

## MAPPING OF GENOMIC REGIONS ASSOCIATED WITH RESISTANCE TO ANGULAR LEAF SPOT IN COMMON BEANS

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Common bean angular leaf spot (ALS) caused by the fungus *Phaeoisariopsis griseola* is a common disease in tropical and sub-tropical regions. In fact, this disease affects bean crops grown in more than sixty different countries causing yield losses that may reach 80% of the expected production. Incorporation of genes determining partial resistance is a promising breeding strategy for developing resistant bean cultivars to ALS. This strategy has been shown to be effective in other cultures leading a more durable resistance (Johnson, 1984). The lack of information on the inheritance mode of the ALS resistance genes in beans is one of the main reasons this strategy is not being used to develop cultivars resistant to this disease.

The present work aimed at evaluating and mapping the loci controlling partial resistance to ALS in common beans. A set of recombinant inbred lines (RILs) at the F<sub>8-9</sub> generation was used. The RILs were produced from a cross between BAT 93 (Mesoamerican) and Jalo EEP558 (andean), performed by Gepts et al. (1993).

### Materials and Methods

The seeds of the 50 RILs used in this work were kindly provided by Dra. Siu Mui Tsai from the Centro de Energia Nuclear na Agricultura (CENA/USP, São Paulo, Brazil). First, the parents BAT 93 and Jalo EEP558 were inoculated with spores from 10 *P. griseola* pathotypes to select the one that would be used to inoculate the RILs. The pathotypes correspond to monosporic cultures isolated in different bean growing regions in Brazil.

The RILs were planted in May 2002, in a greenhouse from BIOAGRO/UFV. The plants were inoculated 25 days after germination with a suspension of  $2 \times 10^4$  conidia/ml. Evaluation of the disease symptoms was done 17 and 21 days after inoculation, based on a 1-to-9 scale in which 1 was assigned to plants with no symptoms and 9 to plants severely affected by the disease.

The molecular data (RFLP) was obtained at <http://agronomy.ucdavis.edu/gepts/gepts.htm>. All statistical analyses were done with the aid of the GQMOL program developed by prof. Cosme Damião Cruz from UFV ([www.ufv.br/dbg/gqmol/gqmol.htm](http://www.ufv.br/dbg/gqmol/gqmol.htm)).

## Results and discussion

In the initial evaluation of the parents for resistance/susceptibility to ALS it became clear that Jalo EEP558 was resistant and BAT 93 was susceptible to pathotype 63.55. So this pathotype was used to inoculate the RILs. One hundred-and-three RFLP markers segregating 1:1 (<http://agronomy.ucdavis.edu/gepts/gepts.htm>) were analyzed together with the phenotypic data. Five RFLP markers (D1367, D1287, D1492, D1157 and D1390) co-segregated with regions associated with partial resistance to ALS at  $P < 0.05$ . An additional marker (D1512) was included at  $P < 0.08$ . These same regions are also linked to partial resistance to other types of diseases in beans. Marker D1512 is associated with resistance to anthracnose (Geffroy et al., 2000). Markers D1390 and D1492 are associated with resistance to common bacterial blight (Nodari et al., 1993; Tsai et al., 1998). Markers D1157, D1367, D1287 and D1390 are linked to the partial control of common bacterial blight and wildfire (Boscariol, 1997). Markers D1157 and D1492 were mapped in linkage group 5 and markers D1287 and D1367 were mapped in linkage group 2 (Gepts et al., 1993).

Disease resistance genes in plants are often organized in clusters. This type of organization favors unequal crossing over, which may lead to different haplotypes associated with partial resistance. The fine mapping and characterization of these clusters may help the breeder to design appropriate breeding strategies to develop disease resistant cultivars.

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## References

- Boscariol, R.L. **Localização de regiões genômicas associadas ao número de nódulos e à resistência a *Xanthomonas campestris* pv. *Phaseoli* e *Pseudomonas syringae* pv. *Tabaci* em feijoeiro (*Phaseolus vulgaris* L.):** Piracicaba: ESALQ 1997 MS Thesis – Escola Superior de Agricultura Luiz de Queiroz, Universidade de São Paulo.
- Geffroy, V., Sévignac, M., Oliveira, J.C.F., Fouilloux, G., Skroch, P., Thoquet, P., Gepts, P., Langin, T., Dron, M. Inheritance of partial resistance against *Colletotrichum lindemuthianum* in *Phaseolus vulgaris* and co-localization of quantitative trait loci with genes involved in specific resistance. **Molecular Plant-Microbe Interactions** 13: 287-296. 2000.
- Gepts, P., Nodari, R., Tsai, S.M., Koinange, R.M.K., Llaca, V., Gilbertson, R., Guzman, P. Linkage mapping in common bean. **Annual Report of the Bean Improvement Cooperative** 36:24-38. 1993.
- Johnson, R. A critical analysis of durable resistance. **Annual Review of Phytopathology**. 22: 309-330. 1984.
- Nodari, R.O., Tsai, S.M., Guzmán, P., Gilbertson, R.L., Gepts, P. Toward an integrated map of common bean. III. Mapping genetic factors controlling host-bacteria interactions. **Genetics** 134: 341-350. 1993.
- Tsai, S.M., Nodari, R.O., Moon, D.H., Camargo, L.E.A., Vencovsky, R. and Gepts, P. QTL mapping for nodule number and common bacterial blight in *Phaseolus vulgaris* L. **Plant and Soil** 204:135-145. 1998.