IDENTIFICATION AND MAPPING OF QTLS ASSOCIATED WITH RESISTANCE TO *Macrophomina phaseolina* AND DROUGHT STRESS IN COMMON BEANS

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IDENTIFICATION AND MAPPING OF QTLS ASSOCIATED WITH RESISTANCE TO 
Macrophomina phaseolina AND DROUGHT STRESS IN COMMON BEANS

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Common beans (Phaseolus vulgaris L.) are native from Mexico. The crop has a great
economic and social importance and it is a major source of protein and essential nutrients.
Drought is the main stress factor on bean production in Mexico and frequently is combined with
high incidences of diseases caused by fungi, bacteria, viruses or nematodes. One emerging
pathogen in beans and other crops is the fungus Macrophomina phaseolina (Tassi) Goid., causal
agent of charcoal rot which incidences are favored by water deficits (Hernández-Delgado
et al., 2011; García-Olivares et al., 2012). This work was developed to apply DNA molecular markers
to develop a genetic map for identification of molecular markers associated to genes that confer
resistance to combined charcoal rot disease/drought stress.

A population of 94 RILs F2:9 from crosses between BAT 477 (resistant to both charcoal
rot and water stresses) and cv. Pinto UI-114 (susceptible) was generated. Evaluations of
reactions to M. phaseolina and drought stress were conducted under both field and controlled
conditions. Controlled evaluations were conducted in Reynosa, México; field experiments were
carried out in Rio Bravo, Cotaxtla and Isla, México and were described by García-Olivares et al.
(2012). A genetic linkage map was built with genotypic data obtained with 30 +3/+3 AFLP
marker combinations which generated 476 polymorphic markers, 190 of them segregating in a
1:1 ratio. Finally, QTls associated with resistance to both stresses were identified using R ver.
2.10.1 (R Development Core Team, 2012)

A genetic linkage map was obtained with 68 AFLP markers distributed in 10 linkage
groups (LG) with coverage of 718.1 cM. This map showed nine QTls associated with resistance
to M. phaseolina and three with resistance to drought stress, while Hernández-Delgado et al.
(2009) only detected one QTL associated to charcoal rot resistance in BAT 477 using a F2
population. Markers BPC40M127 and BPC54M150 (associated with charcoal rot resistance) and
BPC63M217 (near to the genomic site C5.LOC20, and associated to drought resistance) are
proposed as candidates to be transformed as SCAR markers and then used in Marker-Assisted
Selection programs in order to identify and develop bean germplasm with resistance to both
adverse factors (Méndez-Aguilar et al., 2013).

REFERENCES

Fig. 1. Linkage map on F$_{2}$:9 RILs derived from BAT 477 x Pinto UI-114. Linkage Groups (LGs) included 68 AFLP markers (right) and distances between markers (left) are centiMorgans (cM). RMP = QTL of *M. phaseolina* resistance; RS = QTL of drought resistance.