZM_21_008 (5.0), C40 (5.0), Jubileeex9017 (5.0), P39M96 (5.0), Sc6069 (5.0), P51 (5.0), IL100K (5.0), IL112t (5.0), IL303b (5.0), IL328a (5.0), NJ112 (5.0), Slatka Pukanka (5.0), and Golden Bantam

(5.0) (23 *su* entries and 3 *sh2su* entries, Table 3.3). Vigor was significantly positively correlated with stand count (r = 0.5117, $P < 0.0001$). For all of the variables measured, only three lines did better than GSS 3071: C7e (*su*), IL104g (*su*), and 21-396-68B (NA) (Table 3.3).

By 42 dap, a number of the diversity panel entries and GSS 3071 were observed to produce tillers. By 49 dap, 97 of the 182 diversity panel entries had ≥50% of the plants producing tillers in one or both plots. Of the 56 GSS 3071 plots, 26 had 50% of the plants producing tillers. The production of tillers is not an advantageous trait in sweet corn. Over the duration of the trial, 24 entries produced seedlings with abnormal appearances (Fig. 3.3), including pale white (albino) seedlings (IL279xRlpd, ILB5765, Slatka Pukanka, NE_EDR_sh2, and ARZM_21_007), interveinal chlorosis on new and mature leaves (NJ159, IL124a, IL21f, C40, and Chile 335), general chlorosis (Sc6069, IL393a, IaEV3015, IL104g, IL648, MDM 1, C65, IL465, A7, and Separation_from_177642) and leaf dieback (Strain T35-388-68A, IaEV3004, and IL699e) (Fig. 3.3) compared to other plants in the same plot for the two plots of the same line. Chlorosis and dieback of leaves in some plots was only noticed 49 dap. Some of this could have been a result of herbicide injury after the grower-cooperator applied an herbicide mixture to the entire field 40 dap.

3.3.2. 2020 Trial. Over the 49 days of the 2020 trial, minimum daily air temperature ranged from -4.0 to 12.9°C, and maximum daily air temperature ranged from 11.0 to 26.0°C (Table 3.4, Fig. 3.1B). The average daily air temperature over this duration was 12.5°C and ranged from 4.5°C on 4 April to 18.9°C on 10 May. Soil and air temperature generally increased over the duration of the trial and remained >15°C after 15 April (Fig. 3.1B). However, there were six nights during which the air temperature dropped below freezing (3, 4, 6, 12, 13, and 17 May = 1, 2, 4, 10, 11, and 15 dap, respectively). The minimum air temperature and the soil

temperature at a 5-cm depth dropped <15°C on 49 and 11 days of the trial, respectively (Fig. 3.1B), providing relevant conditions for assessing cold tolerance of the sweet corn entries evaluated. There was little precipitation over the 49 days of the trial, with rainfall recorded on 5 days for a total of 12.5 mm (Table 3.4, Fig. 3.1B). The field was irrigated by the grower using a center pivot irrigation system.

Given the cold conditions at the start of the 2020 field trial, almost no seedlings had emerged by 7 dap so stand counts were first recorded 11 dap (Table 3.5). Seed of two of the 580 accessions, B84 plus su and wh10040R, did not emerge in either of the replicate plots over the entire duration of the trial (Tables 3.5 and 3.6). All other entries produced at least one seedling in at least one plot. Stand counts averaged 0.0 ± 0.0 out of the 12 seed planted/plot at the first rating, 11 dap, and increased to 0.9 ± 0.0 seedlings/plot by 14 dap, 6.6 ± 0.1 at 18 dap, 7.8 ± 0.1 at 21 dap, 8.2 ± 0.1 at 25 dap, 8.3 ± 0.1 at 28 dap, and 8.2 ± 0.1 at 35 dap (Table 3.5). In comparison, stand counts for GSS 3951 averaged 0.2 ± 0.1 at 11 dap, 2.2 ± 0.2 at 14 dap, 8.4 ± 0.2 at 18 dap, 9.3 ± 0.2 at 21 dap, 9.5 ± 0.2 at 25 dap, 9.6 ± 0.2 at 28 dap, and 9.5 ± 0.2 at 35 dap (Table 3.5)

Based on the AUEPC values, the greatest mean emergence was recorded for M31-1-1-1-1-1 (*sh2*) (245.5), Black Mexican (Het-*su*) (242.0), Ia5125 (*su*) (241.8), C7e (*su*) (235.0), and Me121Wa (*su*) (235.0) over the first four ratings, i.e., 11, 14, 18, and 21 dap (Table 3.6). In comparison, the standard hybrid GSS 3951 had a mean AUEPC value of 184.0 for this duration. As previously mentioned, no plants emerged for B84 plus su and wh10040R over the duration of the trial. We10401 (1.8), Wh07166R (5.3), K169-1-1-1-2-2 (6.0), K127-1-1-1-2-1-1-1-1 (7.8), and K104-1 (7.8) had the next lowest AUEPC values (Table 3.6). In total, 211 entries had

AUEPC ratings ≥GSS 3951. Of these, 166 entries were of the *su* genotype, 20 of *sh2*, 7 of *se*, 4 were heterozygous for *su*, 3 of *sh2su*, 2 of *sh2se*, and 10 were wild types.

MET for the 580 lines tested in 2020 ranged from 10.5 ± 7.3 (Il279AxRlpd) to 30.0 ± 0.0 (W191218) with an average MET of 18.3 ± 0.0 days. The lowest MET (fastest emergence) was recorded for Il279AxRlpd (10.5 ± 7.3 days), Glancaster_sh2 (11.3 ± 6.3 days), IL200e (12.5 ± 0.5 days), COES 46A-1 (12.6 ± 2.8 days), and K192-1-1-1-1-1-1 (12.9 ± 5.5 days) (Table 3.6). In total, 132 entries (22.8% of the 580 accessions) had a lower MET compared to GSS 3951, which had a MET of 17.5 ± 0.1 days. Of these, 86 were *su*, 25 were *sh2*, 3 were heterozygous for *su*, 2 were *se*, 4 were *sh2su*, 1 was a *sh2se*, 1 was a *sh2suse*, 1 was *sh2* heterozygous for *su*, and 15 were wild types. Wh07166R, We10401, B84 plus su, and wh10040R had either no plants emerge over the course of the trial or the plants that emerged died by 35 dap and, thus, a MET could not be calculated for these entries. The entries with the highest MET values (slowest to emerge) were W191218 (30.0 days), K169-1-1-1-2-2 (*sh2*) (25.0 days), K127-1-1-1-2-1-1-1-1 (*sh2*) (25.0 ± 0.0 days), Wh07165R (*sh2*) (24.5 days), and wh05070a (*sh2*) (24.5 days) (Table 3.6). MET and AUEPC were significantly negatively correlated (r = -0.38915, $P < 0.0001$).

The number of seedlings stunted by ≥25% in each plot ranged from 0 to 5 out of 12 seeds planted/plot, and was greatest when first rated at 28 dap, with an average of 1.6 ± 0.0 stunted seedlings/plot, compared to 2.1 ± 1.3 stunted seedlings/plot for GSS 3951. The average number of stunted seedlings/plot over the whole trial decreased slightly by 35 dap to 1.5 ± 0.0. A total of 365 sweet corn accessions (62.9% of 580 accessions) had less stunting than GSS 3951. Of these, 218 entries were of the *su* genotype, 95 of *sh2*, 19 of *se*, 6 were heterozygous *su*, 8 were *sh2su*, 3 of *sh2* heterozygous for *su*, 2 of *sh2suse*, 1 was *sh2se*, and 13 entries were wild types. The five entries with the least stunting (no stunted seedling/plot) were Ia5125 (*su*), C7e (*su*), C42 (*su*), G8

(*su*), and C7 (*su*). The five entries with the most stunting (with an average of 4.0 stunted plants/plot) at 35 dap included IL21f (*su*), Wh1017R (*sh2*), Separation from 183742 (*su*), wh13037 (*sh2*), and we08408 (*se*) (Table 3.6).

Vigor ratings ranged from 0 to 7 out of a maximum of 9 in comparison to a rating of 5 for the nearest plot of GSS 3951 (Fig. 3.4). Plant vigor ratings at 28 and 35 dap averaged 4.3 ± 0.0 and 4.4 ± 0.0, respectively (Table 3.5). The five Sweet CAPS diversity panel entries with the greatest vigor rating were VIII/221 (6.5 ± 0.5 at 35 dap), North Dakota Yellow Sweet Bulk (6.0 ± 0.0), Separation from 170882 (6.0 ± 0.0), Rhode Island Sweet (6.0 ± 0.0), and Nueta Sweet Corn (6.0 ± 0.0). At this date, 207 of the 580 sweet corn entries (35.7%) had vigor ratings at least as good as that of GSS 3951 (Table 3.6). Of these, 147 were of the *su* genotype, 28 of *sh2*, 7 of *se*, 4 were Heterozygous *su*, 16 were wild type lines, and 5 were *sh2su* lines.

By 49 dap, 201 of the 580 diversity panel entries (34.7%), and GSS 3951 had tillers on ≥50% of the plants in one or both plots (Table 3.6). Similar to the symptoms observed in the 2019 trial, 43 lines produced seedlings with abnormal appearances (Fig. 3.5), including pale white seedlings (8 lines), interveinal chlorosis on new and mature leaves (11 lines), general chlorosis (10 lines), and leaf dieback (17 lines) compared to other plants in the same plot and across the two plots of the same line. Some of the plants with chlorosis and dieback of leaves were only noticed 49 dap, which could have been associated with herbicide injury as the grower cooperator applied an herbicide to the entire field 41 dap.

Stand and AUEPC were significantly positively correlated ($r = 0.4923$, $P < 0.0001$). While stand and MET were negatively correlated ($r = -0.8982$, $P < 0.0001$). Stand count and number of stunted seedlings were positively correlated ($r = 0.1557$, $P = 0.0002$), as were stand count and vigor ($r = 0.6690$, $P < 0.0001$). A total of 36 entries (6.2%) performed better than GSS

3951 for all traits measured. Of these, the five best entries were Black Mexican (Het-*su*), Me121Wa (*su*), C47 (*su*), Chile 335 (Het-*su*), and Luther Hill (*su*).

Of the 182 and 580 entries screened in the 2019 and 2020 trials, respectively, 142 were planted in both trials. Among the three entries (C7e (*su*), IL104g (*su*), and 21-396-68B (*su*)) that performed better than GSS 3071 for all of the variables measured in the 2019 trial, C7e and C7e consistently fared better than GSS 3071 and GSS 3951 in the 2019 and 2020 trials, respectively. IL104g also performed well in 2019 compared to GSS 3071 in 2019. However, in 2020 this line (S190079) only ranked better than GSS 3951 for vigor (5.5 ± 0.0). 21-396-68B was similar to IL104g. In the 2019, trial 21-396-68B was ranked ≥GSS 3071 for all variables measured. However, in the 2020 trial, this entry was only better than GSS 3951 for MET (15.0 ± 2.2) and plant vigor (5.5 ± 0.5), demonstrating variation in relative cold tolerance among trials that was influenced, in part, by seed lots of the same entry, environmental conditions, and the specific standard hybrid used for comparison.

3.4 Discussion

In the 2019 field trial in this study, average air temperature and soil temperature at a 5-cm depth were ≤15°C for the first week after planting, with minimum air temperature remaining ≤15°C for the first 3 weeks. Similarly, average air and soil temperatures were ≤15°C for at least the first two weeks of the 2020 trial. Soil temperature ≤15°C are considered suboptimal for the growth of sweet corn so the first several weeks of both cold tolerance trials in this study provided suitable cold stress to screen for differences in cold tolerance among the sweet corn entries planted (Hassell et al. 2003; Miedema 1982). Air temperature even dropped below freezing temperatures for two days during the 2019 trial and six days in the 2020 trial, which provided

significant cold stress during the early stage of seed imbibition and germination in both years. Exposure of sweet corn to temperatures <6°C can injure, and even kill, sweet corn seedlings (Miedema 1982). By 10 days after planting, the average daily soil temperature was ≥15°C in both the 2019 and 2020 trials, so the first 10 days of each trial provided suitable conditions to screen for cold tolerance.

Of the 182 sweet corn lines screened in 2019, 90, 59, 118, and 26 lines were rated as good or better than GSS 3071 for AUEPC, MET, plant stunt, and plant vigor, respectively. In the 2020 field trial, 212, 132, 365, and 207 of the 580 entries screened were rated as good or better than GSS 3951 for AUEPC, MET, plant stunting, and plant vigor, respectively. Only 36 of the 580 entries (6.2%) were better than GSS 3951 for all the variables measured. These results illustrate the potential to utilize the Sweet CAPS screening panel to select entries with greater cold tolerance than currently available commercial cultivars for breeding sweet corn cultivars with better cold tolerance. GSS 3071 and GSS 3951 are both supersweet hybrids of the *sh2* endosperm genotype that are planted widely across the Columbia Basin for processing crops. Cultivars with the *sh2* genotype commonly have poorer seedling vigor compared to *su* and other sweet corn genotypes even under optimal planting conditions (Parera et al. 1995; Styer and Cantliffe 1984). The Sweet CAPS diversity panel is comprised of hybrids, Plant Introductions (PIs), and inbred lines with entries of *su*, *se*, and *sh2* endosperm genotypes, as well as others. The entries with the best cold tolerance were primarily *su* genotypes, which typically have greater cold tolerance compared to *sh2* genotypes (Hassell et al. 2003). In the 2019 and 2020 trials 165 of the 182 entries (90.7%) and 372 of 580 entries (64.1%) were *su* and *se* genotypes. Only three entries were better than GSS 3071 for all of the traits measured.

In 2019, it was primarily the *su* entries that rated better than GSS 3071 for AUEPC i.e., 88 *su* entries and 2 *sh2su* recombinant entries. Similarly, 23 *su* entries and 3 *sh2su* entries had vigor ratings similar to or better than that of GSS 3071. The three entries that fared better than GSS 3071 for all of the variables measured were all *su* lines, i.e., C7e, IL104g, and 21-396-68B. In the 2020 cold tolerance screening trial, which had a much larger number of entries than the 2019 trial, a number of *sh2* entries rated better than GSS 3951 for the cold tolerance variables measured. For example, 20 *sh2* entries rated better than GSS 3951 for AUEPC and 28 *sh2* entries had vigor ratings that were the same as or better than that of GSS 3951. Of the 36 entries that were better than GSS 3951 for all of the cold tolerance variables measured, 21 were *su*, 2 were *sh2*, 3 were heterozygous for *su*, 1 was *se*, 3 were wild types, and 1 was a *sh2su* entry. This shows the potential for selecting for cold tolerance from the Sweet CAPS germplasm collection, even among *sh2* entries. Some of the *sh2* sweet corn lines evaluated in the study by Hassell et al, (2003) performed similarly to some *su* cultivars. However, many of the *sh2* lines evaluated in this study in the Columbia Basin of Washington did not perform as well as GSS 3951, as ≤95 of 186 *sh2* entries screened, did better than GSS 3951 for the various traits measured. This reflects the results of Ordás et al. (2010) which showed that most *sh2* lines performed worse than other endosperm genotypes under cold conditions. It would be valuable to compare the more cold tolerant lines identified in these trials with some *su* and *se* commercial cultivars of sweet corn.

GSS 3071 and GSS 3951 are supersweet cultivars that are considered moderately vigorous (K. Moe, Syngenta Crop Protection LLC, *personal communication*), but there are differences between these cultivars in their vigor under cool soil conditions, which could have affected the relative vigor ratings in each trial (Ordás et al. 2010). In the 2019 trial, GSS 3071 had a mean MET of 23.2 ± 0.6 days, while GSS 3951 had a mean MET of 17.5 ± 0.1 days in the

2020 trial. Since there was two weeks in the 2020 trial in which air temperatures were ≤15°C, compared to one week in the 2019 trial, GSS 3951 may be slightly more vigorous than GSS 3071, although this could also be confounded by the quality of the specific seed lot planted of each hybrid. The average stand count and number of stunting seedlings for GSS 3071 and GSS 3951 were similar in both trials, although GSS 3071 had a greater average number of stunted seedlings compared to GSS 3951 (3.0 ± 0.2 vs. 1.9 ± 0.1 plants/plot). This could be attributed to the year, however, as the average number of stunted seedlings for all entries evaluated in 2019 (2.6 ± 0.1 plants/plot) was greater than in 2020 (1.5 ± 0.0 in 2020 seedlings/plot).

During the 2019 trial, a plot staking error occurred at planting which resulted in data for approximately 50% of the plots having to be discarded for ratings completed 14 and 21 dap. This reduced the capacity to assess about half of the lines for cold tolerance during the early stage of seed germination and seedling emergence, which is the most critical period for cold tolerance and which was the only period of the trial when cold stress conditions occurred. In addition, 104 plots were affected by bird or rodent feeding during the first 14 dap of the 2020 field trial, so the number of damaged seedlings in these plots was recorded to adjust the ratings accordingly. Following the 2019 cold tolerance screening trial, ratings in the 2020 trial were completed twice a week compared to once a week in 2019 in order to increase the ability to differentiate differences in emergence during the critical first few weeks after planting when cold stress conditions were most impactful on sweet corn growth and establishment (Tracy 1997; Tracy and Juvik 1988).

In the 2019 and 2020 cold tolerance trials, an important confounding factor to detecting genetic differences in cold tolerance among the entries screened was the potential differences in seedborne inoculum of fungi like *Fusarium* and *Penicillium* present on the seed lots planted, as

well as differences in quality of the seed lots (e.g., electrolyte leakage, immature seed). *Fusarium* and *Penicillium* species are common seedborne pathogens of sweet corn and can affect the vigor and emergence of seedlings significantly (Bacon et al. 1994; Halfon-Meire and Solel 1990; Murillo-Williams and Munkvold 2008). Similarly, soilborne inoculum of pathogenic species of *Fusarium, Pythium,* and *Rhizoctonia* could have caused some pre-emergence damping-off or stunting of seedlings (Bakker et al. 2016; Miedema 1982; Munkvold and White 2016). The PNW 127 seed treatment blend used in both trials should have minimized the confounding influence of some of the seedborne and soilborne inoculum on screening for cold tolerance, but would not have eliminated the confounding effects of differences in quality of seed lots.

In summary, this study demonstrated that some entries within the Sweet CAPS diversity panel show potential for use in breeding programs to improve the tolerance of sweet corn to cold stress. In the 2019 and 2020 field trials, 1.6 and 6.2% of the entries screened had potentially greater cold stress tolerance than the commercial hybrids, GSS 3071 and GSS 3951, respectively. Other studies have shown the potential for improving the genetic basis of cold tolerance in sweet corn germplasm (McConnell and Gardner 1979; Rodríguez et al. 2010; Tracy 1990; Viesselmann et al. 2014). Tolerance to cold soil conditions is a much-needed trait when sweet corn crops are planted in regions that regularly experience cold soil conditions, such as spring planting conditions in the Columbia Basin. Further evaluations of the most promising lines identified in these trials is needed to assess the robustness of the results and the potential of these lines for improving cold tolerance in sweet corn.

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Table 3.1. Daily air and soil temperatures and precipitation in Ephrata, WA from 10 April to 29 May 2019[a]

Date (day/month)	Daily air temperature (°C)			Average daily soil temperature at a 5-cm depth (°C)	Total daily precipitation (mm)	Total daily irrigation (mm)[b]
	Minimum	Maximum	Average			
10/4	4.7	14.7	9.8	9.7	0.00	7.57
11/4	5.5	15.1	9.4	11.4	1.27	0.00
12/4	5.1	14.4	9.3	12.6	0.25	0.00
13/4	2.8	13.4	7.5	9.4	0.51	0.00
14/4	1.5	12.6	6.8	8.3	0.00	0.00
15/4	0.0	13.4	7.3	11.0	0.00	0.00
16/4	1.6	16.1	10.4	12.3	0.00	0.00
17/4	4.4	20.4	12.5	14.45	0.00	6.53
18/4	6.3	22.8	13.6	15.3	0.00	11.23
19/4	11.9	20.9	15.8	15.8	0.00	8.38
20/4	6.6	20.2	14.5	16.8	0.00	0.00
21/4	2.6	21.5	13.0	16.7	0.00	0.00
22/4	2.5	21.6	12.8	16.6	0.00	0.00
23/4	9.4	21.4	15.2	17.9	0.00	6.30
24/4	3.5	20.7	12.8	17.7	0.00	2.46
25/4	4.0	19.6	13.3	16.6	0.00	0.00
26/4	9.6	20.9	14.9	18.7	0.00	0.00
27/4	2.9	14.0	9.1	16.4	0.00	5.33
28/4	1.6	15.2	9.0	14.9	0.00	3.35
29/4	-1.2	17.0	9.4	16.3	0.00	0.00
30/4	1.6	18.4	11.1	17.3	0.00	0.00
1/5	1.7	19.1	10.4	16.9	0.00	0.00
2/5	3.7	20.0	12.8	18.3	0.00	0.00
3/5	5.3	21.1	13.3	19.2	0.00	0.00
4/5	3.9	24.0	14.8	20.1	0.00	0.00
5/5	10.4	25.3	18.7	22.3	0.00	0.00
6/5	7.6	25.7	17.3	22.3	0.00	0.00
7/5	10.8	27.3	20.1	23.8	0.00	11.91
8/5	13.3	27.6	19.8	23.8	0.00	4.95
9/5	11.5	25.1	18.2	24.6	0.00	0.00
10/5	6.4	27.5	18.2	24.2	0.00	0.00
11/5	8.2	29.2	19.3	25.1	0.00	0.00
12/5	11.8	26.9	19.3	23.9	0.00	0.00
13/5	8.1	27.6	18.1	23.3	0.00	0.00
14/5	7.8	19.4	13.5	20.0	0.00	0.00
15/5	4.1	18.7	12.6	18.1	0.25	7.72
16/5	9.4	21.3	14.4	18.0	6.86	3.30
17/5	8.5	20.6	14.1	17.6	1.27	0.00
18/5	4.9	20.3	13.7	18.5	0.00	0.00
19/5	11.7	23.1	16.1	21.2	0.00	0.00
20/5	9.7	20.8	15.8	20.7	0.00	0.61
21/5	10.0	20.5	15.5	21.1	0.00	6.10
22/5	13.5	22.4	17.7	21.8	0.00	5.15
23/5	7.2	27.4	19.1	23.5	0.00	3.40
24/5	12.2	19.4	14.9	20.6	3.56	11.50
25/5	11.1	20.4	15.2	19.5	0.00	8.33
26/5	12.4	17.1	14.7	16.7	13.97	10.61
27/5	14.8	26.7	20.4	20.3	0.00	0.00
28/5	13.1	29.1	20.4	23.3	0.00	0.00
29/5	11.8	28.8	20.5	24.7	0.00	2.31
Mean or total	7.0	21.1	14.3	18.4	27.94	127.04

[a] Recorded at the Washington State University AgWeatherNet (weather.wsu.edu) station located near Ephrata, WA (47.18°N, 119.64°W).

[b] The trial was located in a ~50-ha crop of processing sweet corn that was irrigated by center-pivot. Details on the amount irrigation were provided by the grower.

