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Data article

Genetic characterization of inbred lines of Chinese cabbage by DNA markers; towards the application of DNA markers to breeding of F₁ hybrid cultivars



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ABSTRACT

Chinese cabbage (*Brassica rapa* L. var. *pekinensis*) is an important vegetable in Asia, and most Japanese commercial cultivars of Chinese cabbage use an F₁ hybrid seed production system. Self-incompatibility is successfully used for the production of F₁ hybrid seeds in *B. rapa* vegetables to avoid contamination by non-hybrid seeds, and the strength of self-incompatibility is important for harvesting a highly pure F₁ seeds. Prediction of agronomically important traits such as disease resistance based on DNA markers is useful. In this dataset, we identified the S haplotypes by DNA

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Fusarium yellows
Clubroot disease
Self-incompatibility

markers and evaluated the strength of self-incompatibility in Chinese cabbage inbred lines. The data described the predicted disease resistance to Fusarium yellows or clubroot in 22 Chinese cabbage inbred lines using gene associated or gene linked DNA markers.

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Specifications Table

Subject area	Biology
More specific subject area	Plant molecular biology
Type of data	Table, figure
How data was acquired	PCR, Pollination test
Data format	Raw and analyzed data
Experimental factors	Inbred lines of Chinese cabbage used in Kawamura et al. [1] were used for plant materials. DNA isolated from leaves was used as PCR templates.
Experimental features	Gene associated or linked DNA markers were tested to predict the disease resistance. The strength of self-incompatibility was calculated by the number of seeds per flower.
Data source location	Kobe, Japan
Data accessibility	The data is available with this article.

Value of the data

- Prediction of disease resistance by DNA markers is useful for marker-assisted breeding.
- Identification of the *S* haplotype is important for determining suitable combinations of parental lines in Brassica vegetables.
- The strength of self-incompatibility is an important factor for F_1 seed production to avoid inbreeding seed contamination in Brassica vegetables.

1. Data

1.1. Prediction of Fusarium yellows resistance by DNA markers

Fusarium yellows is caused by a soil-borne fungus *Fusarium oxysporum* f. sp. *conglutinans*/*F. oxysporum* f. sp. *rapae*. Plants infected with Fusarium yellows show leaf yellowing, wilting, defoliation, stunted growth, and death of the host plant, and resistance genes have been identified in *Brassica rapa* [2,3].

We developed 22 inbred lines of Chinese cabbage as candidates for parental lines of F_1 hybrid cultivars, especially as seed parents, and the genetic relationship of these 22 inbred lines was evaluated [1]. We have developed dominant DNA markers, Bra012688m and Bra012689m, which are closely linked to the Fusarium yellows resistance locus [3]. Both PCR based and inoculation tests have previously been performed in 7 of the 22 inbred lines using these markers (Table 1) [3], and we assessed these 2 DNA markers against the remaining 15 inbred lines. Twelve of the 15 inbred lines showed PCR amplification of both DNA markers (Table 1), suggesting that these inbred lines have Fusarium yellows resistance.

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