



**HAL**  
open science

## The pea genome

Jonathan Kreplak, Mohammed-Amin Madoui, Karine Labadie, Gregoire Aubert, Philippe Bayer, P. Capal, Anthony Klein, Ayité Kougbéadjó, J. Vrana, K.K. Gali, et al.

► **To cite this version:**

Jonathan Kreplak, Mohammed-Amin Madoui, Karine Labadie, Gregoire Aubert, Philippe Bayer, et al.. The pea genome. 8. International Conference on Legume Genetics and Genomics (ICLGG), Noble Research Institute., Sep 2017, Siófok, Hungary. 128 p. hal-02735156

**HAL Id: hal-02735156**

**<https://hal.inrae.fr/hal-02735156>**

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.

# BOOK OF ABSTRACTS



**8<sup>th</sup> International Conference on Legume Genetics and Genomics**  
**18-22 September 2017**  
**Siófok, Hungary**

## The pea genome

J. Kreplak, M.A. Madoui, K. Labadie, G. Aubert, P. Bayer, P. Capal, A. Klein, A. Kougbéadjó, J. Vrana, K.K. Gali, C. Fournier, L. d'Agata, B. Taran, C. Belser, M.C. Le Paslier, A. Bendahmane, H. Bergès, V. Barbe, R. McGee., J. Lichtenzweig, C. Coyne, T. Warkentin, J. Batley, J. Macas, D. Edwards, J. Dolezel, P. Wincker, **J. Burstin**

### *The International Pea Genome Consortium*

Pea (*Pisum sativum* L.) has long been a model for plant genetics. It is also a widely grown pulse crop producing protein-rich seeds in a sustainable manner. Thanks to large national and international programs, and driven by innovations in sequencing technology, informatics and biotechnology, many genomic resources are now available for pea. An atlas of the expression of its genes in many tissues, high density genetic mapping, and the ongoing sequencing of its genome have provided useful tools for dissecting traits of interest. We will present how the pea genome draft sequence opens the way to explore genetic diversity of pea.

---

#### **How to refer your abstract:**

J. Kreplak, M.A. Madoui, K. Labadie, G. Aubert, P. Bayer, P. Capal, A. Klein, A. Kougbéadjó, J. Vrana, K.K. Gali, C. Fournier, L. d'Agata, B. Taran, C. Belser, M.C. Le Paslier, A. Bendahmane, H. Bergès, V. Barbe, R. McGee., J. Lichtenzweig, C. Coyne, T. Warkentin, J. Batley, J. Macas, D. Edwards, J. Dolezel, P. Wincker, J. Burstin (2017) *The pea genome*; ICLGG 2017 - Book of abstracts, ICLGG2017/PL/106