

ITS ribosomal DNA phylogeny of *Gaeumannomyces graminis*

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ABSTRACT

Gaeumannomyces graminis causes take-all disease on cultivated cereal grasses (wheat, barley, oats, bentgrass, blugrass and other related grasses). In the present study the, 5.8S and the internal transcribed spacers (ITS) regions of the ribosomal DNA from 21 isolates belonging to *G. graminis* varieties [tritici (5), avenae (4), and graminis (9)], *G. incrustans* (1), *G. leptosporous* (1), and *G. cylindrosporous* (1) were sequenced and then compared to each other. Phylogenetic parsimony analysis among the isolates was carried out. Together, including gaps, ITS and 5.8S regions totaled 660 aligned sites, 220 of which were informative. Only 18 of the informative sites were located in the 5.8S rDNA. All of the isolates tested formed a major clade with high bootstrap support value (100%). *G. leptosporous* and *G. cylindrosporous* formed a distinct subclade. *G. graminis* var. *avenae* grouped together as sister isolates. *G. g.* var. *tritici* isolates formed two monophyletic groups. Four *G. g.* var. *graminis* isolates formed two distinct groups, while two additional isolates were associated with *Ggt* and *Gga* groups. The rest of the isolates were randomly positioned. These data support our previous results using Random amplified polymorphic DNA (RAPD) and Restriction fragment length polymorphism (RFLP) of rDNA.

Key words: ITS rDNA, phylogeny, *G. graminis*.

INTRODUCTION

Gaeumannomyces graminis (Sacc.) Arx & D. Olivier, a filamentous soil borne fungus, parasitizes the roots and crowns of susceptible members of the Gramineae family. The species *G. graminis* is subdivided into four varieties: *G. g.* var. *tritici* (Walker), *G. g.* var. *avenae*, *G. g.* var. *graminis* and *G. g.* var. *maydis*.

Gaeumannomyces genera, species and varieties have been classified using morphological characteristics of the teleomorphic, anamorphic and mycelial states; cultural characteristics; and host-parasite

relationships. The most commonly used criteria for separation of *G. graminis* isolates into varietal groups are hyphopodial type, growth on media containing cystine (Turner, 1959; 1961), and morphology and size of asci and ascospores, respectively.

A complementary approach to fungal taxonomy or phylogeny is represented by DNA analysis of specific genome regions. Methods that can be used include random amplified polymorphic DNA (RAPD), restriction fragment length polymorphisms (RFLPs) and Amplified fragment length polymorphism (AFLP) that permit evaluation of phylogenetic relationships without knowing the nucleotide