**Evaluating host resistance to Verticillium wilt in strawberry**

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The 2025–26 season marks the tenth consecutive year of a long-term field trial evaluating strawberry genotypes for resistance to Verticillium wilt caused by *Verticillium dahliae*. This year's trial included 92 cultivar entries from six breeding programs. Driscoll's, Good Farms, Pinnacle Berry Genetics, Planasa, Plant Sciences, and UC Davis. Plots consisted of 20 plants per genotype, with slight variation in some plots due to plant availability. Bareroot transplants were planted in Cal Poly's Field 25, block 3, a field with a well-documented history of Verticillium wilt (Fig. 1). All genotypes were transplanted on 30 October 2025 except for 11 genotypes from Good Farms which were planted on 4 November. The field was not fumigated prior to planting and the soil is naturally infested with *V. dahliae* (8.0 CFU/g soil). Plant mortality was assessed weekly throughout the growing season, with plants classified as dead once 50% or more of the foliage exhibited necrosis (Fig. 2A). Disease symptoms developed gradually, likely reflecting the unusually warm and dry conditions early in the season, which may have been less favorable for Verticillium wilt development. Consequently, symptom progression was delayed, and plant mortality accumulated much more slowly than in previous years.



**Figure 1.** Experimental plot layout for the strawberry cultivar field trial located within Field 25, block 3 at the Cal Poly research field.

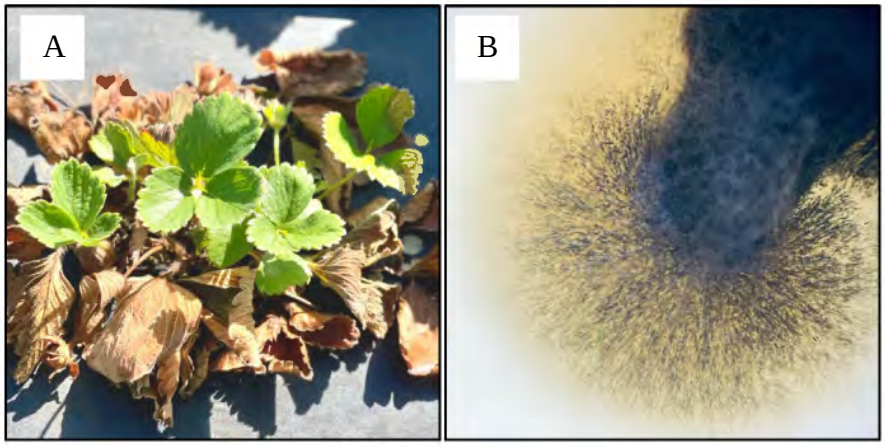



**Figure 2.** A) Symptoms of Verticillium wilt B) *Verticillium dahliae* growing out from one end of an infected strawberry petiole plated on a semi-selective medium (NP-10).

