

identified for progression rate and year specific QTLs were detected for onset of senescence and inflection point. Interesting pleiotropic effects and epistatic interactions between QTLs were also detected when two-way interactions were studied.

### **Glycoalkaloid Contents in a Family from a Cross between a Diploid *S. Tuberosum* and a Diploid *S. Sparsipilum* Clone are Under Polygenic Control**

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Breeders often exploit wild species to introgress new traits into potato varieties. In addition to the favorable traits, undesirable ones like “high content of glycoalkaloids in the tubers” can be introduced. That is why it is very important to identify the different chromosomal regions involved in the glycoalkaloid content in order to be able to detect eventual co-localisation of favorable QTL and undesirable traits, and to select against these last ones. In the present study, tubers of 95 clones from a diploid population between the dihaploid Caspar H3 and a clone of the diploid wild species *Solanum sparsipilum* were analysed for their  $\alpha$ -chaconine and  $\alpha$ -solanine contents by HPLC. The two glycoalkaloid contents were quantitatively distributed. QTL analysis performed according CIM methods allowed to detect nine QTLs involved in the character expression. They are present on both parents. For the  $\alpha$ -chaconine, three QTLs were identified on the map of the *S. sparsipilum* clone on chromosomes I, V and VIII and two QTLs on the map of Caspar H3 on chromosomes IV and VI. For the  $\alpha$ -solanine, two QTLs were identified for each parent. They were mapped on the *S. sparsipilum* chromosomes V and XII and on the Caspar H3 chromosomes IV and VI. Each QTL explained between 8 and 18% of the total variance. In Caspar H3, two QTLs for  $\alpha$ -chaconine and  $\alpha$ -solanine contents co-localised and for *S. sparsipilum* the QTLs were mapped on the same position on chromosome V.

### **Genetic Variation in Potato (*Solanum tuberosum* L.) Canopy Development: A Model Approach Using Standard Cultivars and a Segregating Population**

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We investigated the potential of a model-based approach to assist in the genetic analysis of the environment-sensitive, quantitative crop trait canopy cover in potato

(*Solanum tuberosum* L.). We used a model based on beta functions to analyze the genotype×environment interactions related to the dynamics of canopy cover. The model equations describe three phases of canopy growth: build-up phase (*P1*), maximum cover phase (*P2*), and decline phase (*P3*). The model has five parameters:  $t_{m1}$  indicates the transition from accelerating to diminishing growth during *P1*,  $t_1$  marks the end of *P1* when canopy cover attains its maximum level  $v_{max}$ ,  $t_2$  marks the end of *P2* when canopy cover starts to decline, and  $t_e$  represents the end of the crop cycle when canopy cover has declined to nil. Values of these parameters were estimated for 100 individuals of an F1 population, their parents, and five standard cultivars differing in maturity type, using data collected in six field experiments. The model successfully described differences in canopy dynamics among individual genotypes across environments. Model parameters were used to derive several secondary variables:  $D_{P2}$  (duration of *P2*),  $D_{P3}$  (duration of *P3*), and  $A_{sum}$  (area under the canopy cover curve reflecting the crop's capacity to intercept incoming radiation). The length of *P1* (i.e.  $t_1$ ) was relatively conservative, but  $D_{P2}$ , and  $D_{P3}$  varied greatly. Later genotypes had higher  $A_{sum}$  because they had longer  $D_{P2}$ , and  $D_{P3}$ . Genotypic and phenotypic variance components of the F1 population were estimated for all traits across environments and almost all of them proved significant ( $P<0.01$ ). For most traits, genetic variability and heritability were high. There are opportunities, therefore, for future potato breeding programmes to exploit the genetic variability available in the F1 segregating population and to select for highly heritable traits in order to improve radiation interception efficiency.

### The Role of Molecular Markers in the Bioimpuls Organic Potato Breeding Program

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The organic potato sector urgently needs better adapted, non GMO varieties to deal with the constraints of the low-input, organic farming system. Besides late blight resistance the program focuses on resistance against rhizoctonia, scab, alternaria and PVY. Special attention is also paid to early tuber bulking, dormancy and nutrient-efficiency. Since 2008 a joint breeding program “Bioimpuls” was initiated including Louis Bolk Institute, Wageningen University, six breeding companies, and several farmer breeders. The approach is based on three parallel goals: a) to develop new progenitors through classical introgression breeding with new late blight resistance genes, b) to provide the breeding sector with plant material (seeds/seedlings) for selection and c) to stimulate farmer breeder participation in the selection process, by giving training courses on potato breeding and technical support. A breeding program has been