

# Transcriptome-based mapping of anthracnose resistance gene (*Llur*) in yellow lupin (*Lupinus luteus*)

Florian Haase<sup>1</sup> and Brigitte Ruge-Wehling<sup>1</sup>

<sup>1</sup> Julius Kühn-Institut, Federal Research Centre for Cultivated Plants, Institute for Breeding Research on Agricultural Crops, Rudolf-Schick-Platz 3a, OT Groß Lüsewitz, 18190 Sanitz, Germany

E-mail of corresponding author: [florian.haase@julius-kuehn.de](mailto:florian.haase@julius-kuehn.de)

Yellow lupin (*Lupinus luteus* L.) is a promising legume crop, which is well adapted to poor soils, has a good drought tolerance and higher seed protein content than most legume species. Nonetheless, the yellow lupin has almost disappeared from the fields in Germany due to high susceptibility against the fungal disease anthracnose caused by pathogen *Colletotrichum lupini*.

A screening for anthracnose resistance of the several lupin cultivars revealed a polish variety with a high level of resistance to anthracnose. Segregation of the anthracnose resistance was assessed in a F<sub>2</sub> population (n=200). A 3:1 ratio of resistant to susceptible plants indicates a monogenic dominant inheritance of the resistance locus. The corresponding

resistance gene was previously designated *Llur*. Development of resistance linked selection markers shall be accomplished by methodical combination of bulked segregant analysis and NGS-based transcriptomic analysis. Therefore artificially infected leaf segments of resistant and susceptible genotypes of a F<sub>2</sub> mapping population were sampled and bulked. RNA was isolated and RNA-Seq was performed to reveal the presence and quantity of RNA in post-inoculated *L. luteus* plant material. Comparative expression studies are aimed at identifying exclusive transcripts or SNPs in the resistant bulk and thus can be used as reliable marker resource for the genetic mapping of resistance gene *Llur* in yellow lupin.