Table 3.2. Sweet corn stand counts, number of stunted seedlings, and vigor rating recorded at weekly intervals in a sweet corn cold tolerance screening field trial near George, WA in 2019[a]

Date (days after planting)	Diversity panel vs. GSS 3071	Plant stand (out of 12 seed planted/plot)		Number of stunted plants (out of 12 seeds planted/plot)		Vigor rating (0 to 9)	
		Mean	Range	Mean	Range	Mean	Range
24/4/2019	182 lines	1.1 ± 0.2[b]	0 – 11	-	-	-	-
(14)	GSS 3071	1.3 ± 0.3	0 – 7				
01/4/2019	182 lines	7.1 ± 0.3	0 – 12	-	-	-	-
(21)	GSS 3071	7.9 ± 0.3	4 – 11				
08/4/2019	182 lines	7.8 ± 0.2	0 – 12	2.8 ± 0.1	0 – 8	3.8 ± 0.1	0 – 7
(28)	GSS 3071	8.7 ± 0.3	4 – 12	3.1 ± 0.2	0 – 5	5.0 ± 0.0	3 – 5
15/4/2019	182 lines	7.8 ± 0.2	0 – 12	2.6 ± 0.1	0 – 9	3.9 ± 0.1	0 – 7
(35)	GSS 3071	8.8 ± 0.2	4 – 12	3.0 ± 0.2	0 – 5	5.0 ± 0.0	5 – 5
22/4/2019	182 lines	7.8 ± 0.2	0 – 12	2.5 ± 0.1	0 – 9	3.8 ± 0.1	0 – 7
(42)	GSS 3071	8.9 ± 0.3	4 – 12	2.9 ± 0.1	0 – 5	5.0 ± 0.0	5 – 5
29/4/2019	182 lines	7.8 ± 0.2	0 – 12	2.1 ± 0.1	0 – 9	3.8 ± 0.1	0 – 7
(49)	GSS 3071	9.0 ± 0.3	4 – 12	2.4 ± 0.1	0 – 5	5.0 ± 0.0	5 – 5

[a] Twelve seed were planted into each of two replicate plots for each sweet corn line. GSS 3071 was planted as a standard, *sh2*, processing sweet corn hybrid in 56 replicate plots scattered throughout the trial.

[b] Mean ± standard error.

[c] Counts of the number of stunted seedlings per plot and vigor ratings (0 = no plants emerged, 5 = same vigor as the nearest plot of GSS 3071, and 9 = most vigorous plots in the trial at that rating date) recorded 28 days after planting.

Table 3.3. Area under the emergence progress curve (AUEPC), mean emergence time (MET), plant vigor, stand count, number of stunted seedlings/plot, and lines producing tillers in a sweet corn cold tolerance screening trial planted near George, WA in April 2019

Sweet corn line[a]	Genotype[a]	Entry[a]	AUEPC[b]	MET (days)[cde]	Plant stand (35 dap)[e]	Plant vigor (0 to 9) (35 dap)[ce]	Number of stunted seedlings/12 seed planted (35 dap)[ce]	≥ 50% of plants with tillers (49 dap)[eg]
IL451b	*su*	F170276	390.3	18.7 ± 1.8	12.0 ± 0.0	4.5 ± 0.5	2.5 ± 0.5	+
IaCG4189	*su*	F170099	386.8	19.3 ± 2.3	12.0 ± 0.0	4.0 ± 0.0	3.0 ± 0.0	+
IL44b	*su*	F170273	381.5	20.1 ± 0.9	12.0 ± 0.0	3.5 ± 0.5	2.5 ± 0.5	+
A15	*su*	F170073	374.5	18.9 ± 1.4	11.5 ± 0.5	4.5 ± 0.5	3.5 ± 1.5	
C90	*su*	F170117	374.5	21.3 ± 0.3	12.0 ± 0.0	4.0 ± 0.0	6.0 ± 1.0	
IL699e	*su*	F170179	369.3	21.0 ± 1.7	12.0 ± 0.0	4.5 ± 0.5	4.5 ± 0.5	
STRAIN 465A-421-68B	*su*	F170030	357.0	18.5 ± 2.6	11.0 ± 0.0	5.5 ± 0.5*	3.5 ± 1.5	
Ma5125	*su*	F170216	357.0	22.8 ± 0.0	12.0 ± 0.0	3.5 ± 0.5	4.5 ± 0.5	
C7e	*su*	F170123	353.5	21.6 ± 6.4	12.0 ± 0.0	5.5 ± 0.5*	2.0 ± 1.0	+
A684su	*su*	F170061	344.8	19.7 ± 0.6	11.0 ± 0.0	4.0 ± 0.0	4.0 ± 1.0	
IL328a	*su*	F170093	343.0	23.3 ± 4.7	12.0 ± 0.0	5.0 ± 0.0*	2.0 ± 0.0	+
IL104g	*su*	F170084	339.5	21.0 ± 7.0	11.5 ± 0.5	6.0 ± 0.0*	2.5 ± 1.5	+
MDM 17	*su*	F170172	339.5	21.6 ± 0.0	11.0 ± 0.0	4.5 ± 0.5	3.0 ± 0.0	+
IP39	*su*	F170229	336.0	22.5 ± 5.5	11.5 ± 0.5	4.5 ± 0.5	4.0 ± 0.0	+
P35	*su*	F170034	332.5	20.7 ± 0.3	10.5 ± 0.5	4.5 ± 0.5	2.0 ± 0.0	
IL21f	*su*	F170100	330.8	21.3 ± 0.3	11.0 ± 0.0	2.5 ± 0.5	6.5 ± 1.5	
STRAIN T20-2-68B	*su*	F170024	329.0	25.1 ± 2.2	12.0 ± 0.0	3.5 ± 0.5	3.5 ± 0.5	
P39M94	*su*	F170044	329.0	23.6 ± 4.4	11.5 ± 0.5	4.5 ± 0.5	1.0 ± 1.0	+
IL323a	*su*	F170092	329.0	22.9 ± 5.1	11.5 ± 0.5	4.5 ± 0.5	2.5 ± 0.5	+
IL788a	*su*	F170144	329.0	22.9 ± 5.1	11.5 ± 0.5	5.5 ± 0.5*	3.0 ± 0.0	+
NJ159	*su*	F170048	327.3	20.3 ± 0.7	10.0 ± 0.0	6.0 ± 0.0*	2.5 ± 0.5	+
M5	*su*	F170232	327.3	21.0 ± 0.0	10.5 ± 0.5	4.0 ± 0.0	4.0 ± 0.0	
P39xRp1d	*su*	F170016	323.8	24.5 ± 3.5	11.5 ± 0.5	4.0 ± 0.0	1.5 ± 0.5	+
P51xRp1d	*su*	F170020	320.3	23.2 ± 4.8	11.0 ± 0.0	4.0 ± 0.0	3.5 ± 2.5	+
STRAIN T24-395-68B	*su*	F170022	320.3	23.0 ± 5.0	11.0 ± 1.0	4.5 ± 0.5	3.0 ± 0.0	
IaEV3004	*su*	F170115	320.3	24.8 ± 3.2	11.5 ± 0.5	3.0 ± 0.0	3.0 ± 0.0	
IL100K	*su*	F170120	320.3	24.5 ± 3.5	11.5 ± 0.5	5.0 ± 0.0*	0.5 ± 0.5	+
M822	*su*	F170228	320.3	22.1 ± 0.5	10.5 ± 1.5	3.5 ± 0.5	0.5 ± 0.5	+
IL368a	*su*	S181497	318.5	24.5 ± 3.5	11.5 ± 0.5	3.0 ± 0.0	2.5 ± 1.5	+
P14	*su*	F170027	316.8	25.1 ± 2.9	11.5 ± 0.5	4.0 ± 0.5	3.5 ± 1.5	+
P39	*su*	F170038	316.8	24.8 ± 3.2	11.5 ± 0.5	4.0 ± 0.0	2.5 ± 0.5	+
C40	*su*	F170247	316.8	24.8 ± 3.2	11.5 ± 0.5	5.0 ± 0.0*	2.0 ± 0.0	+
21-396-68B	*sh2su*	F170131	315.0	23.2 ± 4.8	11.0 ± 0.0	6.0 ± 0.0*	1.0 ± 0.0	
STRAIN T33-399-68B	*su*	F170021	313.3	22.8 ± 5.3	11.0 ± 1.0	4.5 ± 0.5	1.5 ± 0.5	

Sweet corn line[a]	Genotype[a]	Entry[a]	AUEPC[b]	MET (days)[cde]	Plant stand (35 dap)[e]	Plant vigor (0 to 9) (35 dap)[ce]	Number of stunted seedlings/12 seed planted (35 dap)[ce]	≥ 50% of plants with tillers (49 dap)[eg]
IL793a	*su*	F170180	311.5	21.4 ± 0.4	10.0 ± 2.0	4.0 ± 0.0	2.0 ± 0.0	
P39LE_261_61	*su*	F170042	309.8	24.2 ± 3.8	11.0 ± 0.0	4.0 ± 0.0	2.0 ± 0.0	+
Luther_Hill	*su*	F170210	309.8	23.9 ± 4.1	11.0 ± 0.0	4.0 ± 0.0	3.5 ± 0.5	+
IL86e	*su*	S181449	308.0	24.5 ± 3.5	11.0 ± 0.0	4.5 ± 0.5	2.0 ± 1.0	
C65	*su*	F170253	306.3	22.6 ± 5.4	10.5 ± 0.5	4.0 ± 0.0	3.0 ± 1.0	
IL325a	*su*	F170088	301.0	25.4 ± 2.6	11.0 ± 1.0	4.0 ± 0.0	3.5 ± 0.5	
IL671a	*su*	F170156	301.0	24.9 ± 3.2	11.0 ± 1.0	4.5 ± 0.5	3.0 ± 0.0	
IL713a	*su*	F170173	301.0	20.7 ± 0.5	9.5 ± 0.5	4.0 ± 0.0	2.5 ± 0.5	+
IL773a	*su*	F170157	299.3	26.4 ± 2.2	11.5 ± 0.5	3.5 ± 0.5	6.0 ± 0.0	
IA2132	*su*	GRIN 487	299.3	22.1 ± 2.5	10.0 ± 0.0	3.0 ± 0.0	3.5 ± 2.5	
Jubileeex9017	*su*	F170193	295.8	24.5 ± 3.5	10.5 ± 0.5	5.0 ± 0.0*	2.5 ± 0.5	
P39M96	*su*	F170043	294.0	28.0 ± 0.0[h]	12.0 ± 0.0	5.0 ± 0.0*	3.0 ± 0.0	+
P51	*su*	F170051	294.0	28.0 ± 0.0[h]	12.0 ± 0.0	5.0 ± 0.0*	2.5 ± 1.5	+
IL395a	*su*	F170078	294.0	28.0 ± 0.0[h]	12.0 ± 0.0	3.0 ± 1.0	5.5 ± 1.5	
NJ618	*su*	F170169	294.0	28.0 ± 0.0[h]	12.0 ± 0.0	4.0 ± 1.0	2.5 ± 0.5	
IL689a	*su*	F170192	294.0	28.0 ± 0.0[h]	12.0 ± 0.0	5.5 ± 0.5*	4.0 ± 1.0	+
SD883	*su*	F170259	294.0	28.0 ± 0.0[h]	12.0 ± 0.0	4.5 ± 0.5	5.5 ± 0.5	
MDM 18	*su*	F170166	292.3	22.1 ± 6.0	10.0 ± 0.0	4.0 ± 1.0	3.5 ± 0.5	+
IL798c	*su*	F170206	292.3	24.1 ± 4.5	10.5 ± 0.5	3.5 ± 0.5	6.0 ± 3.0	
A7	*su*	F170267	292.3	19.0 ± 0.6	9.0 ± 1.0	4.0 ± 0.0	3.5 ± 0.5	
Cuzco_suse	*su*	GRIN 108	292.3	22.9 ± 5.1	10.0 ± 1.0	6.0 ± 1.0*	2.5 ± 0.5	
IL648	*su*	F170146	285.3	22.6 ± 0.4	9.5 ± 2.5	4.0 ± 0.0	3.5 ± 1.5	
SD909	*su*	F170138	283.5	24.2 ± 3.9	10.0 ± 0.0	4.0 ± 1.0	4.0 ± 0.0	+
STRAIN 451B-4-68B	*su*	F170026	281.8	28.0 ± 0.0[h]	11.5 ± 0.5	4.0 ± 0.0	3.0 ± 0.5	+
P39_10_226	*su*	F170036	281.8	24.2 ± 3.9	10.0 ± 0.0	4.0 ± 0.0	3.5 ± 0.5	
IL112t	*su*	F170083	281.8	28.0 ± 0.0[h]	11.5 ± 0.5	5.0 ± 0.0*	3.5 ± 0.5	+
IL303b	*su*	F170096	281.8	28.0 ± 0.0[h]	11.5 ± 0.5	5.0 ± 0.0*	1.5 ± 0.5	+
Me135	*su*	F170125	281.8	28.0 ± 0.0[h]	11.5 ± 0.5	5.5 ± 0.5*	3.5 ± 0.5	+
IL764b	*su*	F170196	281.8	20.6 ± 0.4	9.0 ± 0.0	3.5 ± 0.5	4.0 ± 0.0	
ILB5870	*su*	F170231	281.8	28.0 ± 0.0[h]	11.5 ± 0.5	3.5 ± 0.5	3.5 ± 0.5	
IL430a	*su*	F170080	280.0	28.0 ± 0.0[h]	11.5 ± 0.5	4.5 ± 0.5	3.5 ± 0.5	+
C31	*su*	F170255	280.0	28.0 ± 0.0[h]	11.5 ± 0.5	4.5 ± 0.5	3.5 ± 0.5	
IL393a	*su*	F170070	278.3	23.4 ± 1.1	9.5 ± 1.5	3.0 ± 0.0	4.0 ± 0.0	
GTS1	*su*	F170105	276.5	21.8 ± 0.0	9.0 ± 0.0	3.5 ± 0.5	2.0 ± 0.0	+
IL802b_Ht2	*su*	F170202	273.0	25.2 ± 2.8	10.0 ± 0.0	4.0 ± 0.0	5.0 ± 1.0	
Slatka_Pukanka	*su*	S181053	273.0	24.9 ± 3.1	10.0 ± 1.0	5.00*[f]	3.0 ± 1.0	+
Ia453 su1	*su*	F170103	269.5	28.0 ± 0.0[h]	11.0 ± 0.0	4.0 ± 1.0	2.0 ± 0.0	+
IL678a	*su*	F170154	269.5	25.3 ± 2.7	10.0 ± 1.0	3.0 ± 0.0	4.0 ± 1.0	
NJ112	*su*	F170171	269.5	28.0 ± 0.0[h]	11.0 ± 1.0	5.5 ± 0.5*	3.5 ± 0.5	+
Me121 wb	*su*	F170219	269.5	28.0 ± 0.0[h]	11.0 ± 1.0	4.5 ± 0.5	1.5 ± 1.5	

Sweet corn line[a]	Genotype[a]	Entry[a]	AUEPC[b]	MET (days)[cde]	Plant stand (35 dap)[e]	Plant vigor (0 to 9) (35 dap)[ce]	Number of stunted seedlings/12 seed planted (35 dap)[ce]	≥ 50% of plants with tillers (49 dap)[eg]
C42	*su*	F170249	269.5	28.0 ± 0.0[h]	11.0 ± 0.0	4.0 ± 0.0	2.5 ± 0.5	+
Andjar_bekaa	*sh2su*	GRIN 171	269.5	28.0 ± 0.0[h]	11.0 ± 0.0	7.0 ± 0.0*	3.0 ± 1.0	+
IL11D	*su*	F170081	267.8	25.6 ± 2.5	10.0 ± 0.0	3.5 ± 0.5	4.5 ± 0.5	+
No_156	*su*	S181162	267.8	24.5 ± 3.5	9.5 ± 0.5	3.5 ± 0.5	4.5 ± 0.5	+
IaEV3015	*su*	F170077	264.3	25.6 ± 1.6	10.0 ± 0.0	3.0 ± 0.0	3.0 ± 1.0	
MDM_21	*su*	F170143	264.3	24.5 ± 3.5	9.5 ± 0.5	3.0 ± 0.0	4.5 ± 0.5	+
IL103a	*su*	F170082	262.5	24.9 ± 3.9	9.5 ± 0.5	3.5 ± 0.5	4.5 ± 0.5	
STRAIN T35-388-68A	*su*	F170015	260.8	23.9 ± 4.1	9.0 ± 3.0	5.5 ± 0.5*	2.0 ± 0.0	+
C81	*su*	F170118	257.3	28.0 ± 0.0[g]	10.5 ± 0.5	4.0 ± 0.0	3.0 ± 0.0	+
IL615a	*su*	F170148	257.3	21.3 ± 5.8	8.5 ± 0.5	3.5 ± 0.5	3.5 ± 0.5	
IL767b	*su*	F170195	257.3	28.0 ± 0.0[g]	10.5 ± 0.5	4.0 ± 0.0	3.0 ± 1.0	
ARZM_21_007	su	S181240	255.5	23.1 ± 4.9	8.5 ± 1.5	4.0 ± 0.0	2.5 ± 0.5	+
IL707a	*su*	S181406	255.5	26.7 ± 1.3	10.0 ± 2.0	3.5 ± 0.5	3.5 ± 0.5	+
STRAIN 11D-586-68A	su	F170025	252.0	24.5 ± 3.5	9.0 ± 0.0	3.0 ± 0.0	3.0 ± 2.0	
C8pseudo	*su*	F170270	248.5	28.0 ± 0.0[h]	10.0 ± 2.0	4.0 ± 0.0	4.0 ± 0.0	+
Me123	*su*	GRIN 37	248.5	24.9 ± 3.1	9.0 ± 0.0	3.0 ± 0.0	3.5 ± 0.5	+
SC6069	*su*	F170050	245.0	23.3 ± 4.7	8.5 ± 0.5	5.0 ± 0.0*	3.5 ± 0.5	
IL733a	*su*	F170187	245.0	28.0 ± 0.0[h]	11.0 ± 1.0	3.0 ± 0.0	4.0 ± 0.0	
IL729a	*su*	F170209	245.0	28.0 ± 0.0[h]	10.0 ± 0.0	4.0 ± 0.0	3.5 ± 0.5	
Separation_from_177107	su	GRIN 218	243.3	22.9 ± 0.5	6.0 ± 0.0	3.0 ± 0.0	4.0 ± 0.0	+
AS11_Sweet_corn_poplation	*su*	S181168	243.3	22.9 ± 1.1	8.0 ± 1.0	3.5 ± 0.5	4.0 ± 1.0	
IL454a	*su*	F170266	241.5	22.4 ± 0.6	8.0 ± 1.0	3.0 ± 0.0	3.5 ± 0.5	+
IL124a	*su*	F170068	238.0	24.9 ± 3.9	9.0 ± 1.0	4.5 ± 0.5	4.5 ± 0.5	+
IL31a	*su*	S181413	232.8	28.0 ± 0.0[h]	9.5 ± 0.5	3.0 ± 0.0	3.5 ± 1.5	
IL766a	*se*	F170207	231.0	24.9 ± 3.1	8.5 ± 0.5	4.0 ± 0.0	3.0 ± 0.0	
ARZM_19_057	*su*	S181194	231.0	26.7 ± 1.3	9.0 ± 1.0	4.0 ± 0.0	3.5 ± 0.5	+
Early_Evergreen	*su*	S181218	227.5	25.2 ± 2.7	8.5 ± 0.5	4.0 ± 0.0	4.5 ± 0.5	+
B5870	*su*	F170114	225.8	28.0 ± 0.0[h]	9.0 ± 1.0	3.5 ± 0.5	2.0 ± 1.0	
MDM_1	*su*	F170175	220.5	28.0 ± 0.0[h]	9.0 ± 1.0	3.0 ± 0.0	4.5 ± 0.5	
IL796a	*su*	F170211	215.3	24.9 ± 3.2	7.5 ± 2.5	4.0 ± 0.0	2.5 ± 0.5	
IL366a	*su*	F170085	213.5	22.2 ± 1.2	7.0 ± 1.0	3.5 ± 0.5	2.5 ± 1.5	
Cubano	*su*	GRIN 243	213.5	23.1 ± 1.7	9.5 ± 1.5	5.5 ± 0.5*	2.5 ± 0.5	
MDM_2	*su*	F170161	208.3	28.0 ± 0.0[h]	8.5 ± 0.5	3.0 ± 0.0	3.5 ± 0.5	+
C15	*su*	GRIN 13	208.3	24.5 ± 3.5	7.5 ± 0.5	4.0 ± 0.0	2.5 ± 2.0	+
Chile_335	WT	S181227	208.3	28.0 ± 0.0[h]	8.5 ± 1.5	4.5 ± 0.5	2.5 ± 0.5	+
IL279AxRp1d	*su*	F170111	206.5	18.2 ± 4.2	6.0 ± 1.0	2.0 ± 0.0	5.0 ± 1.0	
Sunshine	*su*	S181228	206.5	24.9 ± 3.1	7.5 ± 0.5	4.5 ± 0.5	2.5 ± 0.5	+
Separation_from_170882	WT	GRIN 217	203.0	24.5 ± 3.5	9.5 ± 0.5	4.5 ± 0.5	3.0 ± 1.0	
P737M20	*sh2su*	S181177	203.0	24.2 ± 2.4	7.0 ± 2.0	2.5 ± 0.5	2.5 ± 0.5	+
IL437a	*su*	F170095	201.3	28.0 ± 0.0[h]	8.0 ± 1.0	4.5 ± 0.5	2.0 ± 1.0	

