

**DEVELOPMENT AND APPLICATION OF A 20K SNP ARRAY TO CHARACTERISE THE TETRAPLOID GENE POOL OF POTATO (*SOLANUM TUBEROSUM*)**

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A non-redundant subset (15138 SNPs) of the ~129000 SNPs identified by (Uitdewilligen et al, 2013) and 4454 SolCap markers from (Hamilton et al, 2011) were combined on a 20k Infinium SNP array for genotyping a total of ~2400 tetraploid genotypes of which 538 were used for this study to characterise the gene pool of potato. Genotypes from different countries and different market segments complemented with heirloom cultivars and important progenitors were used to perform several experiments. An important parameter of this array is the ability to review the introgression breeding over the last 70 years. Furthermore LD-decay, population structure and the effect of breeding on allele frequency changes over time and for different market segments were analysed.

Major results are that 3219 SNPs present on the array are the result of newly introduced alleles, from the 1940-ties onwards, most likely originating from wild species,. Only few of this “new” SNPs reach high allele frequencies in modern potato cultivars. The majority is therefore assumed to be linkage drag, not adding beneficial traits to the gene pool. The variation originating from heirloom cultivars is for 99% still present in modern cultivars.

This is an intriguing observation for two reasons. First it contradicts the suggested genetic erosion caused by modern breeding efforts. Second, it may help to understand the lack of genetic gains over a century of breeding. Linkage disequilibrium (LD) between SNP loci was analysed. The LD in tetraploid potato decays to background level at 1-2 mega bases on average. However stretches with longer LD are present in within population structure groups and in introgression segments.

**References**

- Hamilton et al. (2011) Single nucleotide polymorphism discovery in elite North American potato germplasm. BMC Genomics 12: 302. doi: 10.1186/1471-2164-12-302.
- Uitdewilligen et al (2013) A next-generation sequencing method for Genotyping-By-Sequencing of highly heterozygous autotetraploid potato. PLoS One 8(5):e62355. doi:10.1371/journal.pone.0062355 ;