



Agricultural Journals

Czech Journal of

GENETICS AND PLANT BREEDING

[home](#) [page](#) [about us](#) [contact](#)



us

Table of Contents

IN PRESS

CJGPB 2014

CJGPB 2013

CJGPB 2012

CJGPB 2011

CJGPB 2010

CJGPB 2009

CJGPB 2008

CJGPB 2007

CJGPB 2006

CJGPB 2005

CJGPB 2004

CJGPB 2003

CJGPB 2002

CJGPB

Home

Editorial Board

For Authors

- **Authors
Declaration**
- **Instruction
to Authors**
- **Guide for
Authors**
- **Copyright
Statement**
- **Submission**

For Reviewers

- **Guide for
Reviewers**
- **Reviewers
Login**

Subscription

Czech J. Genet. Plant Breed.

Pea (*Pisum sativum* L.) in biology prior and after Mendel's discovery

Czech J. Genet. Plant Breed., 50 (2014):
52-64

Pea (*Pisum sativum* L.) has been extensively used in early hybridization studies and it was the model organism of choice for Mendel's discovery of the laws of inheritance, making pea part of the foundation of modern genetics. Pea has also been used as model for experimental morphology and physiology. However, subsequent progress in pea genomics has lagged behind many other plant species, largely as a consequence of its genome size and low economic significance. The availability of the genome sequences of five legume species (*Medicago truncatula*, *Lotus japonicus*, *Glycine max*, *Cajanus cajan* and *Cicer arietinum*) offers opportunities for genome wide comparison. The combination of a candidate gene and

synteny approach has allowed the identification of genes underlying agronomically important traits such as virus resistances and plant architecture. Useful genomic resources already exist and include several types of molecular marker sets as well as both transcriptome and proteome datasets. The advent of greater computational power and access to diverse germplasm collections enable the use of association mapping to identify genetic variation related to desirable agronomic traits. Current genomic knowledge and technologies can facilitate the allele mining for novel traits and their incorporation from wild *Pisum* sp. into elite domestic backgrounds. Fast neutron and targeting-induced local lesions in genomes (TILLING) pea mutant populations are available for reverse genetics approaches, BAC libraries for positional gene cloning as well as transgenic and *in vitro* regeneration for proof of function through gene silencing or over-expression. Finally, recently formed International Pea Genome Sequencing Consortium, holds promise to provide the pea genome sequence by 2015, a year of 150 anniversary of

Keywords:

heredity; hybridization; legume; Mendel;
pea

[[fulltext](#)]

© 2011 [Czech Academy of Agricultural
Sciences](#)

XHTML1.1 VALID

CSS VALID