



# Correction to: Mapping of a novel major effect Hessian fly field partial-resistance locus in southern soft red winter wheat line LA03136E71

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At the time of publication, it appears that there was scientific literature which was contradictory to a statement made in the abstract. The contradictory statement is that “This locus was identified on a chromosome where no other Hessian fly resistance/tolerance QTL has been previously identified.” The authors have removed this statement in the corrected abstract below. There appears to have been identified Hessian fly reaction QTL on the 7D chromosome that the newly identified QTL described here may be related to (Collins et al. 2018; Subramanyam et al. 2013; Tan et al. 2018). The author group believes in reputability and transparency in science. They apologize to the scientific community for

unintentionally propagating misinformation, and hope that this Correction ameliorates the situation.

Corrected abstract:

## Abstract

Hessian fly resistance has centralized around resistance loci that are biotype specific. We show that field resistance is evident and controlled by a single locus on chromosome 7D. Hessian flies (*Mayetiola destructor* Say) infest and feed upon wheat (*Triticum aestivum* L.) resulting in significant yield loss. Genetically resistant cultivars are the most effective method of Hessian fly management. Wheat breeders in the southern USA have observed cultivars exhibiting a “field resistance” to Hessian fly that is not detectable by greenhouse assay. The resistant breeding line “LA03136E71” and susceptible cultivar “Shirley” were crossed to develop a population of 200 random F<sub>4:5</sub> lines using single seed descent. The population was evaluated in a total of five locations in North Carolina during the 2019, 2020, and 2021 seasons. A subsample of each plot was evaluated for the total number of tillers, number of infested tillers, and total number of larvae/pupae. From these data, the percent infested tillers, number of larvae/pupae per tiller, and the number of larvae/pupae per infested tiller were estimated. In all within and across environment combinations for all traits recorded, the genotype effect was significant ( $p < 0.05$ ). Interval mapping identified a single large effect QTL distally on the short arm of chromosome 7D for all environment-trait combinations. This Hessian fly partial-resistance QTL is termed QHft.nc-7D. Fine mapping must be conducted in this region to narrow down the causal agents responsible for this trait, and investigation into the mode of action is highly suggested.

The original article can be found online at <https://doi.org/10.1007/s00122-021-03936-6>.

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