

(O1-04)

**Inheritance of anthracnose resistance to *Colletotrichum* spp.
in chili pepper**

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Pepper anthracnose caused by *Colletotrichum* spp. is an economically important disease that causes serious yield loss and quality deterioration in many Asian countries. Recently, several genetic resources resistant to anthracnose were identified and used for genetic analysis and resistance breeding. Since 1980, anthracnose resistance has reported to be controlled dominantly and quantitatively. In contrast, a recent report demonstrated that the resistance of 'PBC932' to *C. capsici* was controlled by a single recessive gene. In this study, we tried to analyze the inheritance of anthracnose resistance to *C. capsici* and *C. acutatum*. Two different pepper lines, 'Daepoong-cho' (*C. annuum*) and 'AR' (*C. annuum*) were used as resistant resources. To analyze the inheritance mode of resistance, F₂ and BC segregating populations derived from the cross between 'Yeoju' and 'Daepoong-cho' and the cross between 'HN 11' and 'AR' were inoculated with *C. capsici* and *C. acutatum*, respectively. In addition, to determine whether the resistances were controlled by the same gene or not, reciprocal crosses between 'Daepoong-cho' and 'AR', which resistant line was derived from 'PBC 932' (*C. chinense*), were made and their F₁ progenies were inoculated with *C. capsici* and *C. acutatum*. As the result, the resistance of 'Daepoong-cho' and 'AR' seems to be controlled by a single recessive gene because segregation ratio of resistance to susceptibility in F₂ and BC_R generation was fitted to 1:3 and 1:1 mendelian model, respectively. In addition, both resistant sources seem to have the same resistance gene to *C. capsici* because all the F₁ progenies between 'Daepoong-cho' and 'AR' were resistant to *C. capsici*. However, 'AR' seems to have an additional resistance gene to *C. acutatum*.

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Inheritance of Long Husk Leaves in Maize

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Husk leaves (or "flag leaves") extend from the tips of ear husks in maize (*Zea mays* L., corn). They are typical of temperate sweet corns, where they facilitate machine-handling and removal of husks prior to canning. Most field corns lack or have very reduced husk leaves, and husk leaves are rare in tropical field and sweet corns. The inheritance of husk leaves was studied by generation mean analysis of progenies derived from crosses of the inbreds Hi38c1 and Ia453sh2. Hi38c1 is a tropical Hawaiian supersweet that lacks husk leaves and is based on the gene *brittle-1*. Ia453sh2 is a conversion to *shrunken-2* of Iowa inbred Ia453 (su) with long husk leaves.

Husk leaf extension was scored in winter and summer seasons on a scale of 1 (no husk leaves) to 9 (very long extension). The parents average scores were 1.2

(Hi38c1) and 5.8 (Ia453sh2). The F₁ hybrids averaged 3.8, while the F₂ averaged 3.6. Backcross families averaged 2.8 and 4.9, respectively. Coefficients of variability averaged as follows: P₁ 37.1%, P₂ 33.8%, F₁ 50.4%, F₂ 65.6%, BC₁ 64.9%, BC₂ 47.6%. Scores were generally lower in winter under low incident light (3.4) than under high incident light in summer (4.0). Generation mean analysis revealed significant departure ($\chi^2 = 11.3$) from a three-parameter model, but good fit ($\chi^2 = 2.4$) to the five-parameter model. Broad-sense heritability averaged 56.2% and narrow-sense heritability averaged 44.3%. The minimum number of effective gene loci, based on Castle and Wright formulas, was 1.10. It is concluded that a single major gene acting without dominance controls husk leaf extension in this material. The gene is provisionally designated *lhl-453* (long husk leaves). In general, tillering accompanied long husk leaf extension.

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Comparison of Resistance Evaluation of Barley Genotypes to *Barley Mild Mosaic Virus* between Improved Mechanical Inoculation and Natural Transmission

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Barley mild mosaic virus (BaMMV) is one of the most economically important virus diseases in barley (*Hordeum vulgare* L.), in East Asian and European countries. BaMMV is a soilborne bymovirus vectored by root-infecting fungus, *Polymyxa graminis*. By this nature of virus transmission, mechanism of cultivar's resistance is difficult to assess. Whereas, available mechanical inoculation methods for BaMMV and other related viruses are labor intensive, give inconsistent results and generally result in low infection rates. Five Korean barley cultivars and 20 barley genotypes with known gene(s) for resistance were mechanically inoculated by the improved method. Infection rates obtained were compared with available field resistance evaluation data. In this study, inoculation method using gauze rolled on a stick was developed for BaMMV. The improved method proved to be simple, efficient, and reliable. The comparative experiments between mechanical inoculation and natural transmission differentiated the cultivars with resistances to the viruses, to their vector *P. graminis* or both. Results further reveal the true resistance mechanism of certain cultivar. Cultivar Naehanssalbori showed resistance to BaMMV in the field tests but was found susceptible by mechanical inoculation, indicating that the field resistance may be due to resistance to *P. graminis*. PCR result of *P. graminis* from BaMMV affected fields amplified only low level of DNA where as other tested cultivars did higher levels. This further indicates that Naehanssalbori carries gene(s) for resistance to *P. graminis*. The resistance to *P. graminis* identified in Naehanssalbori would provide an option to control BaMMV and other *P. graminis* borne viruses.

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