



Population genetic analysis and trichothecene profiling of *Fusarium graminearum* from wheat in Uruguay

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ABSTRACT. *Fusarium graminearum sensu stricto* (*F. graminearum* s.s.) is the major causal agent of *Fusarium* head blight of wheat worldwide, and contaminates grains with trichothecene mycotoxins that cause serious threats to food safety and animal health. An important aspect of managing this pathogen and reducing mycotoxin contamination of wheat is knowledge regarding its population genetics. Therefore, isolates of *F. graminearum* s.s. from the major wheat-growing region of Uruguay were analyzed by amplified fragment length polymorphism assays, PCR genotyping, and chemical analysis of trichothecene production. Of the 102 isolates identified as having the 15-ADON genotype via PCR genotyping, all were DON producers, but only 41 strains were also 15-ADON producers, as determined by chemical analysis. The populations were genotypically diverse but genetically similar, with significant genetic exchange occurring between them. Analysis of molecular variance indicated that most of the genetic variability resulted from differences between isolates within

populations. Multilocus linkage disequilibrium analysis suggested that the isolates had a panmictic population genetic structure and that there is significant recombination occurs in *F. graminearum* s.s. In conclusion, our findings provide the first detailed description of the genetic structure and trichothecene production of populations of *F. graminearum* s.s. from Uruguay, and expands our understanding of the agroecology of *F. graminearum* and of the correlation between genotypes and trichothecene chemotypes.

Key words: *Fusarium graminearum*; Wheat; Genetic structure; Trichothecene; Fusarium head blight