

Phenotyping of an extensive potato germplasm set for nitrogen use efficiency: nitrogen effect on physiological model parameters for canopy development.

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Nitrogen (N) is an essential nutrient for crop growth and its use has great economical and environmental impact. Proper nitrogen management is especially essential in potato production because of the high demands of the crop and its small and shallow root system. Moreover, the EU nitrate directive (91/767/EEC) makes nitrogen use efficiency (NUE) a very important trait and will force to reduce N-supply, thus affecting the physiological and agronomical performance of the potato crop. The challenge is to know which varieties are performing well under low input and to understand the genetics of high NUE under low N. We used an eco-physiological model to analyze canopy cover as a tool to identify and quantify genetic variation among potato varieties. A diverse set of 200 potato genotypes was planted in 2009 and grown under two levels of available nitrogen (75 and 180 N kg/ha) at the breeding station of Agrico Research (Bant, Noordoostpolder, The Netherlands) on a light clay soil. To apply the physiological model for canopy development, the percentage of soil covered by green potato leaves (soil coverage, SC) was assessed weekly throughout the growing season. Using the hourly temperature, obtained from a nearby meteorological station, days after emergence were converted into thermal days to describe crop development as a function of temperature using the beta function and the three cardinal temperatures for potato. Relevant curve fit parameters estimated from the model for each individual genotype showed large differences between nitrogen levels, with lower values for the low level of N input. Especially the maximum value of SC and the period over which this maximum was maintained were strongly affected by nitrogen. These effects resulted in large differences in light interception, yield, tuber size distribution and nitrogen uptake. Differences between genotypes were large and partly associated with maturity type. The results will be confirmed in a second trial in 2010. An association mapping analysis will follow in the second phase of the project to identify candidate genes related with NUE in potato.