

Abstract

Uromyces viciae-fabae, *U. appendiculatus* and *U. vignae* are recognized as important pathogens on cultivated legumes throughout the world and cause great economic losses.

Uromyces viciae-fabae is separated into two varieties, var. *viciae-fabae* and var. *orobi*, based on differences in urediniospore wall-thickness and putative host specificity. Although, the difference in urediniospore wall-thickness of *U. viciae-fabae* was considered an important taxonomic characteristic, it is not necessarily distinct among the species compared. Therefore, there has been confusion in the identity of, and relationship between, the two varieties causing the rust diseases in different geographic areas and occurring on closely related host plants. On the other hand, *Uromyces appendiculatus*, inclusive of three varieties, is distinguished from *U. vignae* primarily by the position of urediniospore germ pores and putative host specificity. However, the taxonomic opinions over these morphological and physiological features as a taxonomic character have varied greatly, and, thus, the distinction of these species has often been confused.

The objectives of the present study are to examine morphological features of urediniospores and teliospores of *U. viciae-fabae*, *U. appendiculatus* and *U. vignae* for detecting morphologically discrete taxa and to assess thus circumscribed taxa by phylogenetic divergence estimated from molecular divergence in the D1/D2 region of LSU rDNA and the ITS region including 5.8 S rRNA gene.

(1) *Uromyces viciae-fabae*

Morphological features of urediniospores and teliospores of 94 rust fungus specimens on species of *Vicia*, *Lathyrus* and *Pisum* collected in Japan were examined by light microscopy (LM) and scanning electron microscopy (SEM). In principal component analyses, these morphological features did not show definite host specific morphological groups. In molecular analyses, 23 *Uromyces* specimens from *Vicia*, *Lathyrus* and *Pisum* formed a single genetic clade based on LSU rDNA (D1/D2) region and ITS regions including 5.8 S rRNA gene. Therefore, it suggests that no different fungal taxa exist in *U. viciae-fabae* and only a single fungal taxon is recognized in Japan. In the present study, the specimens used for morphological analyses had similar morphology with *U. viciae-fabae* var. *viciae-fabae*. Therefore, the morphological and molecular analyses suggest that *U. viciae-fabae* var. *orobi* may not be distributed in Japan.

(2) *Uromyces appendiculatus* and *U. vignae*

For clarifying the taxonomy of the two species, morphological features of urediniospores and teliospores of 225 rust fungus specimens on species of *Phaseolus*, *Vigna*, *Apios*, *Lablab* and *Dunbaria* collected in Japan were examined by LM and SEM. Forty-five specimens were subjected to molecular phylogenetic analyses. As a result, the position of germ pores in urediniospores and the teliospore wall thickness were considered as a good character to separate three morphological groups based on principal component analyses. In molecular analyses, the specimens fell into two and three clades based on the nucleotide

sequence at D1/D2 domain of LSU rDNA and ITS regions including 5.8 S rRNA gene, respectively. One of the D1/D2 clades corresponded to one morphological group, while another D1/D2 clade included two other morphological groups. In contrast, each of the three ITS clades corresponded to a separate morphological group. Neither morphological groups nor molecular clades were host-limited. It is suggested that three morphological groups that corresponded to three distinct ITS clades constitute distinct species.

When considering the specimens of three morphological groups that have not been subjected to molecular analyses, the ITS groups/morphological groups are not restricted to particular host genus as discussed previously. Thus, it is concluded that three rust fungus species occur on *Phaseolus*, *Vigna*, *Apios*, *Lablab* and *Dunbaria* in Japan and the three species are referable to *U. appendiculatus*, *U. azukicola* and *U. vignae*.