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► To cite this version:

Nadim N. Tayeh, Susete Alves Carvalho, Christelle Aluome, Sébastien Carrere, Jonathan Kreplak, et al.. Pea genomic tools for functional and structural approaches. Mendel's legacy - 150 years of the genius of genetics, Masaryk University. CZE., Sep 2015, Brno, Czech Republic. hal-02743963

HAL Id: hal-02743963

<https://hal.inrae.fr/hal-02743963>

Submitted on 3 Jun 2020

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Research in Plant Genetics

7th September – 10th September 2015



Book of abstracts



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PEA GENOMIC TOOLS FOR FUNCTIONAL AND STRUCTURAL APPROACHES

Nadim Tayeh, S. Alves-Carvalho, C. Aluome, S. Carrère, J. Kreplak, A. Klein, M. Falque, C. Cruaud, P. Salloignon, C. Truntzer, J. Gouzy, P. Wincker, M.C. Le Paslier, D. Brunel, G. Aubert, **J. Bursstin**^a

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Pea (*Pisum sativum*) presents a wide phenotypic diversity that has been described since the early days of plant hybridizers in the 19th century, through Mendel's study of the inheritance of 7 striking pea traits, up to the quantitative traits useful to nowadays breeders. For a long time, pea genomics has been behind the genomics of other smaller genome plants and tools have been missing to systematically investigate the control of these traits. We will describe the recent development of a whole toolkit for gene discovery in pea and their use in plant breeding.

Genes *lufivium* dup 17,2K SNP
12 RILs converted → mini NAM
Parents re-sequenced