



HAL
open science

Towards the genome sequence of pea : a tribute to Mendel

Mohammed-Amin Madoui, K. Labadie, Jonathan Kreplak, Gregoire Aubert, Léo d'Agata, P. Capal, Carine Fournier, Ayité Kougbéadjó, J. Vrana, K. Gali, et al.

► **To cite this version:**

Mohammed-Amin Madoui, K. Labadie, Jonathan Kreplak, Gregoire Aubert, Léo d'Agata, et al.. Towards the genome sequence of pea : a tribute to Mendel. 2. International Legume Society Conference - Legumes for a Sustainable World, Legume Society., Oct 2016, Lisbonne, Portugal. 358 p. <hal-01602206>

HAL Id: hal-01602206

<https://hal.science/hal-01602206v1>

Submitted on 3 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.



Distributed under a Creative Commons CC BY-SA 4.0 - Attribution - ShareAlike - International License



Legumes for a Sustainable World

ILS2 | Second International Legume Society Conference

11th - 14th OCT 2016
TRÓIA RESORT | PORTUGAL

ITob UNIVERSIDADE
NOVA
DE LISBOA



Towards the genome sequence of pea

Madoui M.-A.¹, Labadie K.¹, Kreplak J.², Aubert G.², d'Agata L.¹, Capal P.³, Fournier C.², Kougbéadjio A.², Vrana J.³, Gali K. K.⁴, Taran B.⁴, Belser C.¹, Le Paslier M.-C.⁵, McGee R.⁶, Edwards D.⁷, Batley J.⁷, Bendahmane A.⁸, Bergès H.⁹, Barbe V.¹, Tayeh N.², Klein A.², Lichtenzveig J.¹⁰, Aury J.-M.¹, Coyne C.J.¹¹, Warkentin T.⁴, Dolezel J.³, Wincker P.¹, Burstin J.²

1 - CEA - Genoscope, Evry, France

2 - INRA, UMR1347 Agroécologie, Dijon, France.

3 - Institute of Experimental Botany, Olomouc, Czech Republic

4 - University of Saskatchewan, Saskatoon, SK, Canada

5 - INRA, US1279 EPGV, CEA-IG/CNG, EVRY, France

6 - USDA-ARS, Pullman, WA

7 - University of Western Australia, Perth, Australia

8 - INRA, Evry, France

9 - INRA - CNRGV, Castanet Tolosan, France

10 - Curtin University, WA, Australia

11 - USDA-ARS Western Regional Plant Introduction Station, Pullman, WA

Pea (*Pisum sativum* L.) was the original model organism for Mendel's discovery of the laws of inheritance and kept this model status until the advent of molecular biology at the end of the 20th century. Pea is also one of the world's oldest domesticated crops. It is currently the third most widely grown pulse crop, as its seeds serve as a protein-rich food for humans and livestock alike.

While several legume species genome's draft sequences have been produced, progress in pea genomics has lagged behind largely as a consequence of its complex and large genome size. The pea genome is large (ca 4.45 Gb), probably resulting from recent expansion of retrotransposons followed by sequence diversification.

The Pea Genome International Project has undertaken several complementary strategies in order to produce a high-quality draft sequence of the species. We will present how this draft sequence opens the way to renew strategies in pea breeding.