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PEA GENOMIC TOOLS FOR FUNCTIONAL AND STRUCTURAL APPROACHES

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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 *Infium* circ 17,2K SNP
12 RILs connected → mini NAM
Parents re-sequenced