

## Pea genomics for advanced breeding strategies

Judith Burstin<sup>1</sup>

<sup>1</sup> INRA

J. Burstin<sup>1</sup>, K. Avia<sup>1,9</sup>, A. Klein<sup>1</sup>, K. Gallardo<sup>1</sup>, N. Tayeh<sup>1</sup>, G. Aubert<sup>1</sup>, J. Kreplak<sup>1</sup>, M. Leveugle<sup>2</sup>, H. Duborjal<sup>2</sup>, J.P. Pichon<sup>2</sup>, J.F. Herbobomez<sup>3</sup>, P. Declerck<sup>4</sup>, M. Floriot<sup>5</sup>, C. Lecomte<sup>1</sup>, H. Houtin<sup>1</sup>, M. Chabert-Martinello<sup>1</sup>, Cline Rond-Coissieux<sup>1</sup>, E. Vieille<sup>1</sup>, C. Cruaud<sup>6</sup>, M.C. Le Paslier<sup>7</sup>, and The Pea Genome Consortium<sup>§</sup>

*1 Agrocologie, AgroSup Dijon, INRA, Universit Bourgogne, Universit Bourgogne Franche-Comt, 21000 Dijon, France, 2 Biogemma, Chappes, France, 3 KWS MOMONT Recherche, F-59246 Mons-en-Pvle, France, 4 RAGT 2n, F-28150 Louville La Chenard, France, 5 Agri Obtentions, F-78660 Orsonville, France, 6 Genoscope, Institut Franois Jacob, CEA, Universit Paris-Saclay, 91057 Evry, France 7 Etude du Polymorphisme des Gnomes Vgtaux, INRA, Universit Paris-Saclay, 91000 Evry, France*

Pea genomics has significantly progressed in the last decade. The recently published pea genome sequence<sup>§</sup> provides an improved reference and allow progressing in the identification of candidate genes, locating QTLs, and predicting genomic-enabled breeding values. We will show examples of how large-scale transcriptome approaches reveal complex regulatory networks at play during seed filling, multi-environment and multi-population studies allow reducing QTL confidence intervals, and genomic selection holds promises for breeding complex traits.

<sup>§</sup> Kreplak *et al.* 2019 A reference genome for pea provides insight into legume genome evolution. *Nature Genetics* volume 51, pages1411–1422 (2019)  
<https://doi.org/10.1038/s41588-019-0480-1>