Sweet corn line[a]	Genotype[a]	Entry[a]	AUEPC[b]	MET (days)[cde]	Plant stand (35 dap)[e]	Plant vigor (0 to 9) (35 dap)[ce]	Number of stunted seedlings/12 seed planted (35 dap)[ce]	≥ 50% of plants with tillers (49 dap)[eg]
IL794a	*su*	F170142	201.3	28.0 ± 0.0[h]	8.0 ± 2.0	4.0 ± 0.0	4.0 ± 0.0	
Amarillo_dulce	*su*	S181144	201.3	24.9 ± 3.2	7.0 ± 3.0	3.5 ± 0.5	3.0 ± 1.0	+
CHZM_08_129	*su*	S181057	196.0	28.0 ± 0.0[h]	8.0 ± 0.0	4.5 ± 0.5	3.0 ± 1.0	+
C27	*su*	S181345	196.0	28.0 ± 0.0[h]	8.0 ± 0.0	3.5 ± 0.5	3.0 ± 0.0	
ILB5765	*se*	F170222	194.3	28.0 ± 0.0[h]	8.0 ± 0.0	3.0 ± 1.0	4.5 ± 0.5	
IL465a	*su*	F170264	192.5	25.7 ± 2.3	7.0 ± 2.0	4.0 ± 0.0	2.5 ± 0.5	
Ia4189	*su*	F170101	189.0	22.5 ± 0.3	6.5 ± 0.5	3.5 ± 0.5	2.0 ± 1.0	+
Ma32	*su*	F170208	189.0	21.0 ± 0.0	6.0 ± 3.0	4.5 ± 0.5	2.5 ± 2.5	+
Separation_from_177589	*su*	GRIN 219	180.3	22.9 ± 0.6	5.5 ± 2.5	3.0 ± 0.0	3.0 ± 2.0	+
MDM_16	*su*	F170160	173.3	24.9 ± 3.9	6.5 ± 1.5	3.5 ± 0.5	2.5 ± 1.5	
C1540	WT	F170254	173.3	27.6 ± 1.5	7.0 ± 4.0	2.0 ± 0.0	2.5 ± 0.5	
Millersburg_Red_Sweet_No2	*su*	S181187	173.3	25.7 ± 2.3	6.5 ± 0.5	4.0 ± 0.0	3.0 ± 0.0	+
IL676a	*su*	F170145	171.5	28.0 ± 0.0[h]	7.0 ± 1.0	3.0 ± 0.0	3.0 ± 0.0	+
Tawaktci	*sh2*	S181245	169.8	26.3 ± 1.8	6.5 ± 0.5	3.5 ± 0.5	2.5 ± 0.5	+
PAIA_453	WT	GRIN 154	168.0	24.5 ± 3.5	6.0 ± 0.0	4.0 ± 0.0	2.0 ± 0.0	
West_Brookfield_white_sweet	*su*	GRIN 246	168.0	22.5 ± 3.2	4.0 ± 2.0	2.0 ± 0.0	2.0 ± 1.0	+
Maiz_Amarilla_Evergreen	*su*	S181100	162.8	22.9 ± 0.5	5.5 ± 0.5	4.0 ± 1.0	2.5 ± 0.5	+
ARZM_21_018	*su*	S181067	152.3	25.1 ± 1.2	5.5 ± 1.5	3.5 ± 0.5	1.5 ± 1.5	+
Olcott	*su*	S181455	143.5	24.2 ± 2.0	5.0 ± 1.0	4.0 ± 0.0	1.0 ± 1.0	+
Separation_from_183742	*su*	S181166	140.0	28.0 ± 0.0[h]	5.5 ± 0.5	4.5 ± 0.5	2.0 ± 0.0	+
Oregon_Evergreen-1	*sh2su*	S181174	136.5	25.2 ± 2.8	5.0 ± 2.0	4.0 ± 0.0	1.0 ± 0.0	+
ARZM_21_008	*su*	S181171	134.8	28.0 ± 0.0[h]	5.5 ± 2.5	5.0 ± 0.0*	1.0 ± 1.0	+
Golden_Bantam	*su*	S180996	129.5	19.3 ± 1.8	4.0 ± 0.0	4.5 ± 0.5	1.0 ± 0.0	+
IL777a	*su*	F170164	122.5	28.3 ± 1.5	5.0 ± 1.0	3.0 ± 0.0	3.5 ± 0.5	
IL765a	*su*	F170194	117.3	26.8 ± 1.2	4.5 ± 1.5	3.0 ± 0.0	3.5 ± 1.5	
Z07_001	*su*	GRIN 343	117.3	26.8 ± 3.0	4.5 ± 0.5	3.5 ± 0.5	1.0 ± 0.0	+
908	*su*	GRIN 236	115.5	25.4 ± 1.2	3.0 ± 0.0	3.5 ± 0.5	1.0 ± 0.0	
Oregon_Evergreen-2	*sh2su*	S181224	110.3	21.0 ± 0.0	3.5 ± 1.5	4.0 ± 0.0	1.5 ± 0.5	+
Golden_Giant	*su*	S180983	108.5	24.5 ± 3.5	4.0 ± 1.0	3.0 ± 0.0	2.0 ± 1.0	+
83612b	*su*	F170258	101.5	26.3 ± 1.8	4.0 ± 2.0	3.5 ± 0.5	0.5 ± 0.5	
Atkinson	*sh2su*	S181229	101.5	24.5 ± 3.5	3.5 ± 0.5	4.0 ± 0.0	0.5 ± 0.5	+
NJ116Wa	*su*	GRIN 42	98.0	28.0 ± 0.0[h]	4.0 ± 1.0	3.0 ± 1.0	2.0 ± 2.0	+
ARZM_20_006	*su*	S181030	98.0	28.0 ± 0.0[h]	4.0 ± 0.0	3.5 ± 0.5	2.0 ± 0.0	+
IL761a	*su*	F170191	96.3	25.4 ± 2.6	3.5 ± 0.5	3.5 ± 0.5	1.0 ± 0.0	+
Separation_from_177642	*su*	GRIN 222	96.3	27.6 ± 0.4	4.5 ± 0.5	3.0 ± 0.0	2.5 ± 0.5	
NE_HY_13A	*su*	S181111	94.5	21.0 ± 0.00	3.0 ± 2.0	4.5 ± 0.5	0.5 ± 0.5	+
197A-381-68A	*su*	GRIN 280	87.5	28.6 ± 0.6	4.0 ± 0.0	3.5 ± 0.5	1.0 ± 1.0	
IL797a	*su*	F170182	85.8	28.0 ± 0.0[h]	3.5 ± 2.5	4.0 ± 0.0	2.0 ± 2.0	
Late_Mammoth	*su*	S181004	85.8	28.0 ± 0.0[h]	3.5 ± 0.5	3.0 ± 0.0	2.0 ± 0.0	+

Sweet corn line[a]	Genotype[a]	Entry[a]	AUEPC[b]	MET (days)[cde]	Plant stand (35 dap)[e]	Plant vigor (0 to 9) (35 dap)[ce]	Number of stunted seedlings/12 seed planted (35 dap)[ce]	≥ 50% of plants with tillers (49 dap)[eg]
789	*su*	S181028	85.8	28.0 ± 0.0[h]	3.5 ± 0.5	3.5 ± 0.5	1.5 ± 0.5	+
469	*su*	S181173	85.8	28.0 ± 0.0[h]	3.5 ± 0.5	3.0 ± 0.0	1.5 ± 0.5	+
Ranniaya_Zolotaya_401	*su*	S181099	82.3	28.7 ± 0.7	3.5 ± 1.5	3.5 ± 0.5	1.5 ± 0.5	+
AS12	*sh2su*	S181119	73.5	28.0 ± 0.0[h]	3.0 ± 1.0	2.5 ± 0.5	1.5 ± 0.5	
ARZM_19_051	*su*	S181238	70.0	22.8 ± 5.3	2.5 ± 0.5	4.0 ± 0.0	0.5 ± 0.5	+
IL778c	*su*	F170163	63.0	21.0[e]	2.0 ± 2.0	2.0[f]	1.0 ± 1.0	
NE_HY_13b	*su*	S181003	61.3	28.0 ± 0.0[h]	2.5 ± 1.5	4.0 ± 0.0	1.5 ± 1.5	
ARMZ_21_002	*su*	S181129	61.3	28.0 ± 0.0[h]	2.5 ± 0.5	3.5 ± 1.5	1.0 ± 0.0	+
Ia2730	*su*	S181429	57.8	26.3 ± 2.5	2.5 ± 0.0	1.0 ± 0.0	1.0 ± 0.0	
IL673a	*su*	F170158	54.3	21.0 ± 7.0	2.0 ± 1.0	4.0 ± 1.0	0.5 ± 0.5	+
IL125a	*su*	F170067	49.0	28.0[f]	2.0 ± 2.0	3.0[f]	2.0[f]	
Doce_de_Cuba	*su*	S181031	49.0	28.0 ± 0.0[h]	2.0 ± 0.0	1.0 ± 1.0	0.0 ± 0.0	
IL200e	*su*	F170062	45.5	21.0[f]	1.5 ± 1.5	3.0[f]	2.0[f]	+
Sonora_22	*su*	S181054	43.8	24.5 ± 3.5	1.5 ± 0.5	3.0 ± 0.0	0.5 ± 0.5	+
Tesuque_Pueblo	WT	S180977	36.8	28.0 ± 0.0[h]	1.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0	+
K43-1(x7)	*sh2*	S182454	36.8	28.0[f]	1.5 ± 1.5	3.0[f]	1.0[f]	
Golden_Bantam	*su*	S181007	31.5	21.0 ± 0.0	1.0 ± 0.0	3.5 ± 0.5	0.0 ± 0.0	+
Chihuahua_151	*su*	S181068	28.0	24.5 ± 3.5	1.0 ± 0.0	4.0 ± 1.0	0.0 ± 0.0	+
STRAIN T32-397-68B	*su*	S180968	24.5	28.0 ± 0.0[h]	1.0 ± 0.0	3.5 ± 0.5	0.0 ± 0.0	
P737M20	*sh2su*	S181170	24.5	28.0 ± 0.0[h]	1.0 ± 0.0	1.0 ± 0.0	0.0 ± 0.0	
NE_EDR_sh2	*sh2*	S181233	24.5	28.0[f]	1.0 ± 1.0	1.0[f]	1.0[f]	
MDM_15	*su*	F170159	15.8	21.0[f]	0.5 ± 0.5	4.0[f]	0.0[f]	+
Glancaster_sh2	*sh2*	GRIN 81	15.8	21.0[f]	0.5 ± 0.5	4.0[f]	0.0[f]	+
Z07_002	*su*	S181191	15.8	21.0[f]	0.5 ± 0.5	4.0[f]	0.0[f]	+
34f	*su*	F170279	12.3	28.0[f]	0.5 ± 0.5	1.5 ± 1.5	0.0[f]	
Red_NCLB	*su*	S181160	12.3	28.0[f]	0.5 ± 0.5	0.0[f]	0.0[f]	
ARZM_19_051	*su*	S181200	12.3	28.0[f]	0.5 ± 0.5	0.0[f]	0.0[f]	
MSR_su	*su*	S181209	0.0	-	0.0 ± 0.0	-	-	-
GSSS_sh2	*sh2*	S181239	0.0	-	0.0 ± 0.0	-	-	-
GSS 3071	*sh2*	GSS 3071[i]	245.9	23.2 ± 0.6	8.8 ± 0.2	5.0 ± 0.0	3.0 ± 0.2	+
Mean[c]			216.1 ± 7.7	24.6 ± 0.3	7.8 ± 0.2	3.9 ± 0.1	2.6 ± 0.1	-
Range[c]			0.00 – 390.3	18.2 – 28.1	0.0 – 12.0	0.0 – 7.0	0.0 – 9.0	-

[a] The lines included in this trial are a subset of the accession panel of the United States Department of Agriculture National Institute of Food and Agriculture Specialty Crops Research Initiative Project No. 2018-51181-28419. Sweet corn line refers to the designated name of the sweet corn accession. Entry = refers to the sweet corn accession and seed lot. Genotype refers to the endosperm type of the sweet corn accession: NA = no information, field = standard field corn type, *su = sugary 1*, *se = sugary enhanced*, *sh2 = shrunken 2*.

[b] AUEPC = Area under the emergence progress curve as calculated by Sun et al. (2015) for stand counts recorded weekly from 14 to 49 days after planting (dap). Sweet corn lines are arranged in order of largest to smallest mean AUEPC value.

[c] Mean ± standard error. Refer to the main text for details on how mean plant stand/plot, mean number of stunted seedlings/plot, and mean plant vigor were rated. The 24 sweet corn lines with an asterisk after the vigor rating had a mean vigor rating at least as good as that of the standard *sh2* processing hybrid, GSS 3071, planted throughout the trial.

[d] Mean emergence time (MET) in days, as calculated by Demir and Matthews (2010).

[e] '-' = No plants emerged in both replicate plots so stunting, tiller production, and vigor could not be rated.

[f] Lines without a standard error only had plants emerge in one of the two replicate plots.

[g] '+' = Lines with plots in which ≥50% of the plants produced tillers.

[h] An error occurred in staking some the plots at planting, which was recognized 28 dap. As a result, the incorrect stand counts recorded 14 and 21 dap for those plots were excluded from the calculations of AUEPC and MET.

[i] GSS 3071 was planted in 56 plots scattered throughout the trial as a standard, *sh2,* processing sweet corn hybrid commonly grown in the Columbia Basin of central Washington and northcentral Oregon.

Table 3.4. Daily air and soil temperatures and precipitation in Ephrata, WA from 3 April to 22 May 2020[a]

Date (day/month)	Daily air temperature (ºC)			Average daily soil temperature at a 5-cm depth (°C)	Total daily precipitation (mm)
	Minimum	Maximum	Average		
3/4	-4.0	13.7	11.3	7.9	0.0
4/4	-2.4	11.0	4.5	9.2	0.0
5/4	2.6	13.1	6.9	11.0	0.0
6/4	-1.9	18.4	8.1	11.4	0.0
7/4	2.6	20.1	10.9	12.7	0.0
8/4	3.9	20.2	12.5	14.0	0.0
9/4	0.4	23.4	12.5	14.6	0.0
10/4	4.6	24.5	15.0	15.2	0.0
11/4	2.4	15.5	10.7	14.4	0.0
12/4	-3.4	13.6	6.3	13.6	0.0
13/4	-1.4	17.5	9.0	13.8	0.0
14/4	3.1	21.9	13.0	14.2	0.0
15/4	6.4	17.3	12.0	16.0	0.0
16/4	1.1	16.6	9.4	15.6	0.0
17/4	-0.9	22.4	11.7	15.3	0.0
18/4	8.4	20.6	14.5	17.3	0.0
19/4	4.1	21.5	12.8	17.6	0.0
20/4	3.7	23.2	13.9	18.2	0.0
21/4	4.3	21.7	13.7	18.1	0.0
22/4	5.6	13.9	10.3	15.4	1.5
23/4	5.8	19.9	12.9	15.5	0.0
24/4	3.6	19.8	11.8	15.7	0.0
25/4	5.9	20.2	12.2	15.9	0.0
26/4	2.3	19.8	12.0	16.4	0.0
27/4	6.5	20.3	13.6	17.4	0.0
28/4	2.7	20.4	12.5	17.1	0.0
29/4	8.2	23.8	16.2	18.9	0.0
30/4	6.5	19.8	14.0	20.0	0.0
1/5	1.5	19.8	11.1	19.0	0.0
2/5	7.2	23.8	13.2	19.8	1.3
3/5	2.8	16.4	9.5	16.1	0.0
4/5	0.5	18.8	10.4	16.3	0.0
5/5	5.6	25.0	15.9	19.7	0.0
6/5	3.5	17.1	12.1	17.9	4.6
7/5	3.0	20.4	12.4	16.9	0.0
8/5	3.4	22.3	14.1	19.3	0.0
9/5	12.0	26.0	18.7	21.7	0.0
10/5	12.9	24.7	18.9	22.4	0.0
11/5	11.0	22.4	16.9	21.7	0.0
12/5	10.2	22.4	16.6	21.6	0.0
13/5	6.9	20.6	13.9	20.8	0.0
14/5	6.8	17.7	12.3	19.3	0.0
15/5	7.4	21.6	14.7	20.7	0.0
16/5	71	21.8	14.0	19.7	0.0
17/5	8.5	18.0	13.6	18.2	0.8
18/5	6.1	22.7	13.5	18.3	0.0
19/5	9.5	20.8	13.8	18.7	4.3
20/5	11.2	22.7	16.4	18.3	0.0
21/5	5.6	19.0	13.0	17.9	0.0
22/5	2.8	21.6	12.2	17.7	0.0
Mean or total	4.52	19.95	12.48	16.89	12.5

[a] Recorded at the Washington State University AgWeatherNet (weather.wsu.edu) station located near Ephrata, WA (47.18ºN, 119.64ºW).

[b] The trial was located in a ~50-ha crop of *sh2* processing sweet corn that was irrigated by center-pivot.

Table 3.5. Sweet corn stand count, number of stunted seedlings, and vigor ratings recorded in a sweet corn cold tolerance screening field trial near George, WA in 2020

Date (days after planting)	Diversity panel vs. GSS 3951	Plant stand (out of 12 seed planted/plot)		Number of stunted plants (out of 12 seed planted/plot)[c]		Vigor rating (0 to 9)[c]	
		Mean	Range	Mean	Range	Mean	Range
14/4/2020	580 lines	0.0 ± 0.0[b]	0-4	-	-	-	-
(11)	GSS 3951	0.2 ± 0.1	0-5				
17/4/2020	580 lines	0.9 ± 0.0	0-9	-	-	-	-
(14)	GSS 3951	2.2 ± 0.2	0-9				
21/4/2020	580 lines	6.6 ± 0.1	0-12	-	-	-	-
(18)	GSS 3951	8.4 ± 0.2	3-12				
24/4/2020	580 lines	7.8 ± 0.1	0-12	-	-	-	-
(21)	GSS 3951	9.3 ± 0.2	6-12				
28/4/2020	580 lines	8.2 ± 0.1	0-12	-	-	-	-
(25)	GSS 3951	9.5 ± 0.2	6-12				
01/5/2020	580 lines	8.3 ± 0.1	0-12	1.6 ± 0.0	0-7	4.3 ± 0.0	0-7
(28)	GSS 3951	9.6 ± 0.2	6-12	2.1 ± 1.3	0-5	5.0 ± 0.0	5-5
08/5/2020	580 lines	8.2 ± 0.1	0-12	1.5 ± 0.0	0-5	4.4 ± 0.0	0-7
(35)	GSS 3951	9.5 ± 0.2	6-12	1.9 ± 0.1	0-5	5.0 ± 0.0	5-5

[a] Twelve seed were planted into each of two replicate plots for each sweet corn line. GSS 3951 was planted as a standard, *sh2*, processing sweet corn hybrid in 88 replicate plots scattered throughout the trial.

[b] Mean ± standard error.

[c] Counts of the number of stunted seedlings per plot and vigor ratings (0 = no plants emerged, 5 = same vigor as the nearest plot of GSS 3951, and 9 = most vigorous plots in the trial at that rating date) recorded 28 days after planting.

Table 3.6. Area under the emergence progress curve (AUEPC), mean emergence time (MET), vigor, stand count, number of stunted seedlings, and lines producing tillers in a sweet corn cold tolerance screening trial planted near George, WA in April 2020

Sweet corn line[a]	Genotype[a]	Entry[a]	AUEPC[ab]	Mean emergence time (days)[cde]	Plant stand/12 seeds planted (35 dap)[c]	Number of stunted seedlings/12 seeds planted (35 dap)[ce]	Plant vigor (0 to 9) (35 dap)[bd]	Number of albino seedlings (35 dap)	≥ 50% of plants with tillers (49 dap)[eg]	Abnormal seedling characteristics[g]
M31-1-1-1-1-1-1	*sh2*	W190943	245.5	16.3 ± 1.0	12.0 ± 0.0	2.0 ± 1.0	5.0 ± 0.0*	0.0 ± 0.0	+	
Black Mexican	Het-*su*	S190996	242.0	16.6 ± 0.3	12.0 ± 0.0	1.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
Ia5125	*su*	W191917	241.8	15.5 ± 1.0	11.5 ± 0.0	0.0 ± 0.0	4.5 ± 0.5	0.0 ± 0.0		
C7e	*su*	S190062	235.0	16.3 ± 0.0	11.5 ± 0.0	0.0 ± 0.0	5.0 ± 0.5*	0.0 ± 0.0	+	
Me121Wa	*su*	F190108	235.0	17.2 ± 0.5	12.0 ± 0.0	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
C42	*su*	S190603	235.0	17.2 ± 0.3	12.0 ± 0.0	0.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0	+	Variegated plants (25 - 35 dap)
Chile 335	Het-*su*	S190543	235.0	17.3 ± 0.3	12.0 ± 0.0	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
Selection from 231227	*su*	W191175	235.0	17.3 ± 1.3	12.0 ± 0.0	2.5 ± 0.5	6.0 ± 0.0*	0.0 ± 0.0	+	
SD883	*su*	S191127	231.5	17.6 ± 0.7	12.0 ± 0.0	0.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0	+	
W5543	*su*	S191011	231.5	17.6 ± 1.0	12.0 ± 0.0	0.5 ± 0.5	5.5 ± 0.5*	0.0 ± 0.0	+	
G8	*su*	S190035	231.5	17.7 ± 0.3	12.0 ± 0.0	0.0 ± 0.0	5.5 ± 0.5*	0.0 ± 0.0	+	
M822	*su*	S191193	229.8	17.8 ± 0.8	12.0 ± 0.0	1.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
C27red	*su*	W191625	229.5	16.7 ± 0.9	11.5 ± 0.5	2.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0	+	
Luther Hill	*su*	S190089	229.0	16.9 ± 1.1	11.5 ± 0.5	1.0 ± 1.0	5.0 ± 0.0*	0.0 ± 0.0	+	
W6757	*su*	S190520	228.0	17.9 ± 0.7	12.0 ± 0.0	1.0 ± 1.0	5.0 ± 0.0*	0.0 ± 0.0		
W64A	WT	S190532	228.0	17.9 ± 0.0	12.0 ± 0.0	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
C7	*su*	S190085	226.3	16.0 ± 1.0	11.0 ± 1.0	0.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0		
WVG3	*su*	S190340	226.3	18.1 ± 0.5	12.0 ± 0.0	0.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
IL545	*su*	S191190	226.3	18.2 ± 0.2	12.0 ± 0.0	1.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0		
No 1577	*su*	F190105	224.5	17.3 ± 1.3	11.5 ± 0.5	2.5 ± 0.5	5.5 ± 0.5*	0.0 ± 0.0	+	
Golden Gem	*su*	F190103	224.5	18.2 ± 0.9	12.0 ± 0.0	1.5 ± 1.5	5.0 ± 0.0*	0.0 ± 0.0	+	
P39xRp1d	*su*	S190644	224.5	18.2 ± 0.2	12.0 ± 0.0	0.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0	+	
A15	WT	S190083	224.5	18.3 ± 0.3	12.0 ± 0.0	0.0 ± 0.0	4.5 ± 0.5	0.0 ± 0.0		
IL86e	*su*	S190165	224.5	18.3 ± 0.0	12.0 ± 0.0	2.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0	+	
EP83	*su*	S190594	224.5	18.3 ± 0.3	12.0 ± 0.0	1.5 ± 0.5	5.5 ± 0.5*	0.0 ± 0.0	+	
EP62	*su*	S190655	224.5	18.3 ± 0.0	12.0 ± 0.0	0.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0	+	
Hawaiian Sugar	*su*	W190978	223.8	16.3 ± 1.2	11.0 ± 1.0	2.0 ± 1.0	4.0 ± 0.0	0.0 ± 0.0		
C68Rx552 63	*su*	S190623	223.8	16.4 ± 0.9	11.0 ± 0.0	2.5 ± 1.5	5.5 ± 0.5*	0.0 ± 0.0	+	
W3607	*su*	F190098	223.8	17.3 ± 0.4	11.5 ± 0.7	1.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
HI 82	*su*	W191150	223.8	17.4 ± 0.2	11.5 ± 0.5	2.0 ± 1.0	5.5 ± 0.5*	0.0 ± 0.0		
S43	*su*	S191121	223.0	16.4 ± 0.9	11.0 ± 1.0	1.0 ± 0.0	5.5 ± 0.5*	0.0 ± 0.0	+	

