**Genetic analysis of anthrancnose disease resistance gene in narrow-leafed lupin**

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*Lupinus L.* is a large and diverse genus in the legume family (Fabaceae). Like other members in the legume family, lupins can convert atmospheric nitrogen to a usable form through rhizobium root nodule symbiosis to improve soil quality. Therefore, narrow-leafed lupin (*Lupinus angustifolius* L. 2n=40) has been used as a rotation crop in Western Australian agricultural system.

Lupin anthracnose disease is a serious and the most damaging disease in lupin growing areas. This disease has potential to cause complete crop losses in susceptible lupin varieties.

We identified one major QTL on chromosome 11 for anthracnose disease resistance gene from a RIL population derived from the cross between Unicrop (susceptible) and Tanjil (resistant). This QTL can explain 81.5% of phenotypic variations. We narrowed down this QTL to a 12.5 kb region through fine-mapping of ~5000 F2 lines. There were three annotated gene in this region. And one disease-like gene *AnthTjR* was identified as a candidate gene.

cDNA sequence suggested that there were six exons in this gene region. Eight amino acid changes exisited between Tanjil and Unicrop. Re-sequence analysis of 21 lupin accessions showed that two AA changes were highly associated with the disease resistance. The molecular markers have been developed for marker-assisted selectioin in breeding programs.

Functional analysis of resistance genes is beijing performed by virus-induced silencing (VIGS) method.