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## Genetics and mapping of nutritional traits in *Andigena* potato

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Understanding the genetics and genes involved in the accumulation of antioxidants and minerals is of great importance for the potential improvement of food crops through conventional or molecular breeding. For potato, given that most variety development is done at the tetraploid level, it would be advantageous to have this information in a tetraploid context. We used a DArT -based tetraploid linkage map of the haploid progeny of the purple-fleshed Andean cv. Alcatarma to map degree of flesh pigmentation and the concentrations of iron (Fe), zinc (Zn), ascorbic acid (AA), anthocyanin (ACY), and total phenolic compounds (PHEN) of potato tubers. Data from two contrasting environments in Peru were used to locate and determine gene action of QTL, and contribute information on G x E. DArT marker information available from the SPUD database (DB) of the Potato Genomics Resource (<http://potato.plantbiology.msu.edu/index.shtml>) enabled the search for potential candidate genes underlying QTL that were consistent across environments. All traits except flesh pigmentation and ACY concentration showed continuous phenotypic variation, indicating multiple gene action. Thirteen significant QTL for mineral concentrations, 13 for antioxidant content (AA, ACY and PHEN) and a major gene for flesh pigmentation on chromosome X were identified. Most QTL displayed dominant effects of alleles in simplex or duplex condition, while others showed additive or complex gene action. The QTL explained from 7 to 20% of the phenotypic variation for mineral concentration, 7 to 23% for AA, and 7 to 61% for the other antioxidants (ACY and PHEN). Environmental factors had a large effect on QTL detection. For instance, almost half of the genotypes that were pigmented in the highland environment lost their pigmentation in the lowland subtropics. We analyzed segregation for purple (P), red (R), and unpigmented (U) tuber flesh in the highland environment, where the population segregated 1:1 for pigmented and unpigmented tuber flesh. A 1P:1R:2U segregation ratio which fits a model of digenic epistasis ( $p=0.97$ ) was observed. Complete dominance at both P and R genes (P\_R\_) is required for purple fleshed pigment expression, whereas the recessive condition of the R locus masks the expression of P (P\_rr) resulting in unpigmented tubers. A significant QTL consistent across environments, for ACY, PHEN, and degree of flesh pigmentation, was found on chr X at the same position as the major gene for pigmented flesh. The 3-fold greater percent of variance explained by this QTL in the highland than the lowland environment suggested differential expression of the gene. Consistent QTL across environments were also found for AA, Fe, Zn, PHEN and ACY concentrations. A QTL for Zn on chr VII was particularly interesting since a SolCAP SNP ("solcap\_snp\_c1\_500") annotated as a Zn binding protein was identified at ~1.5 cM from its closest DArT marker. Co-localization of significant QTL for Fe and Zn on chr II and IX might account in part for the 40% of the phenotypic variance shared by these traits ( $r=0.63$ ) This DArT- based linkage map and QTL analysis will contribute to both applied and basic potato research.