Sweet corn line[a]	Genotype[a]	Entry[a]	AUEPC[ab]	Mean emergence time (days)[cde]	Plant stand/12 seeds planted (35 dap)[c]	Number of stunted seedlings/12 seeds planted (35 dap)[ce]	Plant vigor (0 to 9) (35 dap)[bd]	Number of albino seedlings (35 dap)	≥ 50% of plants with tillers (49 dap)[eg]	Abnormal seedling characteristics[g]
IL453b	*su*	S191032	222.8	17.5 ± 0.2	11.5 ± 0.5	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
IP39	*su*	S190495	222.8	18.4 ± 0.7	12.0 ± 0.0	0.0 ± 0.0	4.5 ± 0.5	0.0 ± 0.0	+	
NJ618	*su*	S190108	222.0	17.3 ± 2.3	11.5 ± 0.5	1.5 ± 1.5	5.5 ± 0.5*	0.0 ± 0.0		
North Dakota Yellow Sweet Bulk	*su*	F190112	221.3	16.7 ± 0.3	11.0 ± 1.0	1.5 ± 0.5	6.0 ± 0.0*	0.0 ± 0.0		
IL692c	*su*	S191107	221.0	18.5 ± 0.5	12.0 ± 0.0	3.0 ± 0.0	4.5 ± 0.5	0.0 ± 0.0	+	
C22	*su*	S191162	221.0	18.5 ± 0.3	12.0 ± 0.0	1.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		
wh08114	*sh2*	S191075	220.3	17.7 ± 0.5	11.5 ± 0.5	1.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		
W6728	*su*	S190619	220.3	17.7 ± 0.2	11.5 ± 0.5	1.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0	+	
I112-1-1-2-1-1-1-	*sh2*	S191111	220.3	17.8 ± 1.4	11.5 ± 0.5	3.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
SD176	*su*	S191161	218.8	15.9 ± 0.7	10.5 ± 0.5	1.0 ± 0.0	5.5 ± 0.5*	0.0 ± 0.0	+	
W3647	*su*	W192087	218.5	17.7 ± 0.2	11.5 ± 0.5	1.0 ± 1.0	4.5 ± 0.5	0.0 ± 0.0		
Ia453 WT	WT	S190187	217.8	16.1 ± 0.7	10.5 ± 0.5	0.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0	+	
IL318a	*su*	S190130	217.5	17.9 ± 1.4	11.5 ± 0.5	2.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
Strain T32 397 68r	*su*	S190530	217.5	18.8 ± 0.0	12.0 ± 0.0	1.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0		
VIII/221	WT	W191535	216.8	17.1 ± 0.9	11.0 ± 3.0	2.5 ± 0.5	6.5 ± 0.5*	0.0 ± 0.0		Yellow plants (28 - 35 dap)
wuh09093i	*sh2*	S190604	216.8	18.0 ± 0.0	11.5 ± 0.5	2.0 ± 0.0	5.5 ± 0.5*	0.0 ± 0.0		
IL796a	*su*	S191021	216.8	18.1 ± 0.4	11.5 ± 0.5	0.0 ± 0.0	4.5 ± 0.5	0.0 ± 0.0		
SD909	*su*	S191038	216.8	18.1 ± 0.1	11.5 ± 0.5	0.5 ± 0.5	3.5 ± 0.5	0.0 ± 0.0		
P51wx	*su*	W190924	216.0	17.4 ± 0.6	11.0 ± 0.0	0.0 ± 0.0	5.5 ± 0.0*	0.0 ± 0.0	+	
SD884	*su*	S190091	215.0	17.1 ± 1.4	11.0 ± 1.0	2.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0	+	
IL671a	*su*	S190314	215.0	18.2 ± 0.3	11.5 ± 0.5	1.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0	+	
STRAIN 304A-408-68B	*su*	S190182	215.0	18.2 ± 0.1	11.5 ± 0.5	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
IL370a	*su*	S190545	215.0	18.2 ± 0.1	11.5 ± 0.5	0.0 ± 0.0	4.5 ± 0.5	0.0 ± 0.0		
IL303b	*su*	S190910	215.0	18.3 ± 0.3	11.5 ± 0.5	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
STRAIN 675A-415-68B	*su*	S191113	215.0	18.3 ± 0.3	11.5 ± 0.5	1.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0	+	
Jubileeex9017	*su*	S190104	214.3	17.3 ± 0.9	11.0 ± 1.0	1.0 ± 1.0	5.0 ± 0.0*	0.0 ± 0.0	+	
EP60	*su*	W191342	214.3	17.4 ± 0.6	11.0 ± 1.0	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
wuh09183i	*sh2*	S190289	213.5	16.5 ± 0.3	10.5 ± 0.5	1.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0	+	
Late Mammoth	*su*	S191165	213.3	18.3 ± 0.5	11.5 ± 0.5	2.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
W5579	*su*	S190002	213.3	18.4 ± 0.2	11.5 ± 0.5	1.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
IL451b	*su*	S190172	213.3	18.4 ± 0.8	11.5 ± 0.5	1.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0	+	
IL689a	*su*	S190513	213.3	18.4 ± 0.2	11.5 ± 0.5	0.5 ± 0.5	5.5 ± 0.5*	0.0 ± 0.0		
P39M96	*su*	S190559	213.3	18.5 ± 0.5	11.5 ± 0.5	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	

Sweet corn line[a]	Genotype[a]	Entry[a]	AUEPC[ab]	Mean emergence time (days)[cde]	Plant stand/12 seeds planted (35 dap)[c]	Number of stunted seedlings/12 seeds planted (35 dap)[ce]	Plant vigor (0 to 9) (35 dap)[bd]	Number of albino seedlings (35 dap)	≥ 50% of plants with tillers (49 dap)[eg]	Abnormal seedling characteristics[g]
ARZM 21 014	Het-*su*	S190042	212.5	16.6 ± 1.4	10.5 ± 0.5	1.5 ± 0.5	5.5 ± 0.5*	0.0 ± 0.0	+	
Ia5261	*su*	S190681	212.5	17.5 ± 0.3	11.0 ± 0.0	1.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0	+	
CHZM 08 129	*su*	S190139	212.5	17.6 ± 0.0	11.0 ± 1.0	1.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0	+	
IL677a	*se*	S190637	212.3	18.3 ± 0.7	11.5 ± 0.5	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
SD226	*su*	S190895	211.8	17.6 ± 2.2	11.0 ± 0.5	2.5 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0		
L48-1-1-1-1-1	*sh2se*	W191081	211.5	17.6 ± 0.0	11.0 ± 1.0	3.0 ± 1.0	4.0 ± 0.0	0.0 ± 0.0		
Oregon Evergreen -2	*su*	S190693	211.5	18.5 ± 0.4	11.5 ± 0.5	1.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
Z07 003	*su*	W190974	211.5	18.5 ± 0.5	11.5 ± 0.5	0.0 ± 0.0	4.5 ± 0.5	0.0 ± 0.0	+	
P35	*su*	S191061	210.8	17.7 ± 0.6	11.0 ± 1.0	1.0 ± 1.0	5.0 ± 0.0*	0.0 ± 0.0	+	
Early June	*su*	W191376	210.8	17.7 ± 0.5	11.0 ± 0.0	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
Wu00801	*su*	W192086	210.8	17.8 ± 0.2	11.0 ± 1.0	1.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
C27	*su*	S191131	209.8	18.6 ± 0.1	11.5 ± 0.5	1.5 ± 1.5	5.5 ± 0.5*	0.0 ± 0.0	+	
we09425	*se*	S190555	209.8	18.6 ± 0.1	11.5 ± 0.5	2.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		
C5	*su*	S191322	209.8	18.7 ± 1.4	11.5 ± 0.5	2.0 ± 0.0	5.5 ± 0.5*	0.0 ± 0.0		
ARZM 19 057	*su*	S191064	209.0	17.7 ± 1.4	11.0 ± 1.0	1.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
Ia2076	*su*	S190640	209.0	17.9± 0.0	11.0 ± 1.0	1.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0		
ARZM 19 069	*sh2su*	S190131	209.0	17.9 ± 0.1	11.0 ± 1.0	1.5 ± 0.5	5.5 ± 0.5*	0.0 ± 0.0	+	
C81	*su*	S190689	209.0	17.9 ± 0.0	11.0 ± 1.0	0.0 ± 0.0	5.0 ± 1.0*	0.0 ± 0.0		
Me1	*su*	S190511	208.3	16.9 ± 1.3	10.5 ± 0.5	2.0 ± 1.0	5.0 ± 0.0*	0.0 ± 0.0	+	
Separation from 170882	WT	W191227	208.3	17.0 ± 0.2	10.5 ± 0.5	1.5 ± 0.5	6.0 ± 0.0*	0.0 ± 0.0		
IL1171	*su*	S190578	208.3	17.1 ± 0.2	10.5 ± 0.5	1.0 ± 1.0	4.5 ± 0.5	0.0 ± 0.0	+	
IL795a	*su*	S190888	208.0	18.8 ± 0.3	11.5 ± 0.5	2.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0		
NJ159	*su*	S191093	208.0	18.9 ± 0.2	11.5 ± 0.5	1.0 ± 1.0	5.5 ± 0.5*	0.0 ± 0.0	+	
MDM 6	*su*	W191228	208.0	18.9 ± 1.2	11.5 ± 0.5	1.0 ± 1.0	4.0 ± 0.0	0.0 ± 0.0		
CTS62 Su	*su*	W191209	207.3	17.1 ± 0.9	10.5 ± 1.5	3.0 ± 1.0	4.5 ± 0.5	0.0 ± 0.0		
MDM 16	*su*	S191078	207.3	18.1 ± 0.2	11.0 ± 0.0	1.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0	+	
Wu99823	*su*	W191203	207.3	18.1 ± 0.2	11.0 ± 0.0	3.0 ± 0.0	4.5 ± 0.5	0.0 ± 0.0		
C8pseudo	*su*	S190001	207.3	18.2 ± 0.2	11.0 ± 1.0	0.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0	+	
I94-1-1-1-1-1-1-1	*sh2*	S190045	207.0	19.6 ± 0.4	12.0 ± 1.0	3.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
Rhode Island Sweet	*su*	W191254	206.5	15.8 ± 1.5	10.0 ± 2.0	0.5 ± 0.5	6.0 ± 0.0*	0.0 ± 0.0	+	
Nueta Sweet Corn	*su*	W191674	206.5	17.2 ± 1.1	10.5 ± 0.5	1.5 ± 0.5	6.0 ± 0.0*	0.0 ± 0.0	+	Herbicide injury (49 dap)
Aunt Marys	*su*	S191145	206.5	17.3 ± 0.7	10.5 ± 0.5	1.0 ± 1.0	5.5 ± 0.5*	0.0 ± 0.0	+	
Sunshine	*su*	S190067	206.5	18.2 ± 0.6	11.0 ± 1.0	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
wuh08127ia	*sh2*	S190592	205.5	18.3 ± 0.3	11.0 ± 0.0	1.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0		
we09402	*se*	S190529	204.8	17.4 ± 0.5	10.5 ± 0.5	1.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0		

Sweet corn line[a]	Genotype[a]	Entry[a]	AUEPC[ab]	Mean emergence time (days)[cde]	Plant stand/12 seeds planted (35 dap)[c]	Number of stunted seedlings/12 seeds planted (35 dap)[ce]	Plant vigor (0 to 9) (35 dap)[bd]	Number of albino seedlings (35 dap)	≥ 50% of plants with tillers (49 dap)[eg]	Abnormal seedling characteristics[g]
MR14	*su*	S190593	204.8	17.4 ± 0.5	10.5 ± 0.5	2.5 ± 0.5	5.5 ± 0.5*	0.0 ± 0.0	+	
Hotevilla Az white sweet corn 1	*su*	S190194	204.8	17.4 ± 0.9	10.5 ± 0.5	2.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0	+	
A685su	*su*	S191149	204.8	17.4 ± 0.1	10.5 ± 0.5	1.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
IL543c	*su*	S190497	204.8	17.4 ± 0.6	10.5 ± 1.5	1.0 ± 1.0	4.5 ± 0.5	0.0 ± 0.0		Variegated plants (21 - 35 dap)
N99-1-1-1-1-1-1-1	*sh2*	F190321	204.8	17.4 ± 0.2	10.5 ± 0.5	1.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
STRAIN T24-395-68B	*su*	S191082	204.5	19.1 ± 0.2	11.5 ± 0.5	1.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
IL793a	*su*	S191164	203.8	17.3 ± 1.6	10.5 ± 0.5	2.0 ± 1.0	4.5 ± 0.5	0.0 ± 0.0		
West Brookfield white sweet	*su*	S191370	203.8	17.4 ± 0.6	10.5 ± 1.5	0.5 ± 0.5	6.0 ± 0.0*	0.0 ± 0.0	+	
Ma32	*su*	S190501	203.8	18.4 ± 0.1	11.0 ± 1.0	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
IL699e	*su*	S190183	203.8	18.4 ± 0.1	11.0 ± 1.0	1.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		Herbicide injury (49 dap)
IL328a	*su*	S190008	203.8	18.5 ± 0.2	11.0 ± 0.0	0.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		
wuh11812i	*sh2*	S190137	203.8	18.5 ± 0.5	11.0 ± 0.0	2.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		
Ia45 1	*su*	S190688	203.0	16.5 ± 0.8	10.0 ± 0.0	1.0 ± 1.0	4.5 ± 0.5	0.0 ± 0.0		Herbicide injury (49 dap)
Ia453 su1	*su*	S190523	203.0	17.5 ± 0.8	10.5 ± 0.5	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
Separation from 183739	*su*	S191119	203.0	17.5 ± 0.7	10.5 ± 0.5	0.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0	+	
C90	*su*	S190606	203.0	17.6 ± 0.4	10.5 ± 1.5	0.0 ± 0.0	4.5 ± 0.5	0.0 ± 0.0		
SD789	*su*	S190538	203.0	17.6 ± 0.1	10.5 ± 0.5	1.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
IL788a	*su*	S190149	202.0	18.5 ± 1.2	11.0 ± 0.0	1.0 ± 1.0	4.5 ± 0.5	0.0 ± 0.0	+	
EP85	*sh2*	W190885	202.0	18.5 ± 0.2	11.0 ± 1.0	1.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
IL368a	*su*	S191041	202.0	18.6 ± 0.4	11.0 ± 1.0	1.0 ± 0.0	4.5 ± 0.5	0.0 ± 0.0	+	
C40	*su*	S190176	202.0	18.6 ± 1.0	11.0 ± 1.0	2.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
UFI9EC	*sh2*	S190653	202.0	18.7 ± 1.0	11.0 ± 1.0	2.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0	+	
ARZM 21 006	*su*	S191251	201.3	16.5 ± 1.1	10.0 ± 1.0	1.0 ± 1.0	5.0 ± 0.0*	0.0 ± 0.0	+	
EP58	*su*	S191035	201.3	17.7 ± 0.7	10.5 ± 0.5	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
STRAIN T35-388-68A	*su*	S190016	201.3	17.7 ± 0.2	10.5 ± 0.5	1.0 ± 1.0	5.5 ± 0.5*	0.0 ± 0.0	+	
176	*su*	W192127	201.3	17.7 ± 0.1	10.5 ± 1.5	2.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0		
SD592	*su*	S191101	201.3	17.7 ± 0.3	10.5 ± 1.5	1.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
M5	*su*	S190998	201.3	17.8 ± 0.2	10.5 ± 1.5	1.0 ± 1.0	4.0 ± 0.0	0.0 ± 0.0		
Me244Wb	*su*	S190570	201.0	16.5 ± 0.0	10.0 ± 2.0	0.5 ± 0.5	5.5 ± 0.5*	0.0 ± 0.0	+	
ARZM 21 007	*su*	S190573	201.0	18.6 ± 0.1	11.0 ± 0.0	2.0 ± 1.0	5.0 ± 0.0*	0.0 ± 0.0	+	
SD469	*su*	S191088	201.0	19.4 ± 1.5	11.5 ± 0.5	2.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0		

Sweet corn line[a]	Genotype[a]	Entry[a]	AUEPC[ab]	Mean emergence time (days)[cde]	Plant stand/12 seeds planted (35 dap)[c]	Number of stunted seedlings/12 seeds planted (35 dap)[ce]	Plant vigor (0 to 9) (35 dap)[bd]	Number of albino seedlings (35 dap)	≥ 50% of plants with tillers (49 dap)[eg]	Abnormal seedling characteristics[g]
A684su	*su*	S191028	200.3	17.6 ± 1.0	10.5 ± 0.5	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
IL91j	*su*	S191110	200.3	17.7 ± 0.5	10.5 ± 1.5	1.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
wu07812	*su*	S191023	200.3	18.7 ± 0.9	11.0 ± 0.0	1.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
IL611a	*su*	S190188	199.5	17.9 ± 1.1	10.5 ± 0.5	2.0 ± 0.0	4.5 ± 0.5	0.0 ± 0.0	+	
Separation from 204812	*su*	S191144	199.5	17.9 ± 0.1	10.5 ± 1.5	1.0 ± 1.0	4.5 ± 0.5	0.0 ± 0.0	+	
Ma5125	*su*	S190129	198.8	16.9 ± 0.4	10.0 ± 1.0	1.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		Chlorotic banding on leaves (28 - 35 dap), herbicide injury (49 dap)
Whipples Yellow	*su*	S190615	198.5	16.9 ± 0.7	10.0 ± 0.0	1.0 ± 1.0	5.5 ± 0.5*	2.5 ± 1.5	+	Albino and yellow plants (18 - 35 dap)
IL557a	*su*	S190031	197.8	18.0 ± 0.5	10.5 ± 0.5	0.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0		
Stowels Evergreen	*su*	S191185	197.8	18.1 ± 0.2	10.5 ± 0.5	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
wuh11811i	*sh2*	S191062	197.5	19.6 ± 0.8	11.5 ± 0.5	2.0 ± 1.0	4.5 ± 0.5	0.0 ± 0.0		
W6462	*su*	S191189	197.5	19.8 ± 1.8	11.5 ± 0.5	1.5 ± 1.5	4.0 ± 0.0	0.0 ± 0.0		
C38	*su*	S191010	197.0	17.3 ± 0.7	10.0 ± 2.0	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
2	*su*	S191014	196.8	18.9 ± 0.2	11.0 ± 1.0	1.0 ± 1.0	4.0 ± 0.0	0.0 ± 0.0		
Andjar Bekaa	*sh2su*	S190026	196.0	18.2 ± 0.7	10.5 ± 0.5	1.5 ± 0.5	6.0 ± 0.0*	0.0 ± 0.0	+	Variegated plants (28 - 35 dap)
wuh12019i	*sh2*	W190890	196.0	18.3 ± 0.4	10.5 ± 0.5	2.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
wh13022A	*sh2*	S190116	196.0	18.3 ± 0.3	10.5 ± 1.5	2.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		
W6786	*su*	S190201	196.0	18.3 ± 0.3	10.5 ± 1.5	1.0 ± 1.0	5.0 ± 0.0*	0.0 ± 0.0	+	Variegated plants (21 - 35 dap)
IL678a	*su*	S190044	196.0	18.3 ± 0.0	10.5 ± 0.5	0.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0		
IL676a	*su*	S190150	196.0	18.3 ± 0.4	10.5 ± 2.0	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
Moencopi Pueblo	*su*	W190759	195.3	17.1 ± 1.5	10.0 ± 1.0	1.0 ± 1.0	4.5 ± 0.5	0.0 ± 0.0	+	
Doce de Cuba	*su*	S190800	195.3	17.3 ± 0.3	10.0 ± 1.0	0.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		
Separation from 212335	*su*	S190635	195.3	17.3 ± 0.6	10.0 ± 1.0	0.5 ± 0.5	5.5 ± 0.5*	0.0 ± 0.0	+	
AS12	*sh2su*	S190675	195.3	17.3 ± 0.7	10.0 ± 0.5	1.0 ± 1.0	5.0 ± 0.0*	0.0 ± 0.0		
We04401	*se*	S190625	195.0	18.3 ± 0.3	10.5 ± 1.0	1.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		
Hi38C1	Het-*su*	W191097	195.0	19.0 ± 1.0	11.0 ± 1.5	1.5 ± 1.5	4.0 ± 0.0	0.0 ± 0.0	+	
Sonora 57	WT	W191067	194.3	13.5 ± 0.2	8.5 ± 0.5	3.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0	+	Herbicide injury (49 dap)
Z07 001	*su*	S190124	194.3	17.3 ± 1.3	10.0 ± 1.5	2.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		
Ia2003	*su*	S190205	194.3	17.4 ± 0.8	10.0 ± 0.5	0.0 ± 0.0	4.5 ± 0.5	0.0 ± 0.0	+	

