

## **Abstract**

During growing seasons of 1386-87 wheat and weeds infected to take-all were collected from infected samples, 28 isolates from *Gaeumannomyces graminis* var. *tritici* (Ggt) were isolated and purified. Pathogenicity test of the isolates was conducted on wheat, rye and oat. The isolates showed the disease symptom on wheat, but not on oat. The disease symptom and signs was highly significant in wheat and rye compared with oat. After almost 7-8 weeks of pathogenicity, a lot of perithecia were observed on crown and roots. Conventional diagnosis of the pathogen is time-consuming, laborious and often inconclusive. Otherwise complexity of the soil microorganisms enhances difficulty in diagnosis of wheat take-all. For example the *Gaeumannomyces-Phialophora* Complex and the non-pathogen *Gaeumannomyces* and *Phialophora* species found on cereal roots are troublemaker. Therefore, the objective of this study was to develop a rapid, simple and species method for differentiation of *Gaeumannomyces graminis* variety using PCR and molecular-based techniques. Simple hyphopodia which grows on lower sheaths of wheat and average length of ascospores showed that all of the isolates belong to Ggt. The isolated Ggts were divided into two subdivisions, R (infected rye) and N (non infected rye). Reaction of the 28 isolates were positive in PCR technique by a pair of primer (NS5:GGT-RP). The primer was designed from the 18S rDNA region of wheat. The morphological and molecular results showed that all of the isolates belonged to Ggt. Enzyme digestion of some isolates with four enzyme *AluI*, *CfoI*, *HinfI* and *RsaI* showed no genetic diversity.

**Keywords:** *Gaeumannomyces graminis*, Identification, Diversity  
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