**Identification of sweet alkaloid genes in narrow-leafed lupin**

Zhou G1, Xiao C1, Li C1

*E-mail*: [Gaofeng.zhou@murdoch.edu.au](mailto:Gaofeng.zhou@murdoch.edu.au)

*1 Western Crop Genetics Alliance, Murdoch University, WA, Australia*

In wild narrow-leafed lupin (*Lupinus* *angustifolius*) seeds, the quinolizidine alkaloid (QA) content was around 2%. In contrast, the QA content in sweet lupin cultivars decreased 100 times to ~0.02% to meet the industrial limit.

To identify the gene for QA content, we used three recombinant populations, and fine-mapped the major bitter locus to a 0.46 Mb interval region on chromosome 7. The DEG gene *RAP2-7* in this region was considered to be the candidate gene. By investigating >300 lupin re-sequencing data and their phenotypes, one SNP within the gene region was identified to be associated with alkaloid content. Virus-induced gene silencing of *RAP2-7* was conducted in bitter wild lupin plants, and we successfully converted the bitter leaves to sweet leaves in the VIGS plants. It indicated that *RAP2-7* was the gene controlling the sweetness in narrow-leafed lupin cultivars.

In addition, the Australian sweet lupin cultivar Kalya contains 0.015% QA, while the QA content of another sweet cultivar Tallerack contains 0.00166%, around 10 times difference. DNA analysis indicated they carried the same sweet allele of the gene RAP2-7, and different genes should control the sweeter gene in Tallerack. Two new QTLs for sweeter QA in Tallerack were identified on chromosomes 13 and 16, explaining 25% and 12% of phenotypic variations, respectively. Aphid tolerance analysis showed that the QTL for aphid tolerance was mapped to Chr.13, and this QTL was consistent with the relevant alkaloid QTL on Chr.13.