Sweet corn line[a]	Genotype[a]	Entry[a]	AUEPC[ab]	Mean emergence time (days)[cde]	Plant stand/12 seeds planted (35 dap)[c]	Number of stunted seedlings/12 seeds planted (35 dap)[ce]	Plant vigor (0 to 9) (35 dap)[bd]	Number of albino seedlings (35 dap)	≥ 50% of plants with tillers (49 dap)[eg]	Abnormal seedling characteristics[g]
STRAIN T33-399-68B	*su*	S190100	194.3	18.2 ± 2.2	10.5 ± 0.5	2.0 ± 0.0	5.0 ± 1.0*	0.0 ± 0.0		
Z07 002	*su*	F190113	194.3	18.4 ± 0.3	10.5 ± 1.5	2.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0		Herbicide Injury (49 dap)
STRAIN 11D-586-68A	*su*	S191154	194.3	18.4 ± 0.8	10.5 ± 0.5	0.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		
we08424	*se*	S191159	194.3	18.5 ± 0.6	10.5 ± 0.5	1.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
DF14	WT	W191170	194.3	18.5 ± 0.2	10.5 ± 0.5	1.5 ± 0.5	5.5 ± 0.5*	0.0 ± 0.0		
14H-588-68B	*su*	S191141	194.0	19.9 ± 0.3	11.5 ± 0.5	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
Wh00051	*sh2*	S190503	193.5	17.5 ± 1.1	10.0 ± 0.0	1.0 ± 0.0	5.5 ± 0.5*	0.0 ± 0.0	+	
A7	*su*	S190601	193.5	17.5 ± 0.0	10.0 ± 0.0	1.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
Whipples White	*su*	F190119	193.5	17.6 ± 0.1	10.0 ± 2.0	1.5 ± 1.5	5.0 ± 0.0*	0.0 ± 0.0	+	
ARZM 19 051	*su*	S190550	193.5	17.7 ± 0.0	10.0 ± 2.0	1.0 ± 1.0	5.0 ± 0.0*	0.0 ± 0.0	+	
EP82	*su*	S191057	192.5	18.5 ± 0.2	10.5 ± 1.5	1.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
wh10046R	*sh2*	S190525	192.5	18.6 ± 0.3	10.5 ± 1.5	3.5 ± 1.5	3.5 ± 0.5	0.0 ± 0.0		
T-24-56-ILL	*su*	S190517	191.8	17.6 ± 1.3	10.0 ± 1.0	0.5 ± 0.5	4.5 ± .05	0.0 ± 0.0		
L108-1-1-1-1-1-1	*sh2*	W190839	191.8	17.8 ± 0.6	10.0 ± 0.0	0.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0	+	
MDM 19	*su*	S190118	191.5	19.4 ± 0.1	11.0 ± 1.0	3.0 ± 0.0	5.0 ± 1.0*	0.0 ± 0.0		
F7	WT	W191824	191.0	16.7 ± 0.5	9.5 ± 0.5	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
MDM 2	*su*	S191123	190.8	18.6 ± 0.5	10.5 ± 1.5	1.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0		
C6A	*su*	W190883	190.0	17.8 ± 0.5	10.0 ± 2.0	0.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		
C18	*su*	S191335	190.0	17.8 ± 0.4	10.0 ± 1.0	2.5 ± 0.5	5.5 ± 0.5*	0.0 ± 0.0	+	Variegated plants (25 - 35 dap)
Millersburg Red Sweet No2	*su*	S190207	190.0	17.8 ± 0.3	10.0 ± 2.0	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
A10579	*su*	S190151	190.0	17.9 ± 0.4	10.0 ± 0.0	1.5 ± 1.5	4.5 ± 0.5	0.0 ± 0.0		
IL648	*su*	S190837	189.8	19.5 ± 0.5	11.0 ± 0.0	3.0 ± 1.0	4.5 ± 0.5	0.0 ± 0.0		
P51	*su*	S190608	189.8	19.6 ± 1.0	11.0 ± 0.0	2.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0	+	
R853	*su*	W192066	189.0	17.9 ± 1.4	10.0 ± 1.0	3.5 ± 1.5	4.0 ± 0.0	0.0 ± 0.0	+	
GTS1	*su*	S190650	189.0	18.9 ± 0.3	10.5 ± 0.5	1.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0	+	
Ia5145	*su*	W192099	189.0	18.9 ± 0.3	10.5 ± 0.5	1.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		
Ia2132	*su*	S190080	189.0	18.9 ± 0.6	10.5 ± 0.5	1.0 ± 1.0	4.0 ± 0.0	0.0 ± 0.0		
No. 156	*su*	S190577	189.0	18.9 ± 0.9	10.5 ± 0.5	2.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0	+	Chlorotic plants (28 - 35 dap)
IL125a	*su*	W191188	189.0	18.9 ± 0.2	10.5 ± 1.5	4.0 ± 1.0	4.5 ± 0.5	0.0 ± 0.0		
Olcott	*su*	S191007	189.0	19.0 ± 0.7	10.5 ± 0.5	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
592	*su*	S190639	189.0	19.8 ± 1.3	11.0 ± 0.0	1.0 ± 1.0	5.0 ± 0.0*	0.0 ± 0.0	+	
Hayes White Sweet	*su*	S191084	188.5	15.9 ± 0.7	9.0 ± 1.0	1.5 ± 0.5	5.5 ± 0.5*	0.0 ± 0.0		

Sweet corn line[a]	Genotype[a]	Entry[a]	AUEPC[ab]	Mean emergence time (days)[cde]	Plant stand/12 seeds planted (35 dap)[c]	Number of stunted seedlings/12 seeds planted (35 dap)[ce]	Plant vigor (0 to 9) (35 dap)[bd]	Number of albino seedlings (35 dap)	≥ 50% of plants with tillers (49 dap)[eg]	Abnormal seedling characteristics[g]
IL31a	*su*	S190560	188.3	17.9 ± 0.6	10.0 ± 2.0	0.0 ± 0.0	4.5 ± 0.5	0.0 ± 0.0		
STRAIN 451B-4-68B	*su*	S190620	188.3	18.1 ± 0.3	10.0 ± 1.0	1.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0		
Golden Evergreen	*su*	S191133	188.3	18.2 ± 1.0	10.0 ± 2.0	1.0 ± 0.0	5.5 ± 0.5*	0.0 ± 0.0	+	
C2	*su*	S191016	188.3	18.2 ± 0.2	10.0 ± 1.0	0.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0		
W3742	*su*	S190887	188.3	19.2 ± 1.3	10.5 ± 0.5	2.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
Ia45 2	*su*	S190697	188.0	17.9 ± 1.4	10.0 ± 0.0	3.0 ± 1.0	4.5 ± 0.5	0.0 ± 0.0	+	
K115-11-1-1-1-1-1-1B-1	*sh2*	S190126	187.5	17.1 ± 0.8	9.5 ± 0.5	1.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		
Narino 430	WT	W191395	187.5	17.1 ± 0.7	9.5 ± 0.5	1.0 ± 0.0	6.0 ± 1.0*	0.0 ± 0.0	+	
IL14H	*su*	S191079	187.3	19.9 ± 0.5	11.0 ± 0.0	0.5 ± 0.5	5.5 ± 0.5*	0.0 ± 0.0		
L25-1-1-1-1-1	*sh2*	W191098	186.5	18.2 ± 0.3	10.0 ± 1.0	3.5 ± 1.5	5.0 ± 0.0*	0.0 ± 0.0		
AS11	*su*	S191017	186.5	18.2 ± 0.4	10.0 ± 1.0	1.0 ± 1.0	5.0 ± 0.0*	0.0 ± 0.0		
wh08022	*sh2*	S190038	185.8	17.3 ± 1.3	9.5 ± 0.5	2.0 ± 2.0	4.5 ± 0.5	0.0 ± 0.0		
IL713a	*su*	S191142	185.5	18.9 ± 1.5	10.5 ± 1.5	0.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		
Howling Mob	*su*	S190981	185.5	19.2 ± 0.3	10.5 ± 1.5	1.5 ± 0.5	6.0 ± 0.0*	0.0 ± 0.0	+	
Separation from 177604	*sh2*	W190880	184.8	18.4 ± 0.4	10.0 ± 1.0	2.0 ± 0.0	4.5 ± 0.5	0.0 ± 0.0		
A686su	*su*	S191153	184.8	18.5 ± 0.5	10.0 ± 1.0	1.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0		
we08408	*se*	S191389	184.8	18.5 ± 0.2	10.0 ± 1.0	4.0 ± 1.0	4.5 ± 0.5	0.0 ± 0.0		
wuh07428i	*sh2*	S190669	184.8	18.5 ± 0.6	10.0 ± 1.0	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
I31-1-1-1-2-1-1	*sh2se*	S190582	184.0	16.2 ± 0.6	9.0 ± 1.0	2.0 ± 2.0	4.0 ± 0.0	0.0 ± 0.0		
ZARYA 123	*su*	S190504	184.0	17.2 ± 1.4	9.5 ± 2.5	0.5 ± 0.5	5.5 ± 0.5*	0.0 ± 0.0	+	
IL430a	*su*	S191151	184.0	17.4 ± 0.9	9.5 ± 1.5	0.5 ± 0.5	5.5 ± 0.5*	0.0 ± 0.0		
Separation from 177107	*su*	S190169	184.0	17.5 ± 0.1	9.5 ± 0.5	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
We01407	*se*	S191060	184.0	17.5 ± 0.7	9.5 ± 1.0	1.5 ± 1.5	5.0 ± 0.0*	0.0 ± 0.0		
C13	*su*	S191179	184.0	18.6 ± 1.0	10.0 ± 2.0	1.0 ± 0.0	5.5 ± 0.5*	0.0 ± 0.0	+	
471 U6	*su*	S190102	183.3	16.4 ± 0.1	9.0 ± 1.0	1.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0	+	
MDM 18	*su*	S191081	183.0	18.6 ± 0.3	10.0 ± 0.5	2.0 ± 1.0	4.5 ± 0.5	0.0 ± 0.0		
K52-2-1-1-1-1	*sh2*	W191574	183.0	19.5 ± 0.1	10.5 ± 2.0	3.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0	+	
W7151	*su*	S190088	182.3	19.1 ± 1.4	10.0 ± 0.0	2.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
I97-1-1-1-1-1-1	*sh2*	S190546	182.0	18.5 ± 1.0	10.0 ± 0.5	1.5 ± 1.0	4.5 ± 0.5	0.0 ± 0.0	+	
C1540	WT	S190505	182.0	19.4 ± 0.3	10.5 ± 3.0	4.0 ± 1.0	4.5 ± 0.5	0.0 ± 0.0		
wuh11810i	*sh2*	S190125	181.5	16.5 ± 0.5	9.0 ± 0.0	1.0 ± 1.0	4.0 ± 0.0	0.0 ± 0.0		
wh08092	*sh2*	S190128	181.5	16.6 ± 1.3	9.0 ± 0.0	1.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
STRAIN T20-2-68B	*su*	S190068	181.3	17.6 ± 1.3	9.5 ± 0.5	1.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
Me121 wb	*su*	S190052	181.3	18.7 ± 0.4	10.0 ± 1.0	1.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		

Sweet corn line[a]	Genotype[a]	Entry[a]	AUEPC[ab]	Mean emergence time (days)[cde]	Plant stand/12 seeds planted (35 dap)[c]	Number of stunted seedlings/12 seeds planted (35 dap)[ce]	Plant vigor (0 to 9) (35 dap)[bd]	Number of albino seedlings (35 dap)	≥ 50% of plants with tillers (49 dap)[eg]	Abnormal seedling characteristics[g]
N12A-1	*sh2suse*	S190166	181.3	19.6 ± 1.0	10.5 ± 0.5	3.0 ± 1.0	4.0 ± 0.0	0.0 ± 0.0		
EP84	*sh2*	S190093	180.5	17.9 ± 0.4	9.5 ± 0.5	1.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0		
VIA5492	*su*	S190993	180.5	18.2 ± 0.8	9.5 ± 2.5	1.0 ± 1.0	4.0 ± 0.0	0.0 ± 0.0		
Separation from 183742	*su*	S190282	180.3	17.5 ± 1.7	9.5 ± 0.5	4.0 ± 1.0	5.0 ± 0.0*	1.0 ± 1.0	+	Albino plants (18 - 35 dap)
Wh95016a	*sh2*	S191008	180.3	19.6 ± 0.6	10.5 ± 0.5	3.0 ± 0.0	4.5 ± 0.5	0.0 ± 0.0		
IL755a	*sh2suse*	S190627	180.3	19.7 ± 0.4	10.5 ± 1.5	2.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		
STRAIN 18B-5-69	*su*	S191150	179.8	15.5 ± 1.2	8.5 ± 0.5	0.0 ± 0.0	5.0 ± 0.0*	0.5 ± 0.5		Albino plants (18 - 35 dap)
W6720 2	*su*	S190135	179.5	19.1 ± 1.3	10.0 ± 2.0	2.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0	+	
IL802b Ht2	*su*	S190027	178.8	18.1 ± 0.2	9.5 ± 1.5	3.0 ± 1.0	4.5 ± 0.5	0.0 ± 0.0		
ILB5870	*su*	S191158	178.8	18.1 ± 0.2	9.5 ± 0.5	3.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		
SD277	*su*	S190053	178.8	18.1 ± 0.6	9.5 ± 0.5	1.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0	+	
wuh12027i	*sh2*	S191071	178.5	19.8 ± 0.1	10.5 ± 0.5	4.0 ± 1.0	4.5 ± 0.5	0.0 ± 0.0		
IL515a	*su*	S191013	177.8	19.1 ± 0.5	10.0 ± 0.0	2.0 ± 2.0	5.0 ± 0.0*	0.0 ± 0.0		
Sonora 124	*su*	S191098	177.8	19.1 ± 0.7	10.0 ± 1.0	2.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
Banting	*su*	W191619	177.0	16.0 ± 2.4	8.5 ± 0.5	1.5 ± 0.5	5.0 ± 1.0*	0.0 ± 0.0	+	
Hawaii Sugar	*su*	S191124	177.0	18.4 ± 0.4	9.5 ± 0.5	2.0 ± 2.0	5.0 ± 0.0*	0.0 ± 0.0	+	
wuh11801i	*sh2*	S190509	176.8	17.9 ± 0.6	9.5 ± 0.5	1.5 ± 1.5	5.0 ± 0.0*	0.0 ± 0.0	+	
IaEV3004	*su*	S191054	176.8	20.1 ± 0.5	10.5 ± 1.5	1.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		
wuh07186i	*sh2*	S190542	176.3	17.3 ± 0.7	9.0 ± 0.0	1.0 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
NJ116Wb	*su*	S191330	176.0	18.2 ± 0.1	9.5 ± 0.5	2.5 ± 1.5	4.5 ± 0.5	0.0 ± 0.0		
ARZM 21 018	*su*	S190552	175.3	16.2 ± 1.0	8.5 ± 0.5	0.5 ± 0.5	5.5 ± 0.5*	1.5* ± 0.5	+	Albino plants (18 - 35 dap)
IL110K	*su*	S190072	175.3	18.4 ± 0.6	9.5 ± 0.5	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
Il101T	*su*	S190492	174.5	17.5 ± 0.5	9.0 ± 0.0	0.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0	+	
SD42	*su*	S190879	174.5	17.5 ± 0.2	9.0 ± 1.0	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
SYN2 sh2	*sh2*	S190521	173.5	17.0 ± 1.8	9.0 ± 3.0	1.5 ± 1.5	5.0 ± 0.0*	0.0 ± 0.0		
wuh12035i	*sh2*	S190175	173.5	18.5 ± 1.0	9.5 ± 0.5	4.0 ± 1.0	4.0 ± 0.0	0.0 ± 0.0		
Bi #10	WT	S191003	173.5	18.5 ± 0.8	9.5 ± 0.5	2.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
MDM 23	*su*	S190746	173.5	18.6 ± 0.3	9.5 ± 0.5	0.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
81-1	*su*	W191136	172.8	16.4 ± 1.2	8.5 ± 0.5	3.0 ± 1.0	3.0 ± 0.0	0.0 ± 0.0		
wuh07182i	*sh2*	S190596	172.8	17.6 ± 0.4	9.0 ± 0.0	2.0 ± 1.0	5.0 ± 0.0*	0.0 ± 0.0	+	
W6720-1	*su*	S190096	172.8	17.7 ± 0.1	9.0 ± 0.0	1.0 ± 1.0	5.5 ± 0.5*	0.0 ± 0.0	+	
CI540	WT	S191025	172.5	19.6 ± 0.4	10.0 ± 2.0	3.0 ± 1.0	4.5 ± 0.5	0.0 ± 0.0		
IL789b	*su*	S191033	172.0	15.6 ± 2.4	8.5 ± 3.5	2.5 ± 1.5	4.5 ± 0.5	0.0 ± 0.0	+	
442A-431-68D	*su*	S190010	171.8	17.8 ± 1.0	9.0 ± 0.0	1.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		

Sweet corn line[a]	Genotype[a]	Entry[a]	AUEPC[ab]	Mean emergence time (days)[cde]	Plant stand/12 seeds planted (35 dap)[c]	Number of stunted seedlings/12 seeds planted (35 dap)[ce]	Plant vigor (0 to 9) (35 dap)[bd]	Number of albino seedlings (35 dap)	≥ 50% of plants with tillers (49 dap)[eg]	Abnormal seedling characteristics[g]
Chile 332	Het-*su*	S190210	171.5	19.6 ± 0.6	10.0 ± 0.0	2.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0	+	
we05407	*se*	W192134	171.0	17.7 ± 0.8	9.0 ± 1.0	3.5 ± 0.5	5.5 ± 0.5*	0.0 ± 0.0		
Raza Maiz Dulce	*su*	S191086	171.0	17.7 ± 0.8	9.0 ± 2.0	1.0 ± 0.0	5.5 ± 0.5*	0.0 ± 0.0		
wh12014	*sh2*	S190032	171.0	17.9 ± 0.4	9.0 ± 0.0	3.0 ± 1.0	3.5 ± 0.5	0.0 ± 0.0		
IL47A	*su*	S190995	171.0	17.9 ± 0.1	9.0 ± 1.0	2.0 ± 1.0	4.5 ± 0.5	0.0 ± 0.0		
IL764b	*su*	S190007	171.0	17.9 ± 0.4	9.0 ± 0.0	0.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		
S4	*su*	S190565	170.3	16.8 ± 0.0	8.5 ± 1.5	1.0 ± 1.0	5.0 ± 0.0*	0.0 ± 0.0		Yellow plants (28 - 35 dap)
IL615a	*su*	S191030	170.0	13.7 ± 3.1	7.5 ± 0.5	1.5 ± 1.5	4.0 ± 0.0	1.5 ± 1.5		Albino plants (18 - 35 dap)
83612b	*su*	S190081	170.0	18.9 ± 0.2	9.5 ± 1.5	3.0 ± 1.0	5.0 ± 0.0*	0.0 ± 0.0		
we1095407-2	*se*	S191047	169.3	18.0 ± 1.0	9.0 ± 1.0	1.5 ± 1.5	4.5 ± 0.5	0.0 ± 0.0		
Vineland576	*su*	S191051	169.3	18.1 ± 0.1	9.0 ± 2.0	0.5 ± 0.5	5.5 ± 0.5*	0.0 ± 0.0	+	
Me244Wa	*su*	S191171	169.3	18.1 ± 0.1	9.0 ± 2.0	1.0 ± 1.0	5.0 ± 0.0*	0.0 ± 0.0	+	
N12A-1	*sh2suse*	S190612	169.3	18.2 ± 0.2	9.0 ± 0.0	1.5 ± 1.5	3.5 ± 0.5	0.0 ± 0.0		
PAIA 453	WT	S190516	169.3	18.2 ± 0.2	9.0 ± 1.0	0.0 ± 0.0	4.5 ± 0.5	0.0 ± 0.0	+	
wh12004	*sh2*	S191092	168.5	15.6 ± 2.5	8.0 ± 0.0	1.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		Chlorotic leaves and variegated plants (21 - 35 dap)
Slatka Pukanka	*su*	S190607	168.3	15.6 ± 2.3	8.0 ± 0.0	2.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0	+	Pale green plants (28 - 35 dap)
we09413	*se*	S190142	168.3	19.3 ± 0.4	9.5 ± 1.5	2.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
Golden Bantam WI	*su*	S190515	167.5	18.3 ± 0.6	9.0 ± 0.0	1.5 ± 0.5	6.0 ± 0.0*	0.0 ± 0.0	+	
we08414a	*se*	W190758	167.3	14.1 ± 0.9	7.5 ± 0.5	1.5 ± 0.5	4.0 ± 0.0	3.0 ± 1.0		Albino plants (18 - 35 dap)
Ia45 3	*su*	S190686	167.3	19.9 ± 0.7	10.0 ± 1.0	2.5 ± 1.5	5.0 ± 0.0*	0.0 ± 0.0		
21-396-68B	*sh2su*	S190014	166.8	15.0 ± 2.2	8.0 ± 3.0	0.0 ± 0.0	5.5 ± 0.5*	0.0 ± 0.0	+	
IL661a	*su*	S191137	166.5	18.1 ± 1.9	9.0 ± 1.0	1.0 ± 1.0	4.0 ± 0.0	0.0 ± 0.0		
K113-2-1-2-1-1	*Sh2*	W191346	165.8	18.5 ± 0.1	9.0 ± 1.0	2.0 ± 0.0	4.5 ± 0.5	0.0 ± 0.0		
IL765a	*su*	S191104	165.3	20.9 ± 0.6	10.5 ± 1.5	3.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
wuh09150i	*sh2*	S190152	165.0	17.4 ± 0.5	8.5 ± 0.5	2.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
Ma83608	*su*	W190827	165.0	17.5 ± 0.7	8.5 ± 1.5	1.0 ± 1.0	5.5 ± 0.5*	0.0 ± 0.0	+	
Oh43 su	*su*	W191427	164.8	18.3 ± 0.6	9.0 ± 1.0	1.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
wuh12039i	*sh2*	S190642	164.8	18.9 ± 2.0	9.5 ± 2.5	2.5 ± 2.5	4.0 ± 1.0	0.0 ± 0.0		
M90-1-1-1-2-2-1-1	*sh2*	W190863	164.5	17.5 ± 3.2	8.5 ± 1.5	3.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0	+	
A632 susu	*su*	W190873	164.3	16.2 ± 1.2	8.0 ± 0.0	0.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0		

Sweet corn line[a]	Genotype[a]	Entry[a]	AUEPC[ab]	Mean emergence time (days)[cde]	Plant stand/12 seeds planted (35 dap)[c]	Number of stunted seedlings/12 seeds planted (35 dap)[ce]	Plant vigor (0 to 9) (35 dap)[bd]	Number of albino seedlings (35 dap)	≥ 50% of plants with tillers (49 dap)[eg]	Abnormal seedling characteristics[g]
Cubano	*su*	S191278	164.0	17.4 ± 0.5	8.5 ± 0.5	1.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
W5552	*su*	S190506	164.0	17.5 ± 0.9	8.5 ± 0.5	0.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0	+	
Ranniaya Zolotaya 401	*su*	S190999	164.0	17.6 ± 0.4	8.5 ± 2.5	0.5 ± 0.5	5.5 ± 0.5*	0.0 ± 0.0	+	
ILB5765	*se*	S191055	164.0	18.6 ± 0.8	9.0 ± 0.0	3.0 ± 1.0	4.0 ± 0.0	0.0 ± 0.0		
wh10090R	*sh2*	S190168	164.0	18.6 ± 0.3	9.0 ± 1.0	2.0 ± 1.0	5.0 ± 0.0*	0.0 ± 0.0		
IL395a	*su*	S190664	164.0	18.7 ± 1.0	9.0 ± 1.0	1.5 ± 1.5	4.0 ± 0.0	0.0 ± 0.0		
IL124a	*su*	W190946	164.0	18.8 ± 0.5	9.0 ± 1.0	1.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		
34f	*su*	S190203	163.0	19.6 ± 0.4	9.5 ± 1.5	1.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0		
IL465a	*su*	S190598	162.3	18.8 ± 0.1	9.0 ± 1.0	0.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0		
IL369b	*su*	S190324	161.3	17.7 ± 1.1	8.5 ± 0.5	3.0 ± 1.0	4.5 ± 0.5	0.0 ± 0.0	+	
IL103a	*su*	S190101	161.3	18.8 ± 1.3	9.0 ± 0.0	1.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0		
IL14C	*su*	S191186	161.3	18.9 ± 1.3	9.0 ± 1.0	1.0 ± 1.0	5.0 ± 0.0*	0.0 ± 0.0		
Chile 339	*su*	W190918	160.8	16.9 ± 0.7	8.0 ± 1.0	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	Chlorotic plants (28 - 35 dap)
wh03031	*sh2*	S190536	160.5	18.0 ± 0.7	8.5 ± 0.5	1.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
C4	*su*	S190597	160.5	19.3 ± 0.8	9.0 ± 3.0	1.0 ± 1.0	5.0 ± 0.0*	0.0 ± 0.0	+	
W6714	*su*	S190611	159.8	18.1 ± 0.1	8.5 ± 2.5	1.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0		
IL21f	*su*	S190120	159.5	15.2 ± 0.2	7.5 ± 0.5	4.0 ± 0.0	3.5 ± 0.5	1.5 ± 1.5		Albino plants, variegated plants (21 - 35 dap)
NE HY 13b	*su*	S190037	159.0	16.7 ± 1.7	8.0 ± 1.0	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
Country Gentleman	*su*	S190526	159.0	18.4 ± 0.9	8.5 ± 1.5	2.5 ± 0.5	5.5 ± 0.5*	0.0 ± 0.0		
we07403a	*se*	S190646	158.8	18.7 ± 1.5	9.0 ± 3.0	0.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0	+	
ILB6011	*su*	S190575	158.8	18.9 ± 0.9	9.0 ± 3.0	1.5 ± 1.5	5.0 ± 0.0*	0.0 ± 0.0		
ARZM 21 008	*su*	S190136	158.3	15.6 ± 0.1	7.5 ± 0.5	1.0 ± 0.0	5.5 ± 0.5*	0.0 ± 0.0	+	
wh12001	*sh2*	S191218	158.0	18.3 ± 0.3	8.5 ± 0.5	1.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
I152-1-1-1-1-2-1-1	*sh2*	S190988	158.0	18.4 ± 0.9	8.5 ± 1.5	0.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0	+	
wh13053	*sh2*	S190539	158.0	18.4 ± 0.4	8.5 ± 1.5	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
IL733a	*su*	S190153	157.8	20.2 ± 0.5	9.5 ± 0.5	2.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
wuh09144i	*sh2*	S190683	157.0	19.2 ± 0.8	9.0 ± 2.0	1.5 ± 1.5	4.5 ± 0.5	0.0 ± 0.0		
ARZM 16 011	*su*	S191130	157.0	19.3 ± 1.0	9.0 ± 1.0	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
469	*su*	S190696	157.0	19.4 ± 1.4	9.0 ± 0.0	1.0 ± 1.0	5.0 ± 0.0*	0.0 ± 0.0	+	
wu10804R	*su*	S190692	156.8	20.1 ± 0.4	9.5 ± 0.5	1.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
wuh12018i	*sh2*	S191005	156.3	17.1 ± 0.6	8.0 ± 2.0	2.5 ± 2.5	3.5 ± 0.5	0.0 ± 0.0		
L108-2-1-1	*sh2*	W190995	156.3	18.3 ± 1.0	8.5 ± 1.5	0.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
Northrup King Strain 9316	*su*	W191880	155.5	17.7 ± 1.3	8.0 ± 2.0	1.0 ± 0.0	5.5 ± 0.5*	0.0 ± 0.0	+	

