

Development of genomic resources for an important Australian grain legume, narrow-leafed lupin

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Narrow-leafed lupin (NLL; *Lupinus angustifolius* L.) is the main grain legume grown in Western Australia and forms an important part of sustainable farming systems, reducing the need for nitrogenous fertilizer, providing valuable disease breaks and boosting cereal yields. Over the last years we have developed a number of genetic and genomic resources for NLL. These include a draft genome sequence [1], development of various transcriptome libraries [2,3] and a dense reference genetic map [1,2]. The use of these resources has led to the identification of candidate genes for key domestication traits. In addition, candidate genes involved in alkaloid biosynthesis and regulation have been identified [4]. A new four-year project has recently started to expand these resources, including the generation of a pan-genome and a TILLING resource for the species. These resources will significantly improve and accelerate NLL breeding programmes and an overview of the developed resources to date will be presented.

References:

- [1] Hane et al., 2017, *Plant Biotechnol J*, 15, 318-330.
- [2] Kamphuis et al., 2015, *Plant Biotechnol J*, 13, 14-25.
- [3] Foley et al., 2015, *BMC Plant Biol*, 15, 106.
- [4] Frick et al., 2018, *Plant Cell and Environ*, 41, 2155-2168.