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Presenter Information T. Kiyoshi, M. Hirata, T. Takamizo, H. Sato, Y. Mano, and M. Fujimori

## Crown rust resistance of Italian ryegrass cultivar 'Axis' to an isolate from Japan

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**Keywords:** major gene, linkage analysis, pseudo-testcross

**Introduction** Crown rust (*Puccinia coronata*) is one the most serious diseases of Italian ryegrass. Crown rust resistance genes in Italian ryegrass have been identified from 'Yamaiku130' and 'Harukaze'. The aim of this study was to identify novel major resistance genes for gene pyramiding in order to develop cultivars with high levels of durable resistance to crown rust.

Materials and methods The Italian ryegrass cultivar 'Axis' provided basic material for this study. Following artificial inoculation, we selected 8 individuals with high level of resistance (no visible symptoms). In order to produce F<sub>1</sub> populations for analysis, the 8 resistant individuals were crossed with susceptible individuals of the cultivar 'Waseaoba'. In order to evaluate resistance, seedlings were grown in plastic trays and inoculated with a crown rust isolate from the Yamaguchi Agricultural Experiment Station in Japan. Two weeks after inoculation, the resistance of individuals was scored according to the following criteria, i: no visible symptom of infection, 0: tiny necrotic and chlorotic flecks without pustules, 1: tiny necrotic and chlorotic flecks with small sized pustules, 2; chlorotic flecks with medium to large sized pustules. The Yamaguchi isolate has been used in our previous work including identification of major resistance gene from Yamaiku130 and Harukaze.

Results The degree of resistance of Axis and the 8  $F_1$  populations are shown in Fig1. 28 (50%) out of 56 individuals of Axis showed complete resistance (i) and a total of 39 individuals (70%) showed some resistance to crown rust after artificial inoculation (Fig1). Among the 8  $F_1$  populations, there was no significant difference between reciprocal crosses, indicating that a cytoplasmic factor did not contribute resistance to the Yamaguchi isolate. Four out of the 8  $F_1$  populations segregated in a 1:1 ratio for resistance and susceptibility (Axis2, Axis3, Axis4, Axis5). Two populations in particular (Axis4 and Axis5) segregated in a 1:1 ratio without partial resistance, suggesting that a resistance gene with major effect was segregating in these populations. Linkage analysis using these populations is efficient in identifying major resistance genes. A large portion of partially resistant plants in populations such as Axis1 and Axis7 suggests that these populations contain resistance genes.

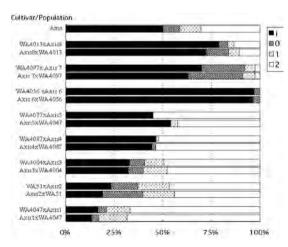


Figure 1 Frequency distribution of the degree of resistance to crown rust in Axis and 8  $F_1$  populations produced by crossing resistant individuals from Axis with susceptible individuals from Waseaoba. The rust scores are explained in the materials and methods

Conclusions
Our data indicate that cytoplasmic factors did not contribute resistance to the Yamaguchi isolate in our populations. This is different from the result obtained by Adams et al. (2000). One possible explanation is a different reaction of the Axis cytoplasm to physiological races. The genetic analysis indicated that Axis possesses at least one dominant resistance gene. In order to identify major resistance genes, we will select 4 populations for linkage analysis in this study.

## Reference

Adams E, Roldan-Ruiz I, Depicker A, van Bockstaele E, de Loose M (2000) A maternal factor conferring resistance to crown rust in *Lolium multiflorum* cv. 'Axis'. Plant Breeding 119 (2): 182-184.

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