**Exploring the Lupin Genome: Uncovering Lipoxygenase Genes to Enhance Flavor**

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Narrow-leafed lupin (*Lupinus angustifolius*) has high protein is currently a good source of animal feed but has untapped potential as a human food. However, the utilisation of lupin in food products is impaired partly due to the undesirable beany flavour caused by lipid oxidation. Reduction of the beany flavour will help increase the overall consumer acceptance of lupin-based products to help make it a valuable protein source for human consumption. Beany flavour in legumes is mostly derived from the catalyzed enzymatic oxidation of linoleic acid and linolenic acid by lipoxygenases. Volatile organic compounds (VOCs) are often associated with the beany flavour. However, the nature of lipid oxidation associated with the beany flavour in lupin is largely unknown.

Biochemical analyses using GC-MS showed that there were qualitive and quantitative variations in fatty acids and VOCs among NLL domesticated and wild accessions. Twenty-one *lox* genes were identified from NLL genomic database. Transcriptomic analysis showed that the expression profiles of the *lox* genes varied among the diversity panel of NLL accessions and among various tissue types and during grain development. Some *lox* gene members were predominantly expressed in lupin grains. Mutations in one or more of LOX isoenzymes were identified in our in-house EMS mutagenic population. These mutants are currently being characterized with regards to changes in lipid content and VOCs. This research deepens our understanding of lipid oxidation in lupins and provides new materials and opportunities to accelerate lupin breeding for flavour improvement to make lupins more attractive in the food market.