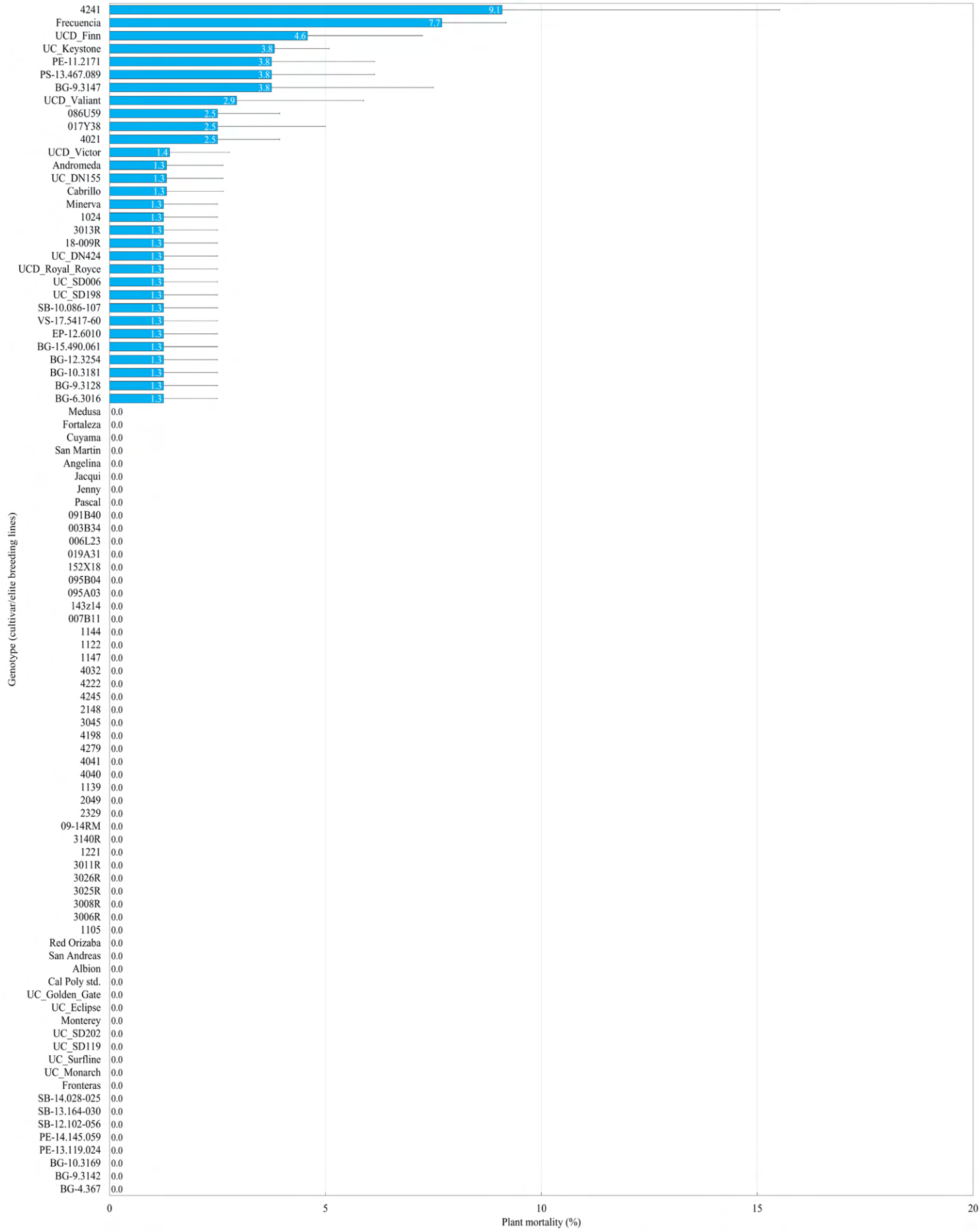



**Figure 3.** Average percent plant mortality due to Verticillium wilt as of 23 June 2026. Error bars represent standard error from four replicates per genotype (n=4).

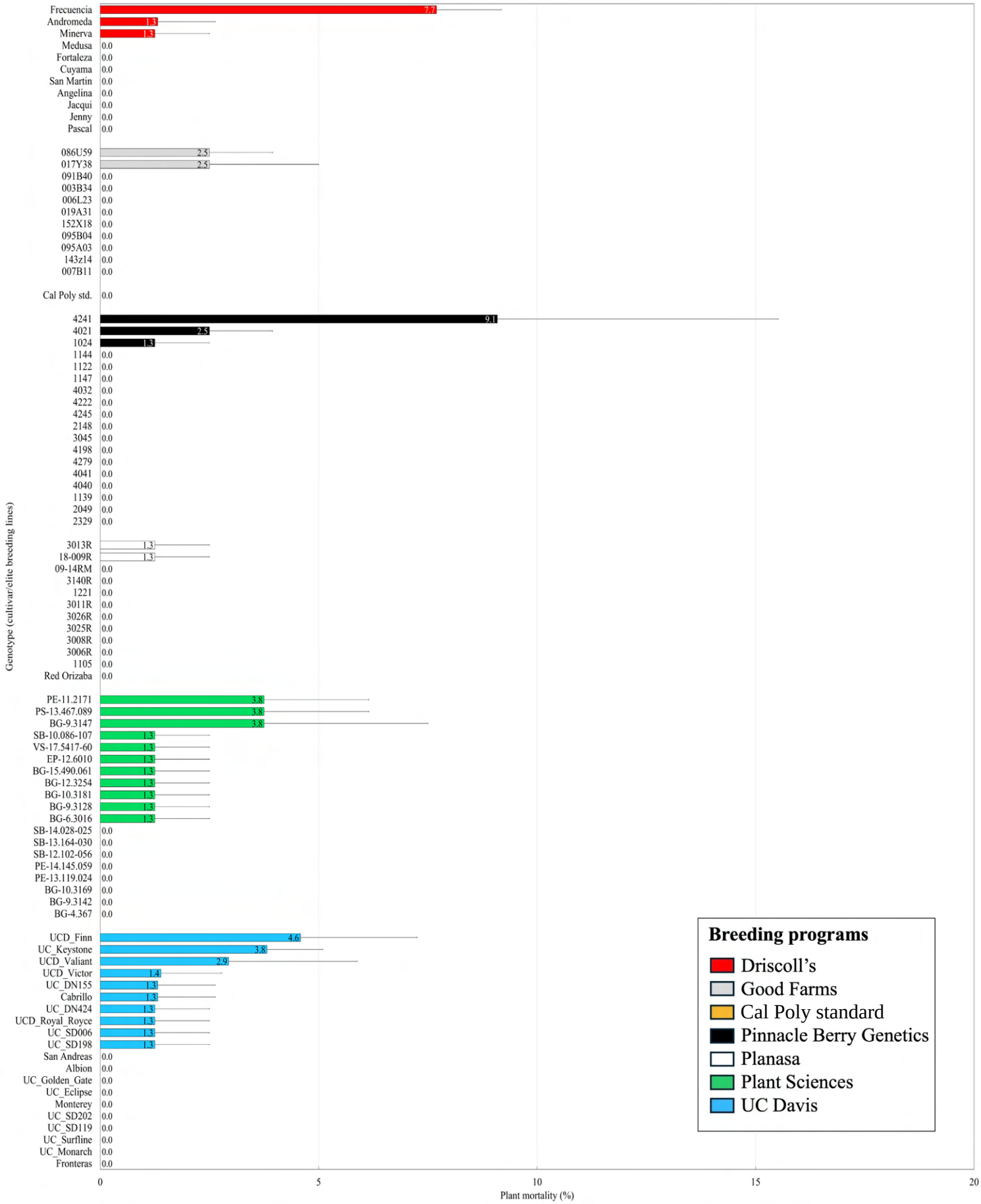



**Figure 4.** Average percent plant mortality due to Verticillium wilt (sorted by breeding program) as of 23 June 2026. Error bars represent standard error from four replicates per genotype (n=4).