

The Canon of Potato Science:

3. Genetic Markers and Maps

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What is it?

Genetic markers are heritable traits, which occur in at least two variants (alleles) in populations of individuals of the same species. They correspond to single genetic loci and segregate in progeny of parents differing in their alleles according to Mendelian rules. The molecular basis of all genetic markers is DNA mutations, either point mutations (exchange of a single nucleotide) or insertions/deletions of one or more nucleotides in one allele versus another. Whereas Mendel analysed the inheritance of DNA mutations by observing morphological variation, molecular techniques are used today to detect DNA polymorphisms directly, for example by restriction fragment length analysis or DNA sequencing (DNA-based markers). Genetic markers located on the same chromosome are physically linked. The distance between the marker loci and their linear order can be determined by estimating the pair wise recombination frequency between all markers located on that chromosome in a segregating population. This results in a genetic linkage map of the chromosome. Such linkage maps can be constructed for all chromosomes of a species. In the F_1 progeny of heterozygous, diploid parents such as diploid potatoes, two linkage maps are constructed derived from meiotic recombination events in the seed and pollen parent. The precision and resolution of linkage maps depends on the number of marker loci and the number of recombination events (population size) analysed. The true physical distance between marker loci is determined by genomic sequencing. The genome sequence of a species is therefore the map with ultimate precision and resolution.

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Why is it Important in Potato Science?

DNA-based markers, linkage maps and ultimately the genome sequence of potato are the basis for:

- *The molecular taxonomy of potato and its relatives.*
DNA-based markers are available in large numbers, for example amplified fragment length polymorphisms (AFLP) or single nucleotide polymorphisms (SNP), and can be used to quantify relationships at the species level between potato varieties, landraces and accessions, at the genus level between *Solanum* species, at the family level between members of the Solanaceae, and within the kingdom of higher plants.
- *The analysis of potato genome structure and evolution in comparison to other plant genomes.*
Using the same set of restriction fragment length polymorphism (RFLP) markers and their sequences, comparative maps have been constructed in different species, for example potato, tomato, pepper, eggplant, allowing the finding of genome segments with similar structure (synteny) and function.
- *The mapping of qualitative and quantitative phenotypic characters.*
Genetic factors controlling characters such as disease resistance, tuber yield, starch content or chip colour are localised in the potato genome by detecting linkage to DNA-based markers of known map position. ‘Know where’ generates ‘Know how’.
- *The positional cloning of potato genes underlying qualitative and quantitative traits.*
Knowledge of the map positions of qualitative and quantitative traits is the starting point for identifying the causal genes by high resolution genetic and physical mapping, sequencing and complementation analysis of candidate genes.

Why is it Important for the Potato Industry?

The customer for the results of research on potato DNA-based markers and linkage maps is the breeding industry. DNA-based markers can be used to fingerprint varieties and breeding clones, facilitating the assessment of clone parentage, identity and purity. Microsatellites or simple sequence repeats (SSR) are the markers of choice for this purpose. DNA-based markers associated with traits important for variety development are diagnostic tools for selecting individuals with superior trait alleles at an early stage in the breeding cycle. Targets for marker-assisted selection are:

- (i) traits, which are difficult to evaluate reliably at the phenotypic level, such as field resistance to late blight (*Phytophthora infestans*) independent of late maturity, or resistance to wart (*Synchytrium endobioticum*);
- (ii) traits, which require several years of tuber multiplication before the trait can be reliably evaluated, such as processing quality.

Knowing the sequences of the genes and their allelic variants that are causal for the genetic variation of agronomic traits leads to ‘precision breeding’: diagnostic DNA-based markers derived directly from natural variants with known effect on a trait assist the choice of parents and progeny in breeding programmes. Cost-effective technology will become available for the parallel analysis of large numbers of markers such as SNPs.

Scientific Developments

Over the past 20 years, at least a dozen linkage maps have been constructed with DNA-based markers, mostly in experimental populations of diploid potato. Numerous qualitative and quantitative traits have been mapped onto potato chromosomes such as resistance to late blight (*Phytophthora infestans*), root cyst nematodes (*Globodera pallida*, *Globodera rostochiensis*), Colorado potato beetle (*Leptinotarsa decemlineata*), viruses (PVX, PVY, PLRV, PVM, PVS), wart (*Synchytrium endobioticum*), tuber soft rot (*Erwinia carotovora* spp. *atroseptica*) and Verticillium wilt (*Verticillium dahliae*); the colour of flowers, tuber skin and flesh; plant maturity; chip quality; tuber starch content; and yield, number and shape of tubers. Knowing their map positions was instrumental for cloning several major genes for resistance to *P. infestans*, *G. rostochiensis* and *Potato virus X*. Candidate genes underlying the quantitative traits chip quality and field resistance to late blight have been identified. Association mapping and population genetics in tetraploid varieties and breeding clones lead to the identification of diagnostic markers for extreme resistance to PVY introgressed from *S. andigena* or *S. stoloniferum*, for high resistance to *G. pallida* pathotype Pa2/3, and for quantitative resistance loci against Verticillium wilt and late blight, the latter being linked to the *R1* gene for resistance to *P. infestans*.

Further Reading

A recent overview on developments over the last 20 years in potato genetics using DNA-based markers, and on all other aspects of potato biology and biotechnology is available in:

Vreugdenhil D, Bradshaw J, Gebhardt C, Govers F, MacKerron DKL, Taylor MA, Ross HA (eds) (2007) *Potato biology and biotechnology: advances and perspectives*. Elsevier, Amsterdam (etc.), ISBN-13: 978-0-444-51018-1