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wh13037	*sh2*	S190087	155.3	18.3 ± 0.5	8.5 ± 1.5	4.0 ± 1.0	4.0 ± 0.0	0.0 ± 0.0		
wu10802R	*su*	S190694	154.5	18.6 ± 0.6	8.5 ± 1.5	1.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
wuh07429i	*sh2*	S191120	154.5	18.7 ± 0.4	8.5 ± 0.5	2.0 ± 1.0	4.5 ± 0.5	0.0 ± 0.0		
wh14082V	*sh2*	W190805	154.5	18.8 ± 0.7	8.5 ± 1.5	2.0 ± 2.0	4.5 ± 0.5	0.0 ± 0.0		
908	*su*	W191533	154.3	18.3 ± 4.6	8.0 ± 0.0	2.0 ± 1.0	5.0 ± 0.0*	0.0 ± 0.0	+	
Wh01001	*sh2*	S191178	154.3	19.6 ± 0.1	9.0 ± 2.0	3.5 ± 0.5	3.0 ± 1.0	0.0 ± 0.0		
Wh98063	*sh2*	W191527	152.8	18.7 ± 0.9	8.5 ± 1.5	2.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
P39Goodman-Buckler	*su*	S191146	152.8	18.9 ± 0.2	8.5 ± 0.5	1.5 ± 1.5	5.5 ± 0.5*	0.0 ± 0.0		
we04806	*se*	S191068	152.8	18.9 ± 0.3	8.5 ± 0.5	1.0 ± 0.0	4.5 ± 0.5	0.0 ± 0.0		
L125-1-1-1	*sh2*	S191112	152.8	20.0 ± 0.1	9.0 ± 1.0	2.0 ± 1.0	4.5 ± 0.5	0.0 ± 0.0		
ARZM 21 013	WT	S191134	152.0	17.6 ± 0.6	8.0 ± 4.0	0.0 ± 0.0	5.5 ± 0.5*	0.0 ± 0.0	+	
IL772a	*su*	S191002	152.0	18.0 ± 0.0	8.0 ± 2.0	2.0 ± 1.0	4.5 ± 0.5	0.0 ± 0.0		
we08405	*se*	S191115	152.0	18.1 ± 0.5	8.0 ± 3.0	1.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		
wuh12020i	*sh2*	W191219	151.8	17.6 ± 0.2	8.0 ± 1.0	3.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
IL731a	*se*	S190082	151.8	18.5 ± 1.7	8.5 ± 2.5	3.0 ± 0.0	3.5 ± 0.5	0.0 ± 0.0		Yellow plants (28 - 35 dap)
ARZM 20 006	*su*	S190671	151.8	19.9 ± 0.3	9.0 ± 1.0	1.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0	+	
I108-2-2-2-2-1-1-1	*sh2*	S190095	151.0	18.9 ± 0.4	8.5 ± 2.5	2.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0		
Maiz Amarilla	*su*	S190679	151.0	19.4 ± 0.9	8.5 ± 2.5	1.5 ± 0.5	5.5 ± 0.5*	0.0 ± 0.0	+	
Evergreen C65	*su*	S190033	150.3	17.8 ± 1.5	8.0 ± 1.0	1.0 ± 1.0	5.0 ± 0.0*	0.0 ± 0.0		
Separation from 177642	*su*	W191446	150.3	17.9 ± 0.6	8.0 ± 2.0	1.0 ± 1.0	4.0 ± 0.0	0.0 ± 0.0		
IL112t	*su*	S190184	150.3	18.0 ± 0.2	8.0 ± 3.0	1.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0		
IL757b	*su*	S191180	150.3	18.0 ± 0.2	8.0 ± 3.0	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
ARZM 20 005	*su*	S190579	149.5	16.9 ± 0.9	7.5 ± 0.5	1.5 ± 0.5	5.5 ± 0.5*	0.0 ± 0.0		
IL696a	*se*	S190022	149.3	18.1 ± 2.3	8.0 ± 0.0	1.0 ± 1.0	4.0 ± 0.0	0.0 ± 0.0		
NJ112	*su*	S190554	149.3	19.3 ± 0.4	8.5 ± 1.5	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
MDM 12	*su*	W191706	149.3	19.3 ± 0.3	8.5 ± 0.5	2.0 ± 1.0	4.0 ± 0.0	0.0 ± 0.0		
we11416	*se*	S190109	149.3	19.4 ± 0.4	8.5 ± 1.5	0.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0	+	
K164-1-1-1-1-1	*sh2*	W191056	149.3	20.3 ± 0.2	9.0 ± 1.0	2.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
IL751a	*su*	S190127	148.5	18.2 ± 0.4	8.0 ± 1.0	2.0 ± 1.0	4.5 ± 0.5	0.0 ± 0.0		
R851	*sh2*	S190982	148.5	18.4 ± 0.5	8.0 ± 1.0	1.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0	+	
I817	*su*	S190028	148.5	18.4 ± 0.4	8.0 ± 0.0	0.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0		
C23 su	*su*	S190634	147.8	13.5 ± 4.7	7.0 ± 3.0	0.0 ± 0.0	4.5 ± 0.5	0.0 ± 0.0	+	
SC1441	*su*	S190680	147.5	20.6 ± 0.7	9.0 ± 0.0	3.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
IL744a	*su*	S190048	147.0	21.7 ± 1.8	10.0 ± 1.0	4.0 ± 1.0	3.5 ± 0.5	0.0 ± 0.0		

Sweet corn line[a]	Genotype[a]	Entry[a]	AUEPC[ab]	Mean emergence time (days)[cde]	Plant stand/12 seeds planted (35 dap)[c]	Number of stunted seedlings/12 seeds planted (35 dap)[ce]	Plant vigor (0 to 9) (35 dap)[bd]	Number of albino seedlings (35 dap)	≥ 50% of plants with tillers (49 dap)[eg]	Abnormal seedling characteristics[g]
SD829	*su*	S190682	146.8	18.2 ± 1.0	8.0 ± 3.0	1.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0	+	
Wh14100V	*sh2*	F190363	146.8	18.4 ± 0.1	8.0 ± 1.0	0.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
wh10117R	*sh2*	W191801	146.5	16.4 ± 2.6	7.5 ± 1.5	4.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0		Herbicide injury (49 dap)
wuh09174i	*sh2*	S190025	146.0	17.3 ± 1.0	7.5 ± 0.5	2.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0		
GSSS sh2	*sh2*	W191365	146.0	17.4 ± 0.6	7.5 ± 0.5	1.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
IL366a	*su*	S190199	146.0	18.6 ± 1.6	8.0 ± 1.0	2.0 ± 1.0	4.5 ± 0.5	0.0 ± 0.0		
N38-2-1-1-1-1-1-1	*sh2se*	W191100	145.8	19.6 ± 0.5	8.5 ± 0.5	3.0 ± 1.0	4.5 ± 0.5	0.0 ± 0.0		
IL801a	*su*	S191012	145.8	19.7 ± 0.1	8.5 ± 0.5	2.0 ± 1.0	4.0 ± 0.0	0.0 ± 0.0		
K1-1-1-1-1-1-2-1-1-1	*sh2*	S190070	145.8	19.7 ± 1.0	8.5 ± 0.5	1.0 ± 1.0	4.5 ± 0.5	0.0 ± 0.0		
If853	*sh2*	W191630	145.8	19.8 ± 1.5	8.5 ± 0.5	2.5 ± 1.5	4.0 ± 1.0	0.0 ± 0.0		
Red NCLB	*su*	W192058	145.8	19.8 ± 2.3	8.5 ± 0.5	2.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
N142A-1	*sh2*	S190213	145.0	18.1 ± 1.3	8.0 ± 4.0	2.5 ± 1.5	4.0 ± 0.0	0.0 ± 0.0	+	
IL437a	*su*	S191156	145.0	18.9 ± 1.6	8.0 ± 1.0	4.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0		
SC6069	*su*	S190645	144.3	17.5 ± 0.5	7.5 ± 1.5	2.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		
CRC 61	Het-*su*	S191249	144.3	17.6 ± 0.6	7.5 ± 0.5	1.0 ± 1.0	5.0 ± 0.0*	0.0 ± 0.0		
IL767b	*su*	S190208	144.0	19.9 ± 0.4	8.5 ± 1.5	3.0 ± 1.0	3.5 ± 0.5	0.0 ± 0.0		
wh08045	*sh2*	S190716	144.0	19.9 ± 1.1	8.5 ± 0.5	3.0 ± 1.0	4.0 ± 0.0	0.0 ± 0.0		
Eskisehir	*su*	S190574	142.5	16.4 ± 1.6	7.0 ± 0.0	0.5 ± 0.5	5.5 ± 0.5*	0.0 ± 0.0	+	
wh07029	*sh2*	S190638	142.3	20.0 ± 0.1	8.5 ± 1.5	2.0 ± 1.0	3.5 ± 0.5	0.0 ± 0.0		
We06409a	*se*	S191177	140.8	17.6 ± 1.8	7.5 ± 1.5	1.5 ± 1.5	4.5 ± 0.5	0.0 ± 0.0		
IL454a	*su*	S190549	140.5	18.4 ± 1.8	8.0 ± 3.0	1.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0		
IL804a HTN	*su*	S190499	140.5	20.2 ± 0.4	8.5 ± 1.5	2.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
MDM 20	*su*	W190933	140.5	20.6 ± 1.3	8.5 ± 1.5	1.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
CTS6 1	WT	S190512	139.8	18.2 ± 0.2	7.5 ± 2.5	1.0 ± 1.0	5.0 ± 0.0*	0.0 ± 0.0		
Ia4189	*su*	S190043	139.8	18.7 ± 1.7	8.0 ± 3.0	1.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0	+	
ARZM 21 009	*su*	S190618	139.8	19.2 ± 1.7	8.0 ± 2.0	0.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0	+	
IL729a	*su*	S190632	137.8	20.6 ± 1.5	8.5 ± 0.5	3.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0		
IL279AxRp1d	*su*	S190107	137.3	10.5 ± 7.3	5.5 ± 0.5	3.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0		Variegated plants (28 - 35 dap)
COES 46A-1	*sh2* Het-*su*	S190186	137.3	12.6 ± 2.8	6.0 ± 2.0	1.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0	+	
wuh09149i	*sh2*	S191152	137.3	18.6 ± 0.6	7.5 ± 1.5	1.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0		
T64S	*sh2su*	S191236	137.3	18.6 ± 0.6	7.5 ± 0.5	1.0 ± 0.0	5.0 ± 1.0*	0.0 ± 0.0		
we05410	*se*	S191106	137.3	20.8 ± 2.8	8.5 ± 0.5	2.5 ± 1.5	4.5 ± 0.5	0.0 ± 0.0		
Amarillo dulce	*su*	S190647	136.5	17.1 ± 0.4	7.0 ± 4.0	1.5 ± 0.5	4.0 ± 1.0	0.0 ± 0.0	+	Herbicide injury (49 dap)
SD908	*su*	S190163	136.5	17.5 ± 0.5	7.0 ± 1.0	1.0 ± 1.0	5.0 ± 0.0*	0.0 ± 0.0	+	Herbicide injury

Sweet corn line[a]	Genotype[a]	Entry[a]	AUEPC[ab]	Mean emergence time (days)[cde]	Plant stand/12 seeds planted (35 dap)[c]	Number of stunted seedlings/12 seeds planted (35 dap)[ce]	Plant vigor (0 to 9) (35 dap)[bd]	Number of albino seedlings (35 dap)	≥ 50% of plants with tillers (49 dap)[eg]	Abnormal seedling characteristics[g]
										(49 dap)
wh14202N	*sh2*	W191205	135.5	17.2 ± 1.5	7.0 ± 1.0	2.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
N132A-1	*sh2* Het-*su*	W192121	135.5	18.9 ± 0.9	7.5 ± 0.5	2.0 ± 0.0	4.5 ± 0.5	0.0 ± 0.0		
Sonora 108	*su*	S191114	134.8	17.8 ± 0.2	7.0 ± 2.0	1.0 ± 0.0	4.5 ± 0.5	0.5 ± 0.5	+	Albino plants (28 - 35 dap)
wh13074A	*sh2*	S191074	133.8	19.2 ± 0.3	7.5 ± 0.5	1.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
wuh09098i	*sh2*	S191369	133.0	17.8 ± 1.5	7.0 ± 0.0	2.5 ± 1.5	5.0 ± 1.0*	0.0 ± 0.0		
T625	*su*	W190868	133.0	20.2 ± 1.2	8.0 ± 2.0	2.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		
COES 28A-1	*sh2se*	S191034	132.8	20.2 ± 0.2	8.0 ± 3.0	2.0 ± 2.0	4.0 ± 0.0	0.0 ± 0.0	+	
wh10127R	*sh2*	S190030	132.0	18.9 ± 1.1	7.5 ± 1.5	1.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
B5765	*se*	S190144	132.0	19.2 ± 1.5	7.5 ± 0.5	1.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
we08417a	*se*	S190024	132.0	19.4 ± 1.0	7.5 ± 0.5	2.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0		
wh14210N	*sh2*	W191208	130.3	19.5 ± 1.0	7.5 ± 0.5	1.5 ± 1.5	3.5 ± 0.5	0.0 ± 0.0		
wuh07469i	*sh2*	S190703	130.3	19.6 ± 0.5	7.5 ± 1.5	2.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
IL803a	*su*	S191095	129.5	17.8 ± 2.1	7.0 ± 1.0	2.5 ± 1.5	4.0 ± 0.0	0.0 ± 0.0		
IL778c	*su*	W191571	129.5	18.2 ± 0.4	7.0 ± 2.0	2.5 ± 1.5	4.0 ± 0.0	0.0 ± 0.0		
Pease Crosby Sweet Corn	*su*	S190121	129.5	18.4 ± 0.0	7.0 ± 0.0	1.0 ± 0.0	4.5 ± 0.5	0.0 ± 0.0	+	
N46A-1	*sh2*	S190535	129.5	18.6 ± 0.5	7.0 ± 4.0	1.0 ± 1.0	4.0 ± 1.0	0.0 ± 0.0		
Wh00033	*sh2*	S190851	128.8	17.1 ± 1.4	6.5 ± 0.5	0.5[e]	5.0 ± 0.0*	0.0 ± 0.0	+	
wh10135R	*sh2*	S191315	128.5	19.6 ± 0.1	7.5 ± 0.5	1.0 ± 0.5	3.5 ± 0.5	0.0 ± 0.0		
COES 25A-1	*sh2*	S190524	127.8	16.9 ± 0.7	6.5 ± 2.5	1.5 ± 0.0	4.0 ± 0.0	0.0 ± 0.0		
Wh98044	*sh2*	S190020	127.8	17.4 ± 1.2	6.5 ± 1.5	0.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		
wuh07492i	*sh2*	W191026	127.0	15.3 ± 0.5	6.0 ± 1.0	2.5 ± 0.5	5.5 ± 0.5*	0.0 ± 0.0	+	
MDM 8	*su*	S190875	127.0	17.6 ± 1.1	6.5 ± 1.5	0.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		
Baxters Golden Bantam	*su*	S190179	126.0	18.9 ± 0.6	7.0 ± 1.0	2.5 ± 0.5	3.5 ± 1.5	0.0 ± 0.0	+	
MSR su	*su*	S190393	125.3	15.9 ± 1.4	6.0 ± 0.0	0.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
wh07061a	*sh2*	S191001	125.3	17.3 ± 0.3	6.5 ± 2.5	2.5 ± 0.5	3.5 ± 0.5	0.0 ± 0.0		
MDM-5	*su*	S191166	124.8	22.1 ± 0.4	8.5 ± 0.5	3.5 ± 1.5	3.5 ± 0.5	0.0 ± 0.0		
P39	*su*	S191140	124.3	18.2 ± 1.5	7.0 ± 4.0	1.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0	+	
We02404	*se*	S191343	123.3	18.9 ± 0.9	7.0 ± 3.0	0.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0		Herbicide injury (49 dap)
K105-1-1-2-1-1	*sh2su*	W190917	122.5	15.1 ± 3.1	6.0 ± 2.0	0.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
wh04020a	*sh2*	S190839	122.5	17.9 ± 1.0	6.5 ± 0.5	0.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
we04819	*se*	S190588	122.3	20.5 ± 0.7	7.5 ± 1.5	3.0 ± 1.0	4.0 ± 0.0	0.0 ± 0.0		
HI 78	WT	W191558	121.8	16.0 ± 0.7	6.0 ± 3.0	0.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0		

Sweet corn line[a]	Genotype[a]	Entry[a]	AUEPC[ab]	Mean emergence time (days)[cde]	Plant stand/12 seeds planted (35 dap)[c]	Number of stunted seedlings/12 seeds planted (35 dap)[ce]	Plant vigor (0 to 9) (35 dap)[bd]	Number of albino seedlings (35 dap)	≥ 50% of plants with tillers (49 dap)[eg]	Abnormal seedling characteristics[g]
K120-1-1-1-1-1-2-1	*sh2*	W191035	121.8	18.0 ± 0.2	6.5 ± 1.5	1.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0		
we11408	*se*	S191188	121.0	16.9 ± 1.1	6.0 ± 1.0	1.0 ± 1.0	5.0 ± 0.0*	0.0 ± 0.0	+	
wh10140R	*sh2*	S191049	120.8	19.6 ± 0.6	7.0 ± 1.0	3.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0		
IaEV3002	*su*	W191470	120.8	19.7 ± 0.0	7.0 ± 1.0	2.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
Ia2730	*su*	S190613	120.8	19.8 ± 1.2	7.0 ± 2.0	1.0 ± 1.0	3.5 ± 0.5	0.0 ± 0.0		Variegated plants (28 - 35 dap)
wh09009	*sh2*	S190105	120.5	20.6 ± 0.6	7.5 ± 0.5	4.0 ± 1.0	4.0 ± 0.0	0.0 ± 0.0		
N72A-1	*sh2*	S190576	120.0	18.1 ± 1.5	6.5 ± 1.5	1.5 ± 1.5	4.0 ± 0.0	0.0 ± 0.0		
Early Evergreen	*su*	S190004	120.0	18.3 ± 0.3	6.5 ± 2.5	2.5 ± 0.5	5.5 ± 0.5*	0.0 ± 0.0	+	Pale green plants (28 - 35 dap)
IL393a	*su*	W192106	119.8	22.3 ± 2.5	8.0 ± 1.0	3.0 ± 0.0	3.5 ± 0.5	0.0 ± 0.0		
wh07051	*sh2*	S190658	119.0	19.9 ± 0.1	7.0 ± 4.0	2.5 ± 2.5	4.0 ± 0.0	0.0 ± 0.0		
B5870	*su*	S191046	118.8	22.9 ± 0.4	8.5 ± 0.5	2.5 ± 0.5	3.5 ± 0.5	0.0 ± 0.0	+	
W6366	*su*	S191009	118.3	19.0 ± 0.5	6.5 ± 4.5	1.0 ± 0.0	4.5 ± 0.5	0.0 ± 0.0		
NE HY 13A	*su*	S191069	117.5	16.9 ± 1.3	6.0 ± 1.0	1.0 ± 1.0	5.5 ± 0.5*	0.0 ± 0.0	+	
wh10067R	*sh2*	S190905	117.5	17.2 ± 0.0	6.0 ± 1.0	1.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
wh13041	*sh2*	S191139	117.3	19.9 ± 1.8	7.0 ± 0.0	1.5 ± 0.5	3.5 ± 0.5	0.0 ± 0.0		
P51xRp1d	*su*	S190528	116.5	18.7 ± 0.9	6.5 ± 0.5	1.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0	+	
IL442a	*su*	S190191	116.5	18.9 ± 0.3	6.5 ± 1.5	1.5 ± 1.5	4.5 ± 0.5	0.0 ± 0.0		
wh08042	*sh2*	S190099	116.5	18.9 ± 0.5	6.5 ± 0.5	0.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
V775	*su*	W191444	114.8	19.2 ± 0.6	6.5 ± 1.5	2.0 ± 0.0	5.0 ± 0.0*	0.0 ± 0.0		
Ia5125B	*su*	S191024	114.8	19.2 ± 0.9	6.5 ± 0.5	0.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		Herbicide injury (49 dap)
Hi 38	WT	W190872	114.8	19.3 ± 0.4	6.5 ± 0.5	2.0 ± 1.0	5.0 ± 0.0*	0.0 ± 0.0		
wuh07422i	*sh2*	S191044	114.8	20.1 ± 2.1	6.5 ± 2.5	1.0 ± 1.0	3.0 ± 0.0	0.0 ± 0.0		
wh10068R	*sh2*	S190003	114.0	18.0[f]	6.0 ± 0.6	1.0 ± 0.0	2.5 ± 2.5	0.0 ± 0.0		
wh10216V	*sh2*	S190571	113.0	15.9 ± 0.9	5.5 ± 2.5	2.0 ± 1.0	4.0 ± 0.0	0.0 ± 0.0		
wh07061b	*sh2*	S191090	113.0	18.0 ± 0.6	6.0 ± 1.0	0.5 ± 0.5	3.5 ± 0.5	0.0 ± 0.0		
wh12048V	*sh2*	S190714	113.0	19.5 ± 0.1	6.5 ± 1.5	1.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0		
wuh09153i	*sh2*	S190985	113.0	20.7 ± 1.0	7.0 ± 1.0	2.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0		
83610b	*su*	S191050	112.8	21.8 ± 0.1	7.5 ± 0.5	2.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0		
789	*su*	S190055	112.3	18.2 ± 0.2	6.0 ± 1.0	1.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0	+	
IL773a	*su*	W191742	112.0	22.3 ± 0.6	7.5 ± 2.5	2.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0		
IL44b	*su*	S190589	111.5	16.5 ± 0.9	5.5 ± 0.5	0.0 ± 0.0	4.5 ± 0.5	0.0 ± 0.0	+	
wuh07177i	*sh2*	S191176	111.3	19.6 ± 1.0	6.5 ± 1.5	3.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0	+	
IL761a	*su*	W192060	111.3	22.2 ± 2.8	6.5 ± 5.5	2.0[e]	4.0 ± 0.0	0.0 ± 0.0		
Ia453 sh2	*sh2*	W192067	110.5	18.3 ± 1.1	6.0 ± 1.0	1.0 ± 1.0	4.0 ± 0.0	0.0 ± 0.0		

