Deletion of the PMR4 genomic region led to the development of the non-transgenic powdery mildew-resistant variety “Tomelo” in less than 10 months, showing the high efficiency and precision of this technology. In addition, CRISPR can be used for rapid domestication of stress-resistant wild materials, keeping their resistance while introducing good agronomic traits.

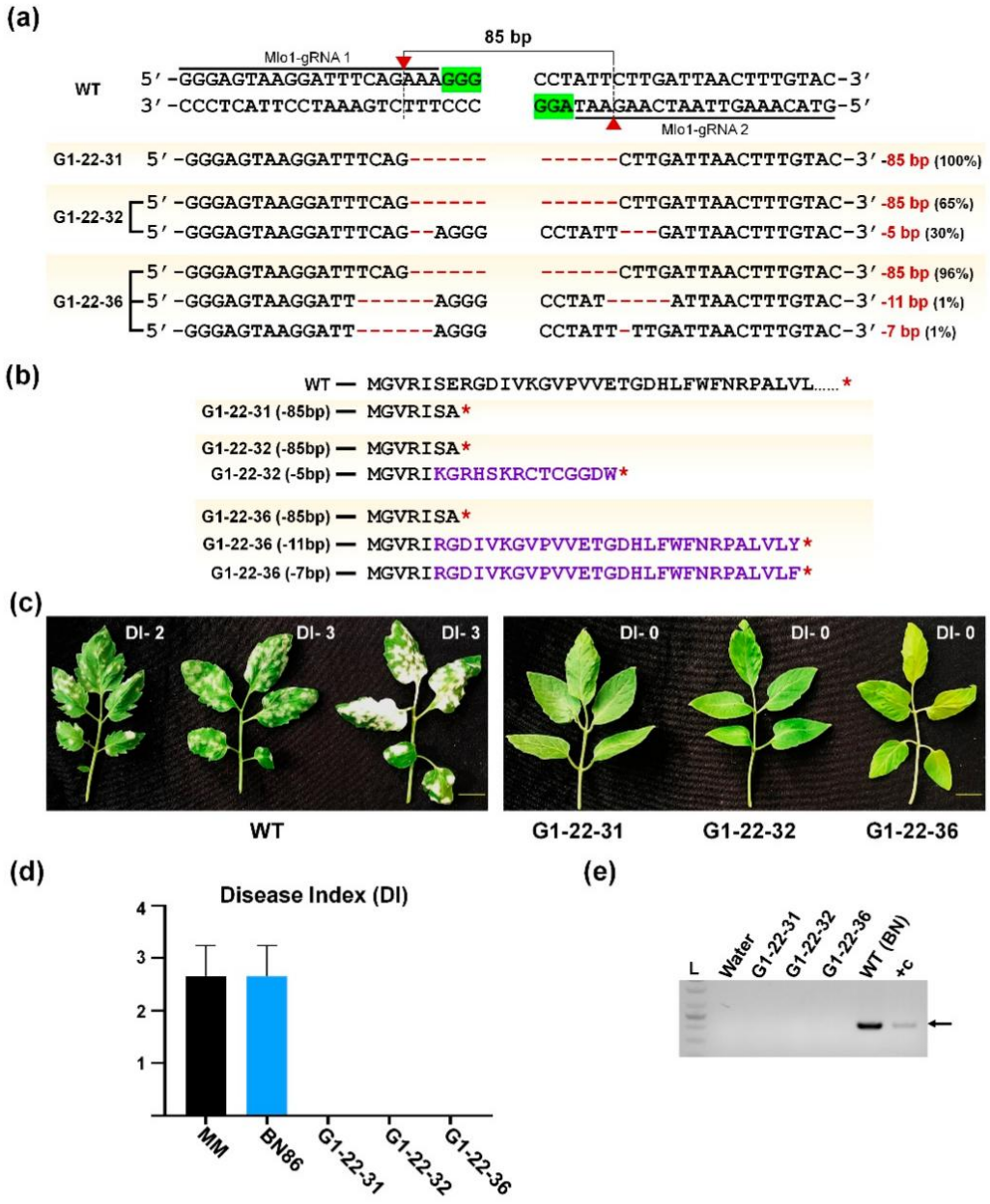

Figure 1 Characterization of CRISPR/Cas9-mediated *SlMlo1* genome-edited tomato lines for powdery mildew resistance. (a) Indel patterns of three *SlMlo1*-knockout plants showing the homozygous (G1-22-31), biallelic (G1-22-32), and chimeric (G1-22-36) genotype. The knockout efficiency (%) of individual lines evaluated using the ICE tool. Red dash indicates the deleted nucleotides; (b) Comparison of amino acid sequence between wild-type (WT) MLO1 protein and truncated region resulting from knockout alleles. Stop codon in red star symbol and altered amino acids in blue was indicated; (c) Analysis of *SlMlo1*-knockout mutant lines tested for resistance against powdery mildew-causing fungus Oidium neolycopersici. The phenotype of the mutant plants evaluated at 21 days post-infection (DPI). Referring to visual fungal growth symptoms, we calculated the disease index; (d) Powdery mildew disease index was calculated with WT (BN-86 and Moneymaker (MM)) and G1 *SlMlo1* mutant lines (G1-22-31, G1-22-32, G1-22-36). Error bars represent SE (three biological replicates); (e) Detection of O. neolycopersici by PCR method using strain-specific 16S ribosomal RNA (rRNA) primers. Non-infected plants used as mock control; fungal DNA used for PCR as a positive control (Adopted from Pramanik et al., 2021)