

Global genetic diversity of *Brassica rapa*

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ABSTRACT

Canola (*Brassica napus*) is an important oilseed crop that has suffered a series of bottlenecks during its development which has reduced its genetic diversity. As one of the parental species that contributed to *B. napus*, *B. rapa* may help to broaden the genetic diversity in canola. By studying genetic diversity in *B. rapa*, some valuable traits could be found for canola improvement. In this study, we studied the global genetic diversity of 374 accessions described as *Brassica rapa*, originally collected from more than 48 countries. Two different treatments were applied at the seedling stage: non-vernalisation and vernalisation at 4°C for 8 weeks. Observations were made on the maturity type (spring, semi-winter or winter type), morphotypes (leafy type, root type, or oilseed type), flowering time, self-compatibility or self-incompatibility, seed yield, and 100 seed weight. Fifty one pairs of SSR primers were used for allelic diversity analysis. In this paper, the global genetic diversity of *B. rapa* will be reported and its potential use in canola breeding will be discussed.

Key words: *Brassica rapa* – genetic diversity – SSR

INTRODUCTION

Knowledge of genetic diversity in the primary gene pool of crop plants is very important from a plant breeding and genetic point of view. Knowledge of wild type species may help humans to overcome obstacles in genetic improvement of crop plants. *Brassica rapa* is a valuable crop species in the *Brassicaceae* family, known by its common names field mustard, turnip, and/or Chinese cabbage. The global distribution of *B. rapa* is broader than most of other *Brassica* species and a genetic study is needed to assess genetic distance within the species, in relation to the phenotypic diversity. Landraces of *B. rapa* are adapted to a broad range of environments, e.g. cold or high temperatures, across a very wide geographic area (Dixon 2007). *B. rapa* is one of the parental species that contributed to *B. napus* (rapeseed or canola) and *B. rapa* may help to broaden the genetic diversity in canola since rapeseed suffered a series of bottlenecks during its development and has reduced genetic diversity (Becker *et al.* 1995; Cowling 2007). The study of genetic diversity of *B. rapa* may lead to the discovery of valuable traits, that can be used for crop improvement and could also aid in the classification of accessions that have unknown origin as well as in the correction of the misclassification of some accessions.

MATERIALS AND METHODS

A total of 374 accessions of *B. rapa* representing 48 countries (from Asia, Europe, America, Africa, and unknown origin) provided by ATFCC (Australian Temperate Field Crops Collection, Horsham, Victoria), IPK (The Leibniz Institute of Plant Genetics and Crop Plant Research, Gatersleben, Germany), and NPZ (Norddeutsche Pflanzenzucht Hans-Georg Lembke KG, Hohenlieth, Germany) were used in this experiment to study phenotypic and molecular genetic diversity. Two different treatments were applied at the seedling stage: non vernalisation and vernalisation at 4°C for 8 weeks. Observations were made on the maturity type (spring, semi-winter or winter type), morphotypes (leafy type, root type, or oilseed type), flowering time, maturity time, self-compatibility or self-incompatibility, total seed, 100 seed weight, and seed colour.

DNA was isolated by collecting young leaves from the plants in a glasshouse. A total of 374 samples plus five other *Brassica* species (*B. juncea*, *B. napus*, *B. oleracea*, *B. carinata*, and *B. nigra*) were evaluated with 51 pairs of SSR primers by multiplex PCR as described previously (Chen *et al.* 2008). Each forward primer from these markers was labelled with one of the following fluorescent dyes: 6-FAM, VIC, NED, or PET. Fragment analysis was done using ABI3730 and the data was extracted using GeneMarker V1.90 from Softgenetics. Dissimilarity matrices were calculated as suggested by Nei and Li (1979) and based on Euclidean distance. Data from this matrix of all accessions were subjected to hierarchical cluster analysis using the unweighted pair group method and arithmetic averages (UPGMA) as proposed by Sneath and Sokal (1973) and ordination by two-dimensional multidimensional scaling (2D-MDS) in PRIMER 6 software (Clarke and Gorley 2006).

RESULTS

In this study we were able to classify the morphotypes and flowering type of 374 *B. rapa* accessions (Table 1). The majority (81.3%) of accessions were oilseed type, and these were found at all places of origin. The leafy types were mostly found in China and root types mostly in Europe. All unknown origin accessions were oilseed type. Approximately 38.5% of the accessions were spring flower type, 35.0% were semi-winter type and 25.9% were winter. The results of phylogenetic analysis supported the *B. rapa* genetic diversity as assessed by Zhao *et al.* (2005) based on AFLP markers.

Table 1. Morphotype and flower type summary

Origin	Morphotype				Flower type				
	Leafy type	Root type	Oilseed type	Total	Spring	Semi -W	Winter	Unknown	Total
Unknown	0	0	18	18	6	10	2		18
Europe	6	16	86	108	16	13	79		108
China	26	0	64	90	52	38	0		90
India	0	0	85	85	43	41	0	1	85
Other Asian countries	12	7	26	45	16	17	12		45
America continent	0	0	7	7	1	4	1	1	7
Canada	0	0	9	9	6	2	1		9
Australia	0	0	8	8	3	3	2		8
Africa	0	3	1	4	1	3	0		4
Total	44	26	304	374	144	131	97		374

DISCUSSION

Results from our research can be used to help classify the unknown origin of some accessions and to give more valuable data to be used for further experiments. We were able to classify the morphotype and flower type of germplasm accessions. Our results can also be used to support further research into the *Brassica* germplasm research and *Brassica* breeding programmes.

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