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IL7	*su*	S191026	110.5	18.4 ± 0.1	6.0 ± 0.0	2.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0	+	
wh09083	*sh2*	W190819	110.5	18.4 ± 0.6	6.0 ± 0.0	2.0 ± 0.0	4.5 ± 0.5	0.0 ± 0.0		
wh05051	*sh2*	W190876	110.5	18.6 ± 0.6	6.0 ± 1.0	2.0 ± 0.0	3.5 ± 0.5	0.0 ± 0.0		
IL18b	*su*	S190185	109.5	18.0 ± 0.0	5.5 ± 5.5	1.0 ± 0.0	2.5 ± 2.5	0.0 ± 0.0		
N7C-1	*sh2* Het-*su*	S191147	109.5	19.6 ± 0.6	6.5 ± 3.5	1.5 ± 0.5	4.0 ± 1.0	0.0 ± 0.0		
I58-1-2-2-1-1-1	*sh2*	W191018	109.5	19.6 ± 1.6	6.5 ± 1.5	3.5 ± 1.5	4.0 ± 0.0	0.0 ± 0.0		
Ill101Q	*su*	S190123	108.8	18.7 ± 0.1	6.0 ± 1.0	1.0 ± 1.0	5.5 ± 0.5*	0.0 ± 0.0	+	
I182-1-2-1-1-1-1	*sh2se*	W191295	108.8	18.8 ± 1.4	6.0 ± 0.0	1.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0	+	
Tesuque Pueblo	*su*	S191173	108.8	19.1 ± 2.3	6.0 ± 1.0	1.5 ± 1.5	4.0 ± 1.0	0.0 ± 0.0		
wuh09164i	*sh2*	S191172	107.0	18.9 ± 0.3	6.0 ± 1.0	2.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
MDM 15	*su*	S190295	107.0	19.0 ± 1.0	6.0 ± 1.0	2.0 ± 1.0	4.5 ± 0.5	0.0 ± 0.0	+	
Wh93016	*sh2*	W191838	107.0	19.1 ± 0.6	6.0 ± 0.0	0.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
IL354a	*su*	W191967	106.3	14.7 ± 2.5	5.0 ± 1.0	0.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		
IL794a	*su*	S190206	106.0	20.7 ± 0.4	6.5 ± 3.5	1.0 ± 1.0	4.0 ± 0.0	0.0 ± 0.0	+	
IL13B	*su*	W191924	105.8	22.7 ± 0.2	7.5 ± 0.5	0.0 ± 0.0	3.0 ± 0.0	0.0 ± 0.0		
wh10137R	*sh2*	S190195	105.3	17.8 ± 0.2	5.5 ± 4.5	0.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0		Herbicide injury (49 dap)
IL766a	*se*	S190666	105.3	19.3 ± 0.3	6.0 ± 0.0	1.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		
wh11001	*sh2*	S190670	105.3	19.3 ± 0.3	6.0 ± 0.0	4.0 ± 1.0	3.0 ± 0.0	0.0 ± 0.0		Herbicide injury (49 dap)
K43-1-1-1-1-1-1-1	*sh2*	W190945	105.3	19.3 ± 0.8	6.0 ± 0.0	1.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0	+	
IL707a	*su*	S190984	105.3	20.9 ± 0.4	6.5 ± 1.5	0.5 ± 0.5	3.5 ± 0.5	0.0 ± 0.0		
UFI2EDbt1-1	*sh2*	S190673	104.3	22.3 ± 1.4	7.0 ± 1.0	2.0 ± 0.0	3.5 ± 0.5	0.0 ± 0.0		
Ma2402	*su*	S190629	103.5	19.3 ± 0.3	6.0 ± 3.0	0.0 ± 0.0	4.5 ± 0.5	0.0 ± 0.0	+	
wh05066a	*sh2*	S191242	103.5	19.4 ± 0.6	6.0 ± 2.0	2.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0		
wh13063A	*sh2*	S190140	103.5	19.7 ± 1.5	6.0 ± 1.0	2.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0		
W85	WT	S190009	102.8	18.3 ± 0.3	5.5 ± 0.5	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0	+	
IL747b	*se*	S190114	101.8	17.6 ± 5.4	5.5 ± 0.5	1.0 ± 1.0	4.0 ± 1.0	0.0 ± 0.0	+	
MDM 1	*su*	S191116	101.0	18.4 ± 0.4	5.5 ± 1.5	1.5 ± 1.5	4.0 ± 0.0	0.0 ± 0.0		
wh10088R	*sh2*	F190362	101.0	18.6 ± 0.2	5.5 ± 0.5	1.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0		
wh10105R	*sh2*	S191117	100.3	16.8 ± 1.2	5.0 ± 0.0	0.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		
wh12008	*sh2*	S190583	99.3	18.5 ± 0.5	5.5 ± 3.5	1.0 ± 1.0	3.5 ± 0.5	0.0 ± 0.0		Variegated plants (28 - 35 dap)
wh10057R	*sh2*	S190291	99.3	18.9 ± 1.1	5.5 ± 0.5	2.0 ± 1.0	4.0 ± 0.0	0.0 ± 0.0		
wuh11813i	*sh2*	S191122	97.5	19.1 ± 0.1	5.0 ± 2.5	1.5 ± 1.5	4.0 ± 0.0	0.0 ± 0.0		
wh09068	*sh2*	S191203	97.3	18.1 ± 3.7	5.5 ± 0.5	3.0 ± 1.0	3.0 ± 0.0	0.0 ± 0.0		
IL607a	*su*	S190651	96.8	18.0 ± 1.0	5.0 ± 2.0	0.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		

Sweet corn line[a]	Genotype[a]	Entry[a]	AUEPC[ab]	Mean emergence time (days)[cde]	Plant stand/12 seeds planted (35 dap)[c]	Number of stunted seedlings/12 seeds planted (35 dap)[ce]	Plant vigor (0 to 9) (35 dap)[bd]	Number of albino seedlings (35 dap)	≥ 50% of plants with tillers (49 dap)[eg]	Abnormal seedling characteristics[g]
wh11017a	*sh2*	W192034	96.5	17.6 ± 3.3	5.5 ± 2.5	2.5 ± 1.5	3.5 ± 0.5	0.0 ± 0.0		
I136-1-1-1-1-1	*sh2*	S190660	96.0	15.1 ± 2.9	4.5 ± 0.5	0.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0	+	
wh05032a1	*sh2*	S190132	95.8	18.9 ± 3.6	5.5 ± 0.5	3.0 ± 1.0	4.0 ± 0.0	0.0 ± 0.0		Herbicide injury (49 dap)
IL104g	*su*	S190079	95.8	19.7 ± 0.1	5.5 ± 1.5	2.0 ± 0.0	5.0 ± 0.0	0.0 ± 0.0	+	
MR10	*sh2*	S190617	95.0	18.0 ± 0.0	5.0 ± 2.0	1.0 ± 1.0	4.0 ± 0.0	0.0 ± 0.0		
MDM-1	*su*	S190103	94.8	20.4 ± 1.7	6.0 ± 2.0	3.0 ± 1.5	4.0 ± 0.0	0.0 ± 0.0		
K192-1-1-1-1-1-1	*sh2*	S190665	93.3	12.9 ± 5.5	4.5 ± 2.5	1.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
IL27a	*su*	S190047	93.3	18.2 ± 0.2	5.0 ± 2.0	1.5 ± 0.0	3.5 ± 0.5	0.0 ± 0.0		
MDM 9	*su*	S190990	90.5	19.3 ± 1.3	5.5 ± 3.5	1.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0		
IL325a	*su*	S190190	89.8	18.9 ± 0.5	5.0 ± 1.0	0.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		
wh10062R	*sh2*	S191056	88.0	19.6 ± 1.6	5.0 ± 1.0	2.0 ± 0.0	3.5 ± 0.5	0.0 ± 0.0		Herbicide injury (49 dap)
wh09086	*sh2*	S191091	87.0	19.0 ± 0.5	5.0 ± 1.0	2.5 ± 1.5	3.0 ± 0.0	0.0 ± 0.0		
L185-1-1-1-1-3-1	*sh2* Het-*su*	W191283	86.3	19.7 ± 3.1	5.5 ± 2.5	1.5 ± 1.5	4.0 ± 1.0	0.0 ± 0.0		
I9-1-1-1-1-1-1	*sh2suse*	S191128	85.5	15.9 ± 2.1	4.0 ± 1.0	1.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
we12401	*se*	S190021	85.5	17.1 ± 1.8	4.5 ± 1.5	2.0 ± 1.0	4.0 ± 0.0	0.0 ± 0.0		
Silver #9	WT	S190039	85.5	17.7 ± 1.5	4.5 ± 0.5	1.5 ± 0.5	3.5 ± 0.5	0.0 ± 0.0		Herbicide injury (49 dap)
IL798c	*su*	W192141	83.8	17.7 ± 1.0	4.5 ± 1.5	1.0 ± 0.0	5.5 ± 0.5*	0.0 ± 0.0	+	
wh09137R	*sh2*	S190071	82.0	18.6 ± 0.3	4.5 ± 1.50	0.5 ± 0.5	5.0 ± 0.0*	0.0 ± 0.0		
N120-1-X-1-1-1-1-1-3	*sh2suse*	F190092	81.0	20.1 ± 1.6	5.0 ± 1.0	3.0 ± 0.0	3.5 ± 0.5	0.0 ± 0.0		
wh07020a	*sh2*	W192003	80.3	19.3 ± 2.1	4.5 ± 0.5	1.5 ± 1.5	4.0 ± 0.0	0.0 ± 0.0		
N45A-1	*sh2su*	S190572	78.5	15.2 ± 2.8	3.5 ± 1.5	0.0 ± 0.0	3.0 ± 0.0	0.0 ± 0.0		
wh10113R	*sh2*	S190541	78.3	19.3 ± 3.9	5.0 ± 2.0	2.5 ± 1.5	3.5 ± 0.5	0.0 ± 0.0		
Cuzco suse	*suse*	W191206	77.8	17.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0	4.5 ± 0.5	0.0 ± 0.0		
wh10070R	*sh2*	S190097	76.8	19.7 ± 0.0	4.5 ± 0.5	3.0 ± 1.0	4.0 ± 0.0	0.0 ± 0.0		
NE EDR sh2	*sh2*	W191708	76.8	20.4 ± 1.9	4.5 ± 1.5	1.0 ± 1.0	3.5 ± 0.5	0.0 ± 0.0		
wh10052Ra	*sh2*	S190564	74.3	18.3 ± 0.3	4.0 ± 0.0	1.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
HI 76	WT	W191462	70.8	16.1 ± 1.8	3.5 ± 0.5	0.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
Hi BT SYN 3	WT	S190540	70.8	21.1 ± 1.6	4.5 ± 0.5	2.0 ± 0.0	3.5 ± 0.5	0.0 ± 0.0		Chlorotic plants (28 - 35 dap)
IL11D	*su*	S190060	70.5	15.3 ± 4.3	3.5 ± 0.5	1.0 ± 0.0	4.0 ± 0.0	0.0 ± 0.0		
Burnell Golden Bantam	*su*	W191399	69.0	18.3 ± 2.3	4.0 ± 2.0	1.5 ± 1.0	4.0 ± 1.0	0.0 ± 0.0	+	
R839	*sh2*	S190076	69.0	19.4 ± 1.4	4.0 ± 1.0	1.0 ± 1.5	4.5 ± 0.5	0.0 ± 0.0	+	
wh10163	*sh2*	W191526	67.8	23.9 ± 1.7	5.5 ± 1.5	1.0 ± 1.0	3.0 ± 0.0	0.0 ± 0.0		

Sweet corn line[a]	Genotype[a]	Entry[a]	AUEPC[ab]	Mean emergence time (days)[cde]	Plant stand/12 seeds planted (35 dap)[c]	Number of stunted seedlings/12 seeds planted (35 dap)[ce]	Plant vigor (0 to 9) (35 dap)[bd]	Number of albino seedlings (35 dap)	≥ 50% of plants with tillers (49 dap)[eg]	Abnormal seedling characteristics[g]
13B-587-68A	*su*	S190698	67.8	24.4 ± 0.4	5.5 ± 0.5	3.0 ± 1.0	3.0 ± 0.0	0.0 ± 0.0		
wuh09170i	*sh2*	S190678	63.8	20.7 ± 0.7	4.0 ± 1.0	2.5 ± 0.0	3.5 ± 0.5	0.0 ± 0.0		
OH43 sh2	*sh2*	S191318	63.0	18.7 ± 0.7	3.5 ± 0.5	0.0 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
wh10006R	*sh2*	S191053	62.0	17.9 ± 1.9	3.5 ± 1.5	1.0 ± 0.0	3.5 ± 0.5	0.0 ± 0.0		
A648	*su*	W191095	62.0	20.7 ± 1.2	4.0 ± 2.0	0.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
We03418a	*se*	S190648	62.0	21.1 ± 1.1	4.0 ± 1.0	1.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
I22-1-1-1-1-1-1	*sh2*	W191587	61.3	16.2 ± 2.8	3.0 ± 0.0	1.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
wh13064	*sh2*	S190652	59.5	20.0 ± 0.3	3.5 ± 0.5	0.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
wh09033	*sh2*	S190181	57.0	18.0 ± 0.0	3.0 ± 1.0	0.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
wuh09191i	*sh2*	S190544	56.8	23.5 ± 1.5	4.0 ± 2.0	1.5 ± 1.5	3.0 ± 0.0	0.0 ± 0.0		
wh13070	*sh2*	S190997	55.0	21.2 ± 2.5	3.5 ± 0.5	1.0 ± 1.0	3.0 ± 0.0	0.0 ± 0.0		
wh09141R	*sh2*	S191368	54.3	21.1 ± 2.1	3.5 ± 0.5	1.0 ± 1.0	3.5 ± 0.5	0.0 ± 0.0	+	
IL778d	*su*	S191040	54.3	21.6 ± 2.1	3.5 ± 0.5	0.5 ± 0.5	3.0 ± 0.0	0.0 ± 0.0		
Ind 5817	*su*	W190773	53.8	17.3 ± 0.7	2.0 ± 1.0	0.5 ± 0.5	3.5 ± 0.5	0.0 ± 0.0		
HI 81	WT	W191934	53.5	19.2[f]	3.0 ± 3.0	2.0 ± 0.0	2.0 ± 2.0	0.0 ± 0.0		
I237-1-2-1-1-1-1-1	Het-*su*	F190345	53.5	19.3 ± 0.3	3.0 ± 1.0	0.5 ± 0.5	3.0 ± 0.0	0.0 ± 0.0		
wh10173V	*sh2*	S190556	52.8	16.2 ± 1.8	2.5 ± 0.50	0.0 ± 0.0	3.5 ± 0.5	0.0 ± 0.0		
wh11005	*sh2*	W192117	52.5	21.9 ± 0.4	3.5 ± 0.5	1.5 ± 0.5	2.5 ± 0.5	0.0 ± 0.0		
wh12005	*sh2*	S191345	51.8	18.6 ± 2.6	3.0 ± 1.0	1.0 ± 1.0	2.5 ± 0.5	0.0 ± 0.0		Yellow plants (28 - 35 dap)
wh04036VW	*sh2*	S190508	51.8	20.1 ± 0.9	3.0 ± 2.0	1.0 ± 0.0	3.0 ± 0.0	0.0 ± 0.0		
IL200e	*su*	S190986	47.5	12.5 ± 0.5	2.0 ± 0.0	0.0 ± 0.0	4.5 ± 0.5	0.0 ± 0.0		
Atkinson	*sh2su*	S190050	47.5	17.8 ± 1.3	2.5 ± 0.5	0.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
Wh9261	*sh2*	S190569	47.5	18.1 ± 1.2	2.5 ± 0.5	0.0 ± 0.0	4.5 ± 0.5	0.0 ± 0.0	+	
IL799b	*su*	W190783	46.5	19.9 ± 3.9	3.0 ± 1.0	1.0 ± 1.0	3.0 ± 1.0	0.0 ± 0.0		
If825	*sh2*	S190591	45.8	18.2 ± 2.2	2.5 ± 0.5	0.5 ± 0.5	4.5 ± 0.5	0.0 ± 0.0		
Wh00050	*sh2*	W191997	45.8	18.3 ± 0.3	2.5 ± 1.5	0.0[f]	3.0 ± 0.5	0.0 ± 0.0		
wuh07481i	*sh2*	S191018	44.8	24.3 ± 3.7	3.0 ± 2.0	3.0[f]	3.0 ± 1.0	0.0 ± 0.0		
245	*su*	S191066	44.0	19.8 ± 1.1	2.5 ± 1.5	2.0[f]	4.0 ± 0.0	0.0 ± 0.0	+	
Glancaster sh2	*sh2*	S190563	43.0	11.3 ± 6.3	2.0 ± 1.0	1.0 ± 1.0	3.5 ± 0.5	0.0 ± 0.0		
wh10034R	*sh2*	S190500	39.5	23.1 ± 1.6	3.0 ± 1.0	1.0 ± 0.0	3.0 ± 0.0	0.0 ± 0.0		
wh10231V	*sh2*	S190092	38.8	20.9 ± 1.4	2.5 ± 0.5	0.5 ± 0.5	3.5 ± 0.5	0.0 ± 0.0		
wh10035R	*sh2*	S190510	38.8	20.9 ± 1.4	2.5 ± 0.5	1.00± 0.0	3.5 ± 0.5	0.0 ± 0.0		
IL673a	*su*	S190086	38.8	21.1 ± 1.6	2.5 ± 0.5	0.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
Wh96011	*sh2*	S190098	38.0	18.0 ± 0.0	2.0 ± 0.0	0.5 ± 0.5	3.5 ± 0.5	0.0 ± 0.0		
wh92047	*sh2*	S191126	36.3	17.0 ± 3.0	2.0 ± 1.0	1.0[f]	4.0 ± 0.0	0.0 ± 0.0		Herbicide injury (49 dap)

Sweet corn line[a]	Genotype[a]	Entry[a]	AUEPC[ab]	Mean emergence time (days)[cde]	Plant stand/12 seeds planted (35 dap)[c]	Number of stunted seedlings/12 seeds planted (35 dap)[ce]	Plant vigor (0 to 9) (35 dap)[bd]	Number of albino seedlings (35 dap)	≥ 50% of plants with tillers (49 dap)[eg]	Abnormal seedling characteristics[g]
wuh12037i	*sh2*	S190595	35.3	18.8[f]	2.0 ± 2.0	1.0 ± 0.0	2.0 ± 2.0	0.0 ± 0.0		
K15-1(X9)	*sh2*	W190768	31.0	21.2 ± 0.2	2.0 ± 1.0	2.0[f]	3.0 ± 0.0	0.0 ± 0.0		
HI 70	WT	W191280	30.3	16.7[f]	1.5 ± 1.5	0.0[f]	2.0 ± 2.0	0.0 ± 0.0		
Wh14201N	*sh2*	S190054	28.5	18.0 ± 0.0	1.5 ± 0.5	0.0 ± 0.0	3.0 ± 0.0	0.0 ± 0.0		
wh14102V	*sh2*	W191420	26.8	19.5 ± 1.5	1.5 ± 0.5	0.5 ± 0.5	4.0 ± 0.0	0.0 ± 0.0		
Wh96034	*sh2*	S191020	23.3	20.0 ± 3.0	1.5 ± 0.5	1.0[f]	3.0 ± 0.0	0.0 ± 0.0		
IL777a	*su*	S191103	23.3	21.0 ± 0.0	1.5 ± 0.5	0.0[f]	4.0 ± 0.0	0.0 ± 0.0		
MDM 21	*su*	S190626	23.3	21.3[f]	1.5 ± 1.5	1.0[f]	2.0 ± 2.0	0.0 ± 0.0		
wh13048	*sh2*	S191094	21.5	21.5 ± 3.5	1.5 ± 0.5	0.0 ± 0.0	3.0 ± 1.0	0.0 ± 0.0		
FL32	*sh2*	W191089	21.5	22.0 ± 1.0	1.5 ± 0.5	0.0[f]	3.0 ± 0.0	0.0 ± 0.0		
Shrunken Zapalote Chico	*sh2*	S190744	19.0	17.5 ± 3.5	1.0 ± 0.0	0.0[f]	3.0 ± 0.0	0.0 ± 0.0		
wh09126R	*sh2*	S190502	19.0	18.0[f]	1.0 ± 1.0	0.0 ± 0.0	2.0 ± 2.0	0.0 ± 0.0	+	
wh14119V	*sh2*	W191754	19.0	18.0 ± 0.0	1.0 ± 0.0	0.0[f]	3.0 ± 0.0	0.0 ± 0.0		
wh05070a	*sh2*	S190202	16.3	24.5[f]	1.0 ± 1.0	1.0 ± 0.0	3.0 ± 0.0	0.0 ± 0.0		
Mexican Dent sh2	*sh2*	S191042	13.8	23.0 ± 5.0	1.0 ± 0.0	-	3.0 ± 0.0	0.0 ± 0.0		
wh07165R	*sh2*	S190015	12.0	24.5[f]	1.0 ± 1.0	1.0 ± 0.0	1.5 ± 1.5	0.0 ± 0.0		
Mo17 su/su	*su*	W191218	12.0	30.0[f]	1.0 ± 1.0	0.0[f]	1.5 ± 1.5	0.0 ± 0.0		
K104-1	*sh2*	W191357	7.8	21.0[f]	0.5 ± 0.5	-	2.0 ± 2.0	0.0 ± 0.0		
K127-1-1-1-2-1-1-1-1	*sh2*	S190610	7.8	25.0 ± 0.0	0.5 ± 0.5	0.0[f]	1.5 ± 1.5	0.0 ± 0.0		
K169-1-1-1-2-2	*sh2*	F190350	6.0	25.0	0.5 ± 0.5	0.0 ± 0.0	1.5 ± 1.5	0.0 ± 0.0		
wh07166R	*sh2*	S190115	5.3	-	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	-	
we10401	*se*	S191063	1.8	-	0.0 ± 0.0	-	0.0 ± 0.0	0.0 ± 0.0	-	
B84 plus su	*su*	F190111	0.0	-	0.0[f]	0.0[f]	0.0[f]	0.0[f]	-	
wh10040R	*sh2*	S190527	0.0	-	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	-	
GSS 3951	*sh2*	GSS 3951[h]	184.0	17.5 ± 0.1	9.5 ± 0.2	1.9 ± 0.1	5.0 ± 0.0	0.0 ± 0.0	+	
Mean			152.8 ± 2.3	18.3 ± 0.1	8.3 ± 0.1	1.5 ± 0.0	4.4 ± 0.0	0.2 ± 0.2	-	-
Range			0.00 – 245.5	10.5 – 30.0	0.0 – 12.0	0.0 – 5.0	0.0 – 7.0	0.0 – 3.0	-	-

[a] The lines included in this trial are a subset of the accession panel of the United States Department of Agriculture National Institute of Food and Agriculture Specialty Crops Research Initiative Project No. 2018-51181-28419 accession panel. Sweet corn line refers to the designated name of the sweet corn accession. Entry refers to the specific sweet corn accession and the seed lot. Genotype refers to the endosperm type of the sweet corn accession: NA = no information, field = standard field corn type, *su = sugary 1*, *se = sugary enhanced*, *sh2 = shrunken 2*.

