

Genetic and phenotypic characterization of *Xanthomonas* species pathogenic of wheat in Uruguay

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Bacterial diseases affecting wheat production worldwide have been an issue of growing concern in the last decade. Nevertheless, the main bacterial diseases of wheat in Uruguay remain largely uninvestigated. To identify bacterial pathogens associated with diseased wheat fields, 61 fields were surveyed from 2017 to 2019 in western Uruguay, yielding a collection of strains identified as *Xanthomonas* spp. by 16S rDNA sequencing. These strains were further characterized via multilocus sequence analysis (MLSA) and typing (MLST), as well as in planta pathogenicity assays. MLSA grouped 44 strains with reference strains for *Xanthomonas translucens* pv. *undulosa*, the pathovar predominantly associated with bacterial leaf streak of wheat (BLS). To evaluate the genetic diversity among strains, MLST was applied, revealing a low diversity among Uruguayan strains identified as *X. translucens* pv. *undulosa*. In addition, 17 strains in the collection were assigned to a separate clade distant from the *X. translucens* species, grouping together with previously unreported *Xanthomonas* strains isolated from wheat in Minnesota, USA. In planta pathogenicity assays were performed on BLS susceptible wheat seedlings. The 44 *X. translucens* pv. *undulosa* strains caused greasy, dark brown necrosis symptoms typical of BLS, while the 17 non-*translucens* *Xanthomonas* sp. strains caused distinctly different dry tan necrosis symptoms. These results reveal that the main bacterial pathogen affecting wheat crops in Uruguay is *X. translucens* pv. *undulosa*, the causal agent of BLS; and that other pathogenic *Xanthomonas* species are associated with wheat crops in South and North America.