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Legumes for a Sustainable World

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ITob UNIVERSIDADE
NOVA
DE LISBOA



Towards the genome sequence of pea

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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.