Scientists unravel the genetic coding of the pea

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The pea is one of many important crop species that is unsuited to the Agrobacterium-based genetic modification techniques that are commonly used to work with crops. Researchers, reporting in the open access journal Genome Biology have now discovered the first high-throughput forward and reverse genetics tool for the pea (Pisum sativum), could have major benefits for crop breeders around the world.

Researchers from the INRA Plant Genomics Research Unit at Evry, and the INRA Grain Legumes Research Unit at Bretenières, both in France, both in France developed a high-quality genetic reference collection of Pisum sativum mutants within the European Grain Legumes Integrated Project. Abdelhafid Bendahmane and colleagues used plants from an early-flowering garden pea cultivar, Caméor, to create a mutant population, which they then systematically phenotyped for use in both forward and reverse genetics studies.

The team set up a pea TILLING (Targeting Induced Local Lesions IN Genomes) platform with DNA samples from 4,704} plants. The TILLING technique overcomes the pea's natural unsuitability to genetic modification techniques, and provides a powerful tool for investigating the role of essential genes.

This new tool has implications for both basic science and for crop improvement. TILLING is an alternative to Agrobacterium-based techniques, and uses EMS (ethane methyl sulfonate) mutagenesis coupled with a gene-specific detection of single-nucleotide mutations.

This reverse genetic strategy can be applied to all types of organisms and can be automated for high-throughput approaches.

Following this study, the researchers created a database called UTILLdb, which described each mutant plant at different developmental stages, (from seedling through to fruit maturation), and also incorporates digital images of the plants. UTILLdb contains phenotypic as well as sequence information on mutant genes, and can be searched for TILLING alleles of genes of interest, using the 'BLAST' tool, and for plant traits of interest, using keyword searches.

"By opening UTILLdb to the community, we hope to fulfil the expectations of both crop breeders and scientists who are using the pea as their model of study," said research coordinator Abdelhafid Bendahmane.

Citation: UTILLdb, a Pisum sativum in silico forward and reverse genetics tool, Marion Dalmais, Julien Schmidt, Christine Le Signor, Francoise Moussy, Judith Burstin, Vincent Savois, Gregoire Aubert, Veronique Brunaud, Yannick de Oliveira, Cecile Guichard, Richard Thompson and Abdelhafid Bendahmane, *Genome Biology* (in press)

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