

## Differential Sets

### *Exserohilum turcicum* (Et) - **Sweet corn**

Northern corn leaf blight (NCLB) resistance is achieved by the combined effect of multiple small effect race unspecific resistance genes/QTL and optionally the use of large effect, race specific genes referred to as Ht genes. The most common used gene is *Ht1* which contributes around 50% of the resistance. However, races, able to overcome the *Ht1* gene are known. In case of *Ht1* breaking isolates, the % resistance can drop to 20% or less.

Race unspecific NCLB resistance is highly polygenic and around 30 QTL's with a small effect are identified.

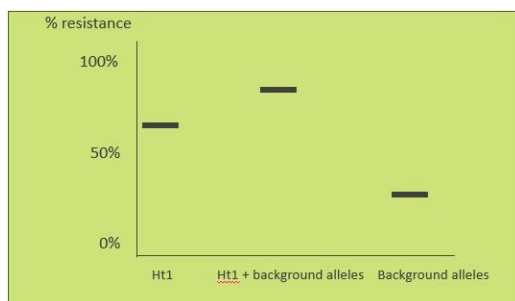
Race unspecific NCLB resistance is often referred to as the genetic background resistance and could add 20 – 40% to the resistance level in common sweetcorn varieties. However, in tropical field corn germplasm much higher resistance levels are known.

There are more major Ht genes known (*Ht2*, *Ht3*, *Htn*) but these are mostly applied in field corn and have not been commonly used in sweetcorn.

Publications do describe variation in symptom expression however, it is not clear if this is due to different alleles of *Ht1* or the genetic background.

The final level of resistance is a result of:

- **PRESENCE OF THE *HT1* GENE.**
- **THE GENETIC BACKGROUND RESISTANCE OF THE PLANT.**
- ***HT1* VIRULENT OR AVIRULENT RACE OF THE PATHOGEN**
- **DIFFERENCES IN AGGRESSIVENESS AMONG THE PATHOGEN ISOLATES.**



Based on the above-mentioned it can be concluded that resistant response in presence of *Ht1* is not black and white and different levels might be observed in practice.

For more information contact the ISF Secretariat at [isf@worldseed.org](mailto:isf@worldseed.org)

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