

Identification of Two New Bacterial Pathogens of Peanut, Causing Early Seedling Decline Disease in the Texas Panhandle

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In 2020 we identified in Spanish-type peanut varieties a new disease of peanut in the Texas Panhandle caused by two bacterial pathogens. The observed disease symptoms included seed rot, pre- and post-emergence damping-off, poor seedling vigor, poorly developed root systems with little or no nodule formation, and whole-plant death. Subsequent diagnosis of symptomatic seedlings recovered two bacterial species identified by BLAST using 676- and 661-bp 16S rRNA fragments as a *Ralstonia* sp. and a *Pantoea* sp., respectively. Investigations conducted under greenhouse conditions, using a Valencia-type peanut variety, relying on Koch's postulate established a causative role for both bacteria in the observed disease with the successful reproduction of field symptoms. Symptoms observed on inoculated plants included seed-rot, pre- and post-emergence damping-off, poor seedling vigor, and poorly developed root systems. Given the early onset of symptom development in affected seedlings, a potential seedborne origin of the disease described as *Bacterial Early Decline Disease* (BEDD) was investigated in the same batches of seeds planted and seeds later harvested in the affected fields. In both seeds, identical bacterial species, on the basis of 16R rRNA identity, were recovered indicating that the bacteria are both seedborne and seed-transmissible. Multi-locus sequence analysis involving six genes (*dnaK*, *fumC*, *gyrB*, *murG*, *trpB*, and *tuf*) showed the bacteria are most closely related to *R. pickettii* and *P. dispersa*, but also phylogenetically distinct and thus have been designated *Ralstonia* sp. strain B526 and *Pantoea* sp. strain B270. Losses from the disease in affected fields in 2020 averaged 50% (US \$1.12 million). Findings from this study provide evidence for two new bacterial pathogens of peanut capable of infecting Spanish and Valencia peanut varieties.