

Genetic mapping and QTLs of popping traits in nuña bean

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Nuña beans are a type of ancient common bean adapted to humid and tropical Andean region of South America. Nuñas do not produce grain in the temperate zones of cultivation due to their late maturity and extreme sensitivity to photoperiod. One of the traits of interest for crop diversification of these varieties is the character named pop or the ability of the dry seed to expand and burst the cotyledons when they are subjected to high temperatures. To elucidate the genetic basis of popping ability, a mapping population of 185 recombinant inbred lines derived from a cross between two Andean genotypes, PMB0225 (dry bean) and PHA1037 (nuña bean), was evaluated for the popping expansion response under both short- and long-day conditions. Genetic analysis performed indicated that popping ability traits showed a polygenic inheritance. The dominant and epistatic effects of genes were the most important genetic parameters, despite the significant result for additive effects. Transgressive segregation was observed suggesting that combination of alleles from both parents have similar effects, which was also supported by QTL analyses. The genetic linkage map developed herein includes 193 loci (85 AFLP, 95 SSR, and 13 SNP markers) across 12 LGs that cover a genetic distance of 822.1 cM with an average of 4.3 cM per marker. The map constructed shows higher number of markers and saturation as well as higher genome coverage than the Andean maps previously reported (Cichy et al. 2009; Blair et al. 2011), and a similar marker density and a genome coverage than the core common bean map (Freyre et al. 1998; Hanai et al. 2010). Several co-localized QTLs were identified on LGs 3, 5, 6, and 7, which accounted together for 31% of the phenotypic variance. QTL pyramiding approach would permit to combine QTL alleles with positive effects for popping ability on a day-length-insensitive genotype through molecular breeding.

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