

## A DIAGNOSTIC PANEL OF HIGHLY INFORMATIVE SNP MARKERS FOR POPULATION STRUCTURE AND GENETIC DIFFERENTIATION IN POTATO

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With the advent of genome-wide analytical technologies, single nucleotide polymorphism (SNP) markers are increasingly favored as population genetic markers, because they are highly abundant and widespread in the genome. Numerous SNPs have been identified in potato and the SolCAP Infinum 8303 Potato SNP array is available for genotyping. The objective was to identify an optimum set of most informative SNP markers to create a diagnostic panel that can effectively differentiate potato individuals and populations. We evaluated two panels: a diverse panel with 250 clones, including genetic stock, wild species and different ploidy levels (1x, 2x, and 4x) scored with 6,117 SNP markers with three call (AA, AB, BB) model, and a cultivated one with 205 potato varieties and elite breeding clones scored with 3,836 SNP markers with five call (AAAA, AAAB, AABB, ABBB, BBBB) model. Diagnostic panels with increasing number of most informative (higher *In* values) markers were created and compared with the original panel with Spearman (*Rho*) rank order correlation analysis. The diagnostic panel of 243 SNPs was identified based upon the *In* and *Rho* values. The selected SNPs have less than 10% no call and are at least 0.3 Mb apart in the potato genome. The most informative SNP markers are not even distributed in the potato genome. The diagnostic panel with the optimum set of SNP markers reduces labor and genotyping cost for potato population structure and diversification studies.

Palavras-chave: *Solanum* spp.; population genetics; Informativeness; molecular markers.

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