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TRYING TO UNDERSTAND THE GENETICS BEHIND A DOMINANT SUSCEPTIBLE PHENOTYPE TO ASIAN SOYBEAN RUST DISEASE. Xing Wu¹, Alexandre Garcia², Matthew Hudson¹, and Steven Clough^{1,3}, ¹University of Illinois, Department of Crop Sciences, Urbana, IL USA, ²Tropical Melhoramento e Genética, LTDA, Cambé, PR, Brazil, ³US Department of Agriculture, Urbana, IL USA

Normally, plant disease resistance genes (*R* genes) are inherited in a dominant fashion, and susceptibility is recessive. Not surprisingly, the *R* gene *Rpp1* in soybean is normally dominant over susceptibility for the disease Asian Soybean Rust (ASR). However, a reversal of this dominance/susceptibility was discovered during the breeding process, and line TMG06-0011 was found to be dominant susceptible over *Rpp1* carrying genotypes (Garcia et al. Crop Science 2011). An initial hypothesis to explain the mechanism of how the susceptibility of TMG06-0011 overpowers the dominance of *Rpp1*, was that TMG06-0011 was making small RNA that interfered with *Rpp1* transcription or translation. Therefore, we conducted extensive RNA-Seq and small RNA sequencing projects to gather data that might support this hypothesis. The transcription patterns show that the two resistant plant introductions (PIs) tested, PI 594760B and PI 561356, share some common defenses, and that many of these defenses are reduced in the dominant susceptible; however, so far our data does not support that the suppression mechanism is due to small RNA interference. We have subsequently sequenced the genome of TMG06-0011 using the new Chromium technology of 10X Genomics (www.10xgenomics.com) and succeeded to produce a high quality, whole genome assembly. Based on the sequence analysis of TMG06-0011, our current hypothesis is that the dominant susceptible *rpp1* allele produces a defective product that inactivates the normally dominant Rpp1 protein.

Keywords: Soybean Asian Rust, Ferrugem da soja, dominance suppression