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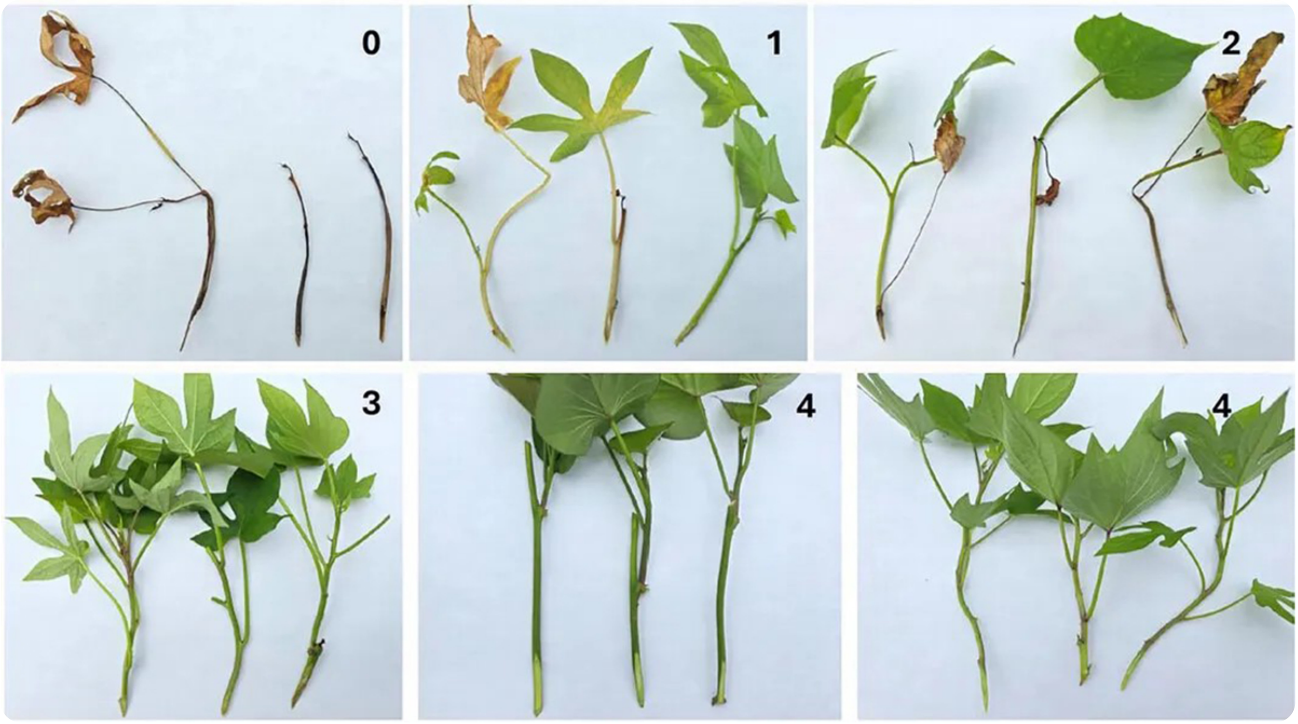
The genetic basis behind *Fusarium* wilt resistance in ‘Covington’ sweetpotato cultivars

April 23, 2026

Dr. Simon Fraher holding a 'Covington' sweetpotato, the major U.S. sweetpotato cultivar. 'Covington' is resistant to Fusarium wilt disease and is widely known for its resistance to other pests and diseases, agronomic performance, and culinary quality. Photo courtesy of D'Lyn Ford, North Carolina State University.

Fusarium wilt (*Fusarium oxysporum* f.sp. *batatas*; Fob) was once considered the most serious disease of sweetpotato (*Ipomoea batatas*). Sweetpotato is propagated from vine cuttings, leaving a wound that Fob can colonize, clogging the vascular tissue and causing the characteristic wilt that impacts stand count, yield, and quality. However, cultivar resistance has led to many growers being unaware of this pathogen; ‘Covington,’ a North Carolina State University (NC State) cultivar that now dominates the U.S. market, is resistant to Fob. Little is known about the genetic basis for this resistance, making it difficult to efficiently develop sweetpotato varieties that have enhanced Fob resistance in addition to other agronomic traits.

The segregating population (454 progenies) from susceptible parent ‘NCDM04-0001’ x resistant parent 'Covington' was used by NC State researchers in greenhouse bioassays in three to four replicates across three trials. Progenies and checks were evaluated using a 0–4 scale, where 0 = dead and 4 = asymptomatic. Including relevant experimental parameters, Best Linear Unbiased Estimates (BLUEs) were calculated; across progenies, the adjusted mean resistance was 2.02 ± 0.69, where scores of 2–4 span moderately to highly resistant.



Fusarium wilt disease rating scale. Disease scores are indicated in the top right corner of each image. 0 = highly susceptible (HS; i.e., dead), 1 = susceptible (S; vascular discoloration, minor to heavy foliar dieback), 2 = moderately resistant (MR; some vascular discoloration, minor foliar wilt), 3 = resistant (R; minor vascular discoloration, minor or no foliar wilt), 4 = highly resistant (HR; asymptomatic). Photo courtesy of Simon Fraher, North Carolina State University.

A continuous segregation for resistance motivated a genetic association study (QTL analysis), which identified a major locus consistently across trials on Chromosome 10, explaining 33.8% of variance for resistance. A Basic Local Alignment Search Tool (BLAST) against the diploid *I. trifida* reference genome revealed gene families associated with *Fusarium* resistance in other crops. These genes are now being targeted for marker-assisted selection to accelerate the development of resistant sweetpotato cultivars.

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Fraher, S., Kinczyk, J., Gesteira, G. S., Heim, C., Williamson, S., Olukolu, B. A., Pereira, G. S., Mollinari, M., Hamilton, J. P., Buell, C. R., Zeng, Z.-B., Quesada-Ocampo, L., & Yencho, G. C. (2026). Discovery of a major QTL for resistance to *Fusarium* wilt (*Fusarium oxysporum* f. sp. *batatas*) in the hexaploid Covington sweetpotato. *Crop Science*, *66*, e70239. https://doi.org/10.1002/csc2.70239

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