[b] AUEPC = Area under the emergence progress curve as calculated by Sun et al. (2015) for stand counts recorded weekly from 14 to 49 days after planting (dap). Sweet corn lines are arranged in order of largest to smallest mean AUEPC value.

[c] Mean ± standard error. Refer to the main text for details on how mean plant stand/plot, mean number of stunted seedlings/plot, and mean plant vigor were rated. The 24 sweet corn lines with an asterisk after the vigor rating had a mean vigor rating at least as good as that of the standard *sh2* processing hybrid, GSS 3071, planted throughout the trial.

[d] Mean emergence time (MET) in days, as calculated by Demir and Matthews (2010).

[e] '-' = No plants emerged in both replicate plots so stunting, tiller production, and vigor could not be rated.

[f] Lines without a standard error only had plants emerge in one of the two replicate plots.

[g] '+' = Lines with plots in which ≥50% of the plants produced tillers.

[h] GSS 3951 was planted in 88 plots scattered throughout the trial as a standard, *sh2,* processing sweet corn hybrid commonly grown in the Columbia Basin of central Washington and northcentral Oregon.

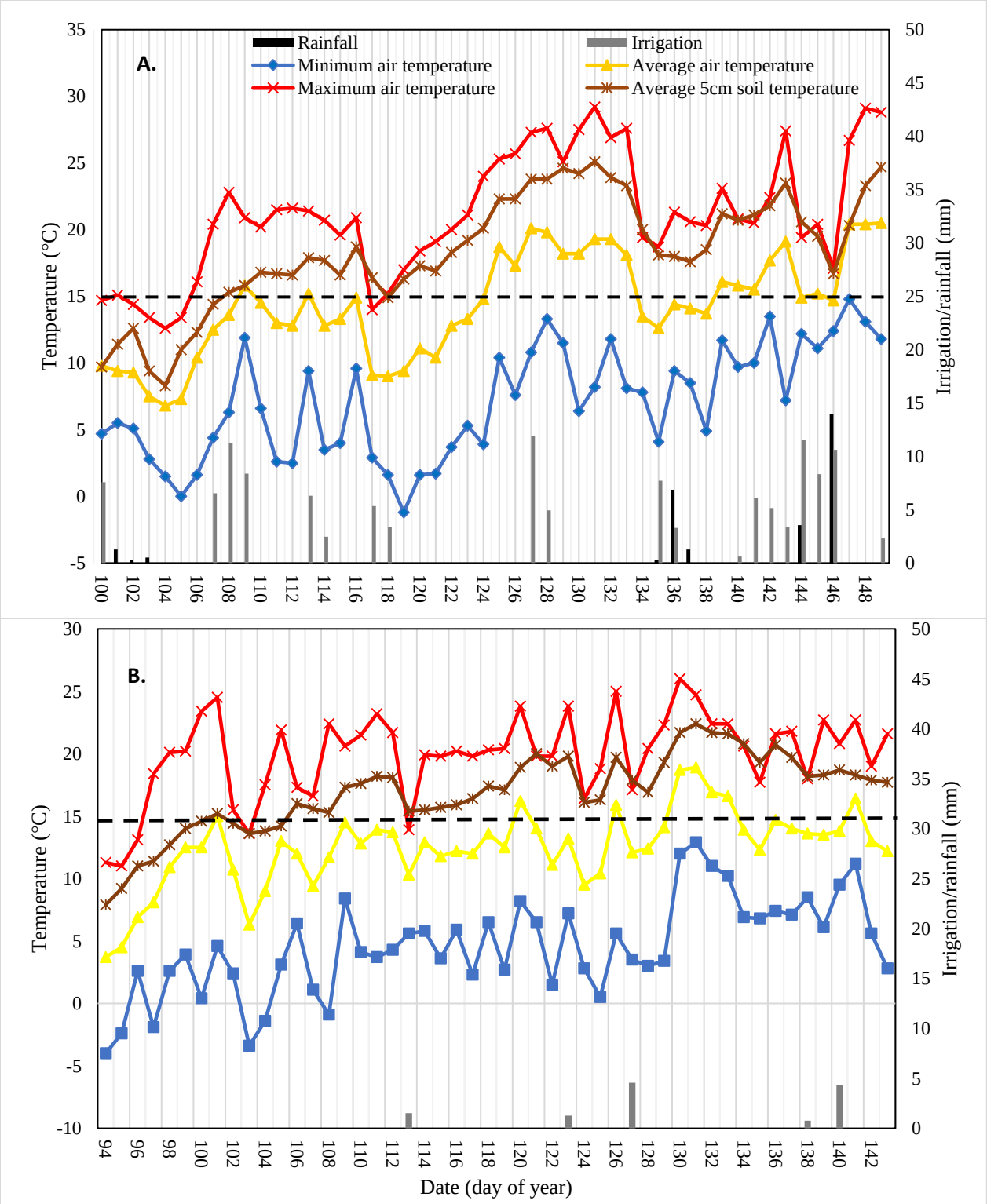

Fig. 3.1. Minimum, maximum, and average air temperature as well as average soil temperature (5-cm depth) measured by the Washington State University AgWeatherNet station near Ephrata,

WA (47.18^{o}N, 119.64^{o}W) over the duration of a sweet corn cold tolerance trial planted near George, WA in 2019 (**A**) and 2020 (**B**). In 2019, the days of the year were from 10 April (100), to 29 May (149). In 2020, 3 April (planting = 94 days) and 22 May (143 days). The black dashed line represents the threshold of 15^{o}C soil temperature for planting sweet corn. In 2019, the minimum air and soil temperatures dropped below this threshold during 49 and 8 days, respectively, of the 49 days of the trial. In 2020, the minimum air and soil temperatures dropped below this threshold during 49 and 11 days, respectively, over the 49 days of the trial.

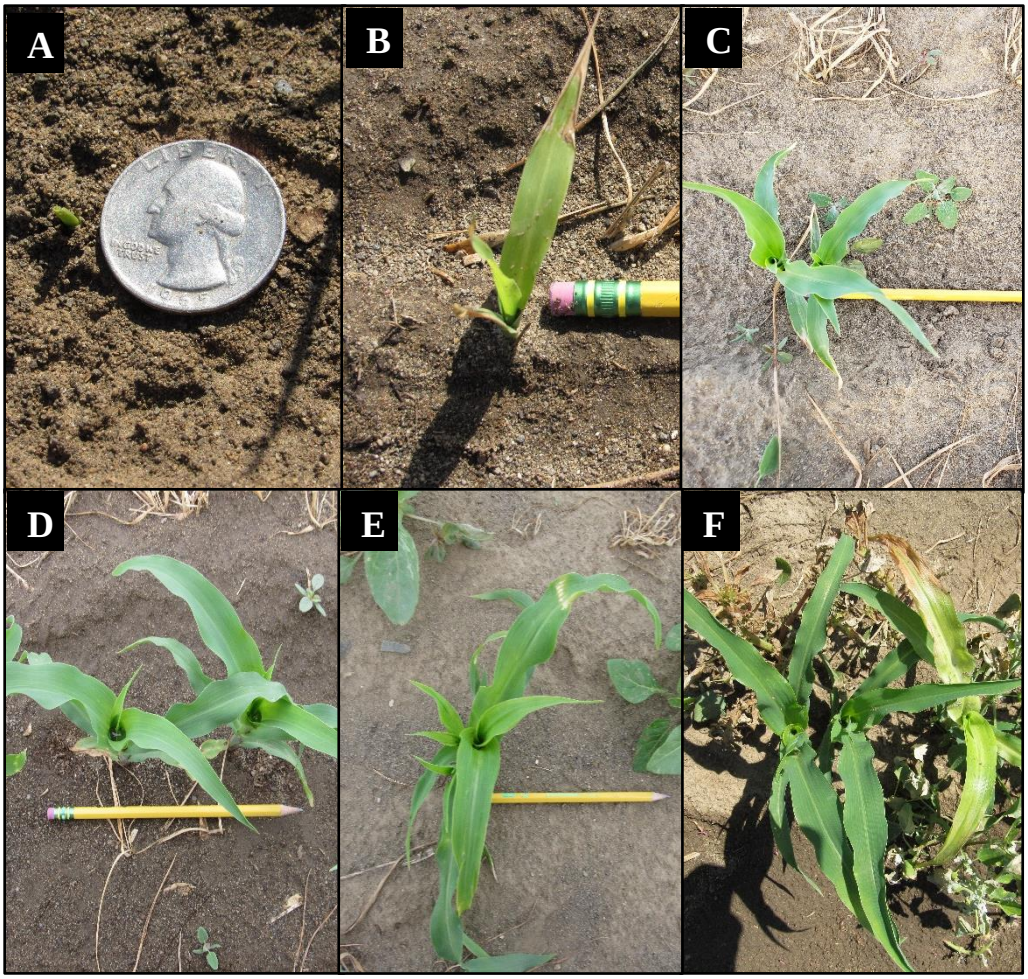

Fig. 3.2. Development of the processing sweet corn hybrid, GSS 3071, from 14 to 49 days after planting (dap) this hybrid as a standard entry in a sweet corn cold tolerance screening trial near George, WA in April 2019. Seedling growth stages shown represent 14, 21, 28, 35, 42, and 49 dap, respectively (**A-F**).

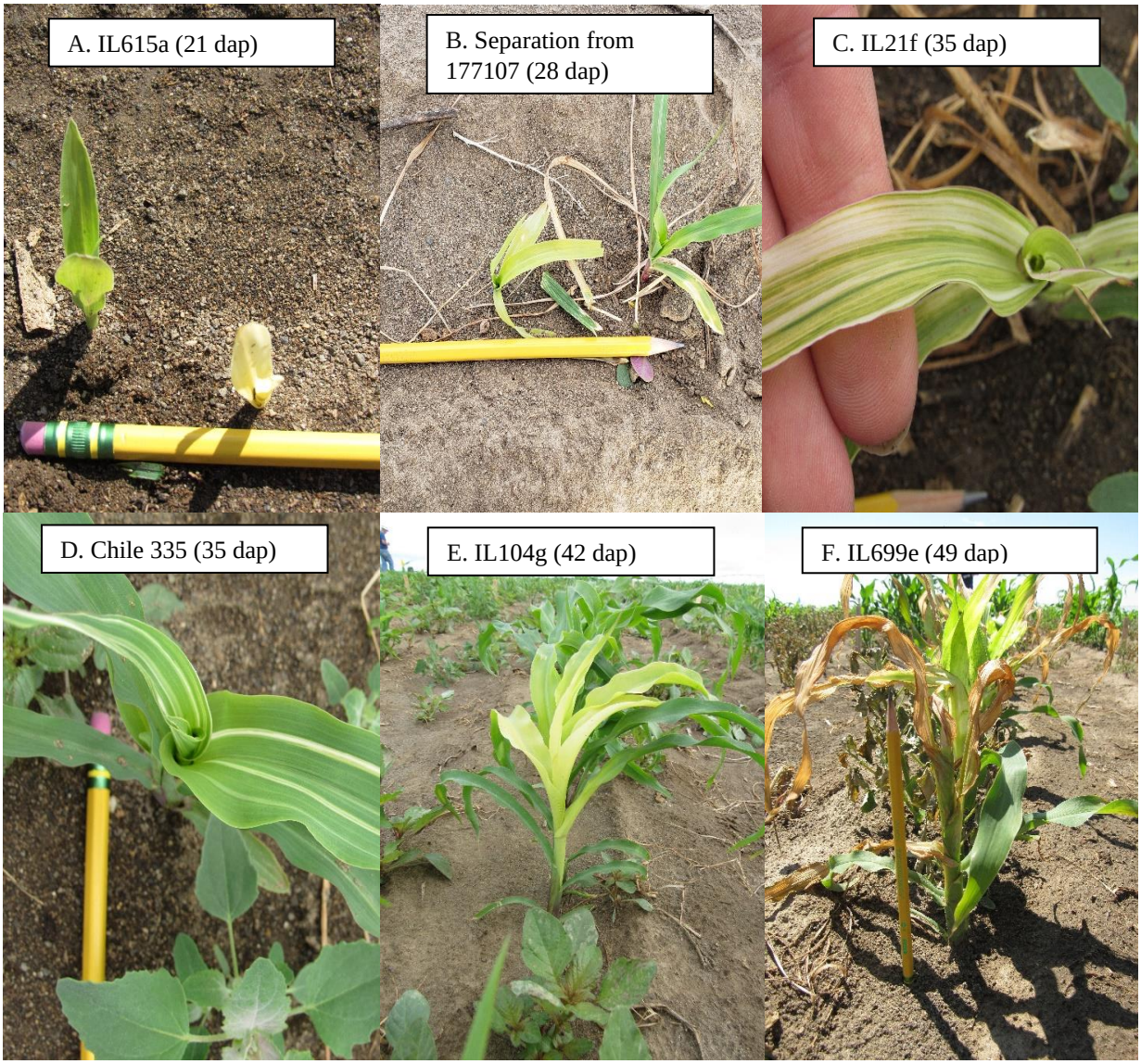

Fig. 3.3. Abnormal development of some plants in a sweet corn cold tolerance screening trial planted near George, WA in April 2019. (**A**) Sweet corn accession IL615a with an albino seedling 21 days after planting (dap). (**B**) A yellow seedling of Separation from 177107 observed 28 dap. (**C**) A plant of IL21f with interveinal chlorosis 35 dap. (**D**) A plant of Chile 335 with interveinal chlorosis 35 dap. (**E**) A plant of IL104g with severe chlorosis 42 dap. (**F**) A plant of IL699e with chlorotic new growth and leaf dieback 49 dap.

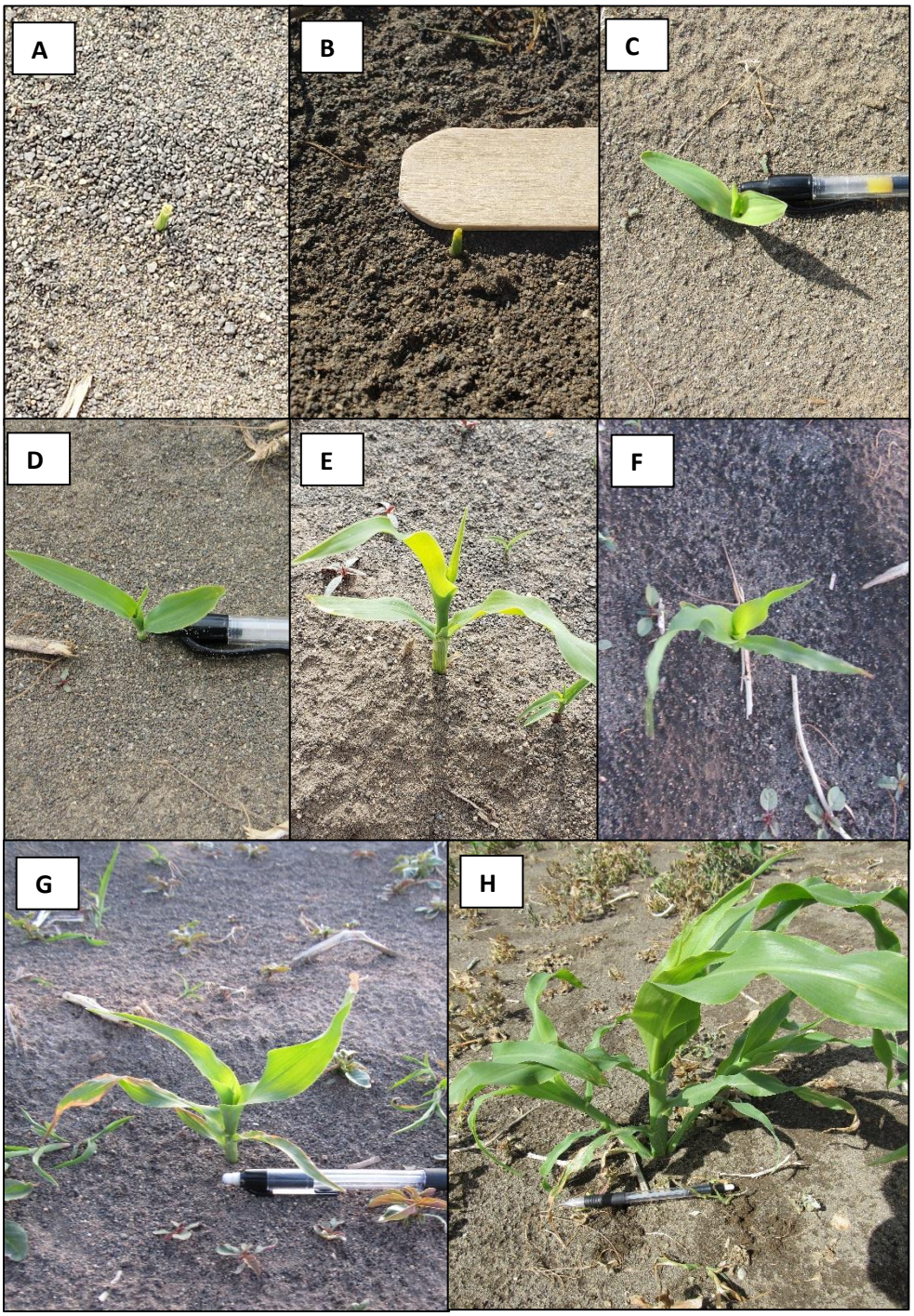

Fig. 3.4. Development of the processing sweet corn hybrid, GSS 3951, in a sweet corn cold tolerance screening trial planted near George, WA in April 2020. Photos were taken 11, 14, 18, 21, 25, 28, 35, and 49 days after planting (dap), respectively (**A**-**H**). GSS 3951 was used as a

standard, supersweet (*sh2*), processing hybrid for comparison with 580 entries from the diversity panel of the United States Department of Agriculture National Institute of Food and Agriculture Specialty Crops Research Initiative (USDA NIFA SCRI) Sweet CAPS Project No. 2018-51181-28419.

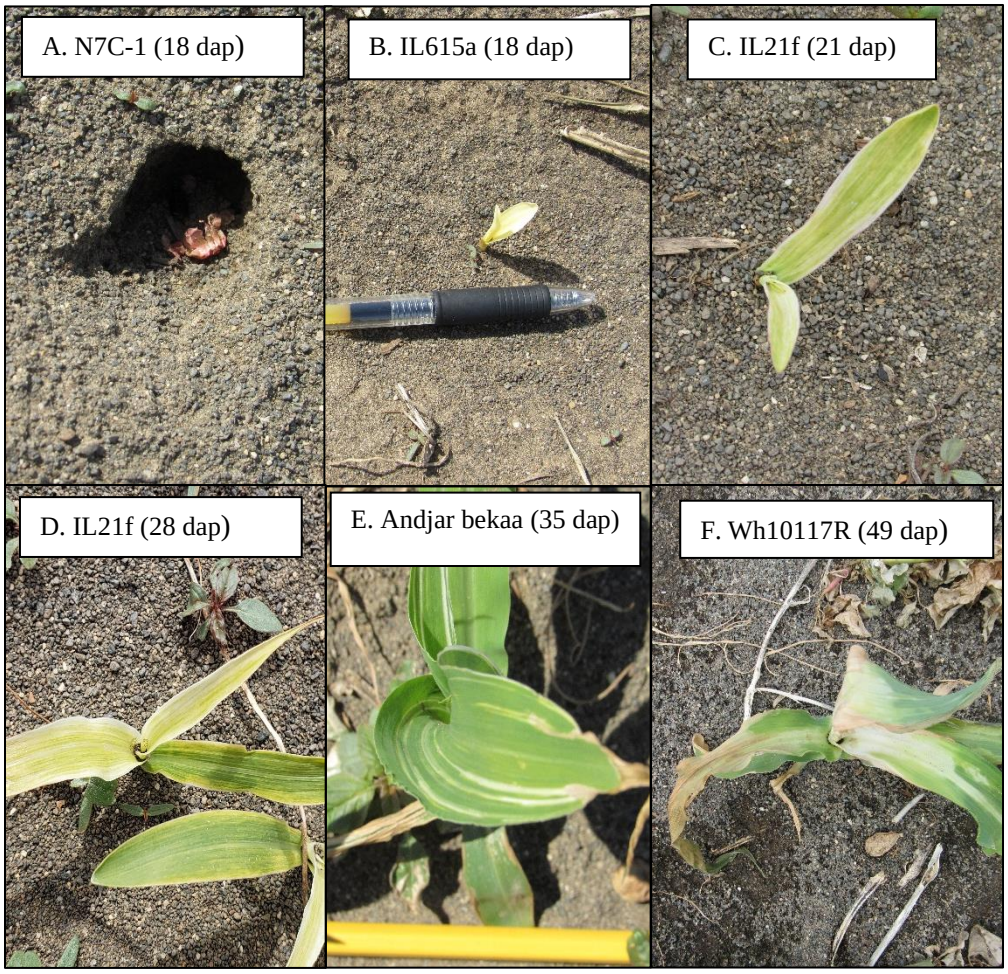

Figure 3.5. Issues and abnormal development observed in a sweet corn cold tolerance screening trial planted near George, WA in April 2020. (**A**) Bird damage to a seedling of N7C-1 18 days after planting (dap). (**B**) Albino seedling of IL615a 18 dap. (**C**) A yellow seedling of IL21f observed 21 dap. (**D**) A plant of IL21f with chlorotic new growth 28 dap. (**E**) A plant of Andjar bekaa with interveinal chlorosis 35 dap. (F) A plant of Wh10117R with chlorotic new growth and leaf dieback 49 dap.