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Heritability and gene effects for tiller number and leaf number in non-heading Chinese cabbage using joint segregation analysis

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ABSTRACT

Non-heading Chinese cabbage is one of the most popular leafy vegetables. Three cultivars, ‘Maertou’, ‘Rugaomaocai’ and ‘Suzhouqing’, were crossed to study gene effects and heritability involved in tiller and leaf development. The joint segregation analysis in six generation populations, P_1, P_2, F_1, F_2, B_1 and B_2, indicating the influence of major genes mixed with polygenes. The results revealed the traits of tiller number and leaf number in non-heading Chinese cabbage were controlled by two major genes and polygenes with dominant, additive and epistasis effects, respectively. The heritability of the two major genes in F_2 was over 60%, indicating that the genetic factor was the main influence to the leaf number and tiller number traits. Data from the present study revealed that it had a significant positive correlation between tiller number and leaf number in non-heading Chinese cabbage.

1. Introduction

Non-heading Chinese cabbage (*Brassica campestris* ssp. *chinensis* Makino) ($2n = 2x = 20$) is one of the most popular leafy vegetables with significant economic value (Hou, 2012). It is originated from China and widely grown in most areas of China (Hou, 2003). Non-heading Chinese cabbage was divided into 5 varieties. Among of them, only the variety of var. *multiceps* Hort. showed tillering (shoot branching) trait.

The tillers (basal branches) arise from near-surface of dwarf-stem at the base of the parent shoot. They are additional inflorescence branches growing out from the axillary buds, subtended by rosette leaves (Kebrom et al., 2013). Generally considered, tillers are quantitative trait controlled by multiple genes, and susceptible to environmental conditions (Ehrenreich et al., 2007; Kebrom et al., 2013). In rice, several genetic loci that control tiller angle have been identified using both classical and molecular methods of genetic analysis (Yu et al., 2007). In *Arabidopsis thaliana*, it has been shown that significant variation in branching and other quantitative aspects of shoot architecture exactly existed (Ungerer et al., 2002). However, breeding for yield improvement by adjusting tiller has not been achieved due to the poor knowledge of controlling factors in non-heading Chinese cabbage. As a leafy vegetable, more tillers and more leaves mean more yield. Interestingly, the tiller number and leaf number showed a correlation, more tiller numbers corresponded more leaf numbers to some extent. So, it is very important to understand the genetic models for tiller trait and leaf trait in non-heading Chinese cabbage.

Various methods have been proposed for statistical inference of major genes by segregation analysis, Morton and Maclean (1974) proposed a mixed model of major locus, polygenic variation, and both common and random environment for testing genetic hypotheses about a quantitative trait. Wang and Gai (1998, 2001); Gai and Wang (1998) proposed the joint segregation analysis (JSA) of multiple populations for mixed major genes plus polygene inheritance. It is aimed to estimate genetic parameters describing the variation of a quantitative trait in plants. QTL mapping and GWAS have been widely used to uncover the genetic structure of variation relevant to breeding. QTL mapping requires molecular data and GWAS need to high-throughput sequencing with much more money. However, the segregation analysis could be used to analyze the mixed inheritance model even without the aid of molecular data. It is easy and quick to analysis the field data. It has been reported the two procedures (the segregation analysis and QTL mapping) could be used as a mutual check and supplement (Gai

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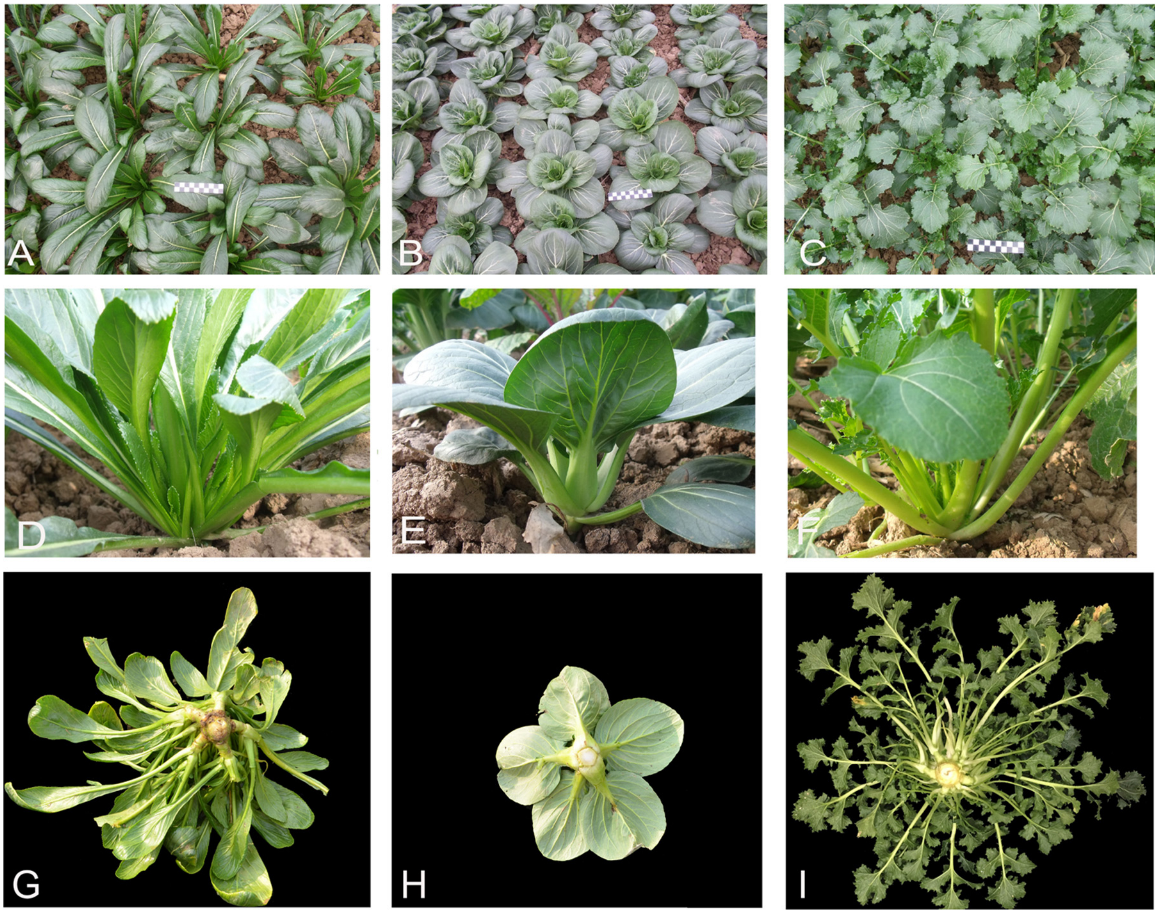

