

BROADENING AND EXPLOITING THE GENETIC BASE OF WHITE LUPIN

Paolo ANNICCHIARICO¹, Nelson NAZZICARI¹, Dimitrios N. VLACHOSTERGIOS², Abco DE BUCK³, Barbara FERRARI¹, Avraam KOSKOSIDIS⁴, Dennis HEUPINK³, Tommaso NOTARIO¹, Luciano PECETTI¹

¹ Council for Agricultural Research and Economics, Research Centre for Animal Production and Aquaculture, Lodi, Italy,

² Institute of Industrial and Forage Crops, Hellenic Agricultural Organization “Demeter”, Larissa, Greece,

³ Louis Bolk Instituut, Bunnik, The Netherlands,

⁴ School of Agricultural Sciences, University of Thessaly, Volos, Greece

paolo.annicchiarico@crea.gov.it

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White lupin is a European crop with a long history of domestication and high potential interest for high-protein food or feedstuff. This report aims to summarize the research steps that were undertaken to (i) verify the extent of genetic diversity exploited by modern breeding, (ii) identify elite bitter-seed landraces and sweet-seed germplasm aimed to broaden the genetic base for European breeding, (iii) assess the genetic variation for tolerance to key abiotic stresses in the germplasm of the novel genetic base, and (iv) verify the potential of genomic models based on genotyping-by-sequencing (GBS) SNP data to select simultaneously and cost-efficiently for some complex traits. Molecular diversity patterns of 83 landraces from nine major historical cropping regions and 15 commercial varieties confirmed that modern plant breeding exploited only a modest part of the crop genetic variation. Germplasm evaluation experiments for adaptation to severe drought or calcareous soil revealed substantial genetic variation (Annicchiarico and Thami-Alami, 2012; Annicchiarico et al., 2018), which, along with other information, was exploited to identify four elite landraces and four elite, sweet-seed lines that acted as parents of a broadly-based population. Some 144 sweet-seed lines extracted from this population were evaluated for grain yield under severe drought in a managed environment of Italy and for adaptation to moderately calcareous soil in a spring-sown environment of the Netherlands and an autumn-sown environment of Greece. We report on the observed line variation for these traits, and on the construction of genomic selection models and their ability to predict the line adaptation to drought or lime soil based on cross validations. Genome-enabled models may be used also to select for tolerance to anthracnose and the sweet-seed trait.

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