



HAL
open science

LEGumes for the Agriculture of TOMorrow (LEGATO project)

Richard Thompson, Gérard Duc, P Annichiarico, Diego Rubiales, Christophe Salon, C Vaz Patto, E Jensen, S Belcher

► **To cite this version:**

Richard Thompson, Gérard Duc, P Annichiarico, Diego Rubiales, Christophe Salon, et al.. LEGumes for the Agriculture of TOMorrow (LEGATO project). 6. International Food Legumes Research Conference (IFLRC VI), University of Saskatchewan. CAN., Jul 2014, Saskatoon, Canada. 225 p. hal-02740641

HAL Id: hal-02740641

<https://hal.inrae.fr/hal-02740641>

Submitted on 2 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



IFLRC VI & ICLGG VII

6th International Food
Legume Research
Conference

7th International
Conference on Legume
Genetics and Genomics

PROGRAM & ABSTRACT BOOK



TCU Place

Saskatoon, Saskatchewan, Canada

July 7-11, 2014



genotypes is used to generate mapping populations for candidate and interval mapping of respective gene(s) together with aforementioned anatomical and chemical analyses. This research is funded by Grant Agency of Czech Republic, 14-11782S project and Operational Program Research and Development for Innovations (CZ.1.05/2.1.00/03.0058).

121	Seeds and Nutrition	Thompson, R.D.	LEGumes for the Agriculture of TTomorrow (LEGATO project)
-----	---------------------	----------------	---

LEGumes for the Agriculture of TTomorrow (LEGATO project)

Thompson, R.D.^{1*}, Duc, G.¹, Annichiarico, P.², Rubiales, D.³, Salon, C.¹, Vaz Patto, C.⁴, Jensen, E. S.⁵, and Belcher, S.^{6,7}. ¹INRA, UMR1347 Agroécologie, DIJON, FRANCE; ²CRA, LODI, ITALY; ³CSIC ISA CORDOBA SPAIN; ⁴ITQB LISBON PORTUGAL; ⁵SLU ALNARP SWEDEN; ⁶PGRO Research, PETERBOROUGH, UK; ⁷ON BEHALF OF THE EU-KBBE LEGATO PROJECT CONSORTIUM. *(thompson@dijon.inra.fr)

The four year FP7 European project LEGATO (Legumes for the Agriculture of Tomorrow) is aimed at improving the competitiveness of legumes in European agriculture. Grain legumes represent less than 2% of cultivated arable land in Europe, which relies heavily on imported plant protein sources. The project brings together 17 research institutions and 10 companies or professional associations from 12 European states to focus on breeding and management methods for the principal grain legumes or pulses grown in Europe, the pea and faba bean. Among the actions proposed will be the use of advanced breeding methods taking advantage of recent genomics data, exploitation of genetic resource collections, techniques of high-throughput phenotyping including non-destructive root imaging, legume-based cropping systems including intercropping, and exploration of new food products incorporating legume flours. Project Web site: <http://www.legato-fp7.eu/>

122	Seeds and Nutrition	Timmerman-Vaughan, G.M.	Candidate gene based association mapping of allelic polymorphisms associated with variation in seed starch chain length distribution
-----	---------------------	-------------------------	--

Candidate gene based association mapping of allelic polymorphisms associated with variation in seed starch chain length distribution

Carpenter, M.A.¹, Cooper, R.², Frew, T.J.¹, Butler, R.¹, Murray, S.R.¹, Moya, L.¹, Coyne, C.J.³, and Timmerman-Vaughan, G.M.^{1*}. ¹New Zealand Institute for Plant and Food Research, PO Box 4704, Christchurch New Zealand; ²New Zealand Institute for Plant and Food Research, 120 Mt Albert Rd, Mt Albert, Auckland New Zealand; ³USDA-ARS, Washington State University, Pullman, Washington, USA. *(gail.timmerman-vaughan@plantandfood.co.nz)

A candidate gene association mapping approach was taken to understand how allelic variation in 25 sucrose or starch metabolism pathway genes and *R* locus affect the variation in pea seed amylopectin chain length distribution (CLD); a structural attribute related to starch functional properties. Using 97 single seed derived USDA-ARS Plant Introduction (PI) lines that were grown in two replicated trials, starch CLD variation was quantified by fluorophore-assisted carbohydrate electrophoresis. The lines consisted of both round (*R*₋, n = 86) and wrinkled seeded types (*rr*, n = 11). In addition, polymorphisms were identified in alignments of partial sequences of the 25 candidate genes by resequencing PCR products. Association mapping was conducted using the mixed linear model (MLM) implemented using TASSEL software with population structure and kinship accounted for using a Q matrix (k = 4, four subpopulations, estimated using STRUCTURE software) and a K (kinship) matrix (the MLM + Q + K model). Q-values were used to determine significant associations that met or exceeded a false discovery rate (FDR) criterion of $\alpha \leq 0.05$. With the 97 lines, *R* locus accounted for most of the variation in CLD (81% and 87% from the trials). Allelic variation in ADP glucose pyrophosphorylase S2 subunit, UDP glucose pyrophosphorylase and phosphoglucan water dikinase were also associated with CLD variation in starch from both trials, and an additional four genes from one trial