Fig. 1. The differences between parents in leaf number and tiller number traits. A, B, C were vertical view of each parent block; D, E, F were side view of each parent per plant; G, H, I were vertical view of each parent per plant to show the tiller. A, D, G: 'Maertou'; B, E, H: 'Suzhouqing'; C, F, I: 'Rugaomaocai'.

et al., 2007). So, it is still a powerful tool that has been used to study various quantitative traits in crops such as time to flowering in chickpea (Anbessa et al., 2006), seeds per silique in Brassica oilseed (Zhang et al., 2010), flag leaf area in wheat (Khan et al., 2012), and seed coat color in sesame (Zhang et al., 2013). In Brassica, some economic traits like vitamin C (Lin et al., 2014), plant height (Han et al., 2008), bolting trait (Zhuo et al., 2009) had been analyzed using JSA.

The tiller trait and leaf trait of non-heading Chinese cabbage has been studied by Zeng and Cao (1996, 1998). They thought tiller trait was a qualitative trait, controlled by two overlapping genes. But for further observation of tiller trait, we think tiller number is a quantitative trait. In this study, the JSA of six generation populations in tiller number and leaf number was analyzed, and correlations between tiller number and leaf number were also be estimated in non-heading Chinese cabbage.

2. Materials and methods

2.1. Plant materials

'Maertou' and 'Rugaomaocai', cultivars which showed tillering phenotype were chosen as female parents. 'Suzhouqing', no-tillering cultivar which belong to var. *communis* Tesn et Lee was the male parent (Fig. 1). Parents and/or crosses involving 'Maertou'(P_1) with 'Suzhouqing'(P_2) or 'Rugaomaocai'(P_1) with 'Suzhouqing'(P_2) were used to produce six generations (P_1, P_2, F_1, B_1, B_2 and F_2). All of them were developed separately.

2.2. Experimental design

The six generations (P_1, P_2, F_1, B_1, B_2 and F_2) of the two crosses were grown in experimental field of Nanjing Agricultural University. In September 2010, three cultivars were planted and in the next year, April 2011, two crosses were made by hand pollination, i.e., 'Maertou'(P_1) × 'Suzhouqing'(P_2) (crossI) and 'Rugaomaocai'(P_1) × 'Suzhouqing'(P_2) (crossII). In the second season, September 2011, seeds of two F_1 were planted. Then, in April 2012, they were used to produce F_2 by strictly pollination self and backcrossed to both parents to produce B_1 ($F_1 \times P_1$), B_2 ($F_1 \times P_2$). In the third season, September 2012, the obtained seeds of the six populations (P_1, P_2, F_1, B_1, B_2 and F_2) of both crossI and crossII were sown and evaluated using a randomized complete block design with three replications. Plants spaced 30 cm from each other. Measurement was performed after planted 80 d when the tillers were occurring on a large numbers. As a replication, the six populations (P_1, P_2, F_1, B_1, B_2 and F_2) of two crosses were sown in September 2014, and the measurement was performed after planted 90 d. Results are expressed herein as two populations.

2.3. Statistical and joint segregation analysis

Initially, field data were combined to determine phenotype and genotype effects, the data from each population were calculated separately. Statistical analyses were performed using SPSS.

Joint segregation analysis of the six generations (P_1, P_2, F_1, B_1, B_2, and F_2) was performed according to Gai and Wang (1998). The details of the JSA were described by Hao et al. (2008). The main steps