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Development of PCR-based Markers for Genetic Mapping based on BAC-end Sequence and ESTs in Chinese cabbage

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Objectives

We have developed the PCR-based markers for genetic mapping based on BAC-end sequence and ESTs in Chinese cabbage. These markers have benefit in working co-dominantly and have used the construction of genetic mapping.

Materials and Methods

- Plants: *Brassica rapa* L. ssp. *pekinensis* inbred line Chiifu and Kenshin type
- BAC-end sequencing: Chinese cabbage *Hind*III BAC library, ABI 3700
- ESTs sequencing: Chinese cabbage cDNA library, ABI3700
- Primer design: Primer3 program, Map construction: JoinMap v.3.0

Results and Discussion

SSR markers were developed using the known BAC-end sequence information. Out of 2,376 BAC-end sequencing data, we found 58 clones containing repeat motif using Repeatmasker program, and designed 41 primer pairs with Primer 3 software. Thirteen pairs out of 41 designed primer allow the polymorphism as SSR marker in *Brassica rapa.*, the frequency of primer sets showing a polymorphism is a 31.7%.

One hundred and fifty sequences out of 1,736 ESTs were selected to design specific ESTs primers for PCR. The amplified products were separated by 1.2-3.0% agarose gel to check polymorphism. To date, about 23.3% of primers represent the polymorphism among the parents and 89 DH lines. These markers distributed in each linkage group as adapt in genetic mapping.

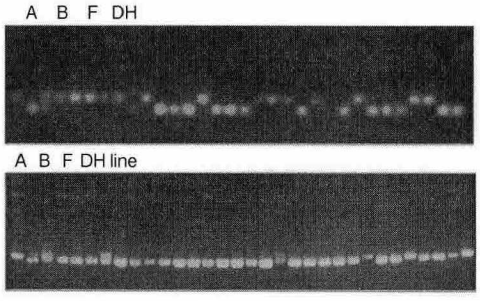

Figure 1. Polymorphism among A, B and DH lines revealed by PCR using specific SSR primer

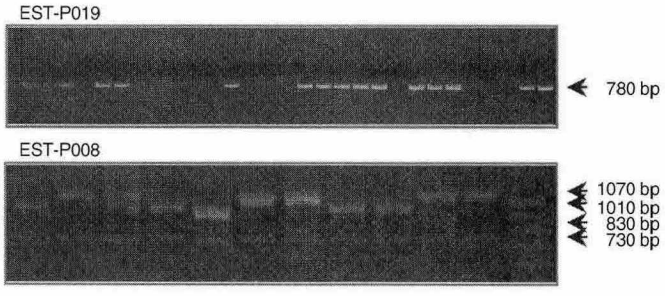

Figure 2. Polymorphism among A, B and DH lines revealed by PCR using specific EST primer

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