PlantsProFood - New varieties of narrow-leafed lupin for application in human nutrition

Kristin Fischer¹, Brigitte Ruge-Wehling¹, Eicke Rudloff¹, Anne-Kathrin Schmalenberg², Björn Rotter³, Peter Winter³ and Peter Wehling¹

¹Julius Kühn-Institut, Institute for Breeding Research on Agricultural Crops, Groß Lüsewitz
²Saatzucht Steinach GmbH, Bocksee
³GenXPro GmbH, Frankfurt/Main

The seed protein of narrow-leafed lupin (Lupinus angustifolius) is known for its exceptional functional properties as food ingredient and, thus, represents a resource of vegetable protein for human consumption. To take advantage of this potential for a broad range of food applications the regional R&D network 'PlantsProFood' was set up in Northern Germany. Lupins shall be enhanced as a protein resource for food purposes, like ice cream, sausages, bakery products or pasta.

The network consists of four research institutions and ten local companies and aims at processing the value chain from the development of (I) high-yielding varieties, (II) new processing approaches towards (III) innovative and healthy food.

Requirements for these efforts are high and stable yields of narrow-leafed lupins. This may be achieved by plant breeding as far as sufficient genetic variability is available. To expand the genetic variability of advanced lupin breeding material an EMS (ethyl methanesulfonate) mutagenesis of cv. 'Boruta' was performed and the offspring screened for novel phenotypes. Phenotypes with a conspicuous novel growth type, such as vigorous growth or high branching compared to the wildtype 'Boruta', were identified and devised to homozygous and stable mutant (M) lines.

The yield potential of the M lines was evaluated under field conditions and for some lines the potential was confirmed by significant increase in kernel yields. For genetic analyses, crosses of the respective M lines with genebank accessions as well as with the wildtype 'Boruta' were carried out. Segregation analysis of F2 populations indicated a monogenic-recessive inheritance of novel growth types.

Promising M lines are going to be subjected to an analysis of differentially expressed sequences of mutant lines and the wildtype via RNAseq techniques and SNP identification. Currently, selected SNPs are analyzed via high-resolution melt analysis to develop selection tools for marker-assisted selection.