

New tools for maize lethal necrosis virus in Africa CIMMYT and Corteva Agriscience collaborate on plant breeding innovations

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Abstract: The high-tolerance maize lethal necrosis qualitative trait loci MLN QTL on chr 6L, identified by CIMMYT, has been narrowed to a small region via positional cloning. Through this collaborative effort involving custom marker development and coordinated cycles of mating and high quality phenotyping, the MLN QTL has been narrowed over 100-fold. Analysis of recombinants continues to further narrow the interval. Full genome optical mapping, sequencing, and assembly is on-going and analysis will help define a genome editing strategy for CRISPR-edits to provide MLN tolerance in four CIMMYT elite parent lines, all of which show promising responses in early transformation testing. We will do controlled environment phenotyping to confirm phenotypes in edited materials. The whole genome sequence approach is now feasible and a valuable tool for exploring genetic diversity, especially for specific traits e.g. MLN and for informing important tropical and sub-Saharan diversity for future solutions.