

Genetic Contribution of Vegetative Traits to Yield Traits Among Subspecies or Varieties in *B. Campestris* L.

Wang Xuefang, Wang Junsheng, Zhang Zhi, Li Dianrong, Tian Jianhua, Zhang Yanfeng

Hybrid Rapeseed Research Center of Shaanxi Province, Shaanxi Rapeseed Branch of National Oil Crops Genetic Improvement Center, Dali, China, 715105

Abstract To reveal the genetic contributions of 8 vegetative traits (No. of leaves (NL), petiole weight (PW), maximal leaf length (MLL), maximal leaf width (MLW), petiole length (PL), root length (RL), root weight (RW), fresh weight per plant (FWPP)) to seed yield per plant (SYPP) and its components and find specific genetic mechanism of different type parents in *B. campestris* L., 12 different parents and their 35 F₁ crosses were planted for multivariable conditional analysis based on a genetic model containing additive-dominance effects and their interactions with environments in 2004-2006 in Shaanxi province, China. The results showed that only additional contribution of RL to SYPP was positive very significant (25.4%), and the dominant contribution ratios of vegetative traits to SYPP (35.2%~70.0%) were all significantly difference. In 3 yield components, the additive contribution ratios of RL to 1000-seed weight (1000-SW) and seeds per siliques (SPS) (39.2%, 24.9%), NL to siliques per plant (SPP) (70.3%) were the highest; The dominant contributions of FWPP and MLL to 1000-SW (26.3%, 24.4%), FWPP and RW to SPS (56.1%, 55.2%) were the highest too. In addition, different type of parents had different additive genetic contribution ways in vegetative traits to SYPP, the additive contribution effects of above-ground vegetative traits were major for vegetable type of *B. camp.* L, but these effects of RW and RL were greater for rapeseed of *B. camp.* L. There are 3 combinations whose dominant effect value was above zero in 10 subspecies or varieties, however, there 16 combinations whose dominant effect value was above zero in 24 subspecies or varieties, so it was easier to obtain higher yield combinations from crosses between subspecies or mutations. Therefore, the utilization of vegetable of *B. campestris* will be a new chance in rapeseed *B. Campestris* L breeding.

Key Words *B. Campestris* L ; Vegetative traits; Yield traits; AD-model; Contribution analysis

Introduction

B. campestris L originated from China, has a long cultivation history (Liu, 1984; He, et. al, 2002), rich germplasms and plentiful genetic diversify in China. It is one of important crop not only oil but also vegetable. It is greatly limited in production now because of lower yield and difficulty on utilizing heterosis. However, some outstanding peculiarities in Chinese-cabbage, No-heading Chinese-cabbage, purple Tcai-tai and Caixin, and the *heterosis* between different subspecies in *B. campestris* L, syn. *B. rapa* L (Wang et. al., 2004, 2005 and 2007) was very greater and provided a new way of improving seed yield of *B. camp. var. oleifera*.

Vegetative traits are basis of yield traits, but it is difficult to measure how much and how way contribution of vegetative traits to yield traits. A new statistical method, however, has been proposed for analyzing net genetic effects and genetic variance components of specific traits to aimed trait in the period (t-1) to t. in several crops.

In this paper, contribution analysis of vegetative traits to SYPP and yield component in subspecies and(or) mutations in *B. Campestris* L. was conducted to ascertain the genetic mechanism of seed yield in different type parent by multivariable conditional analysis method developed by Zhu (Sarawgi et. al., 1997; Zhu, 1995; Atchley et. al., 1997; Wen et. al., 2005), and explored high yield theoretical foundation between subspecies or varieties, which may be useful in indirect selection for breeding high yield cultivars.

Materials and Methods

Experiment design and materials

The experiment was conducted in 2004-2006 in Hybrid Rapeseed Research Center of Shaanxi Province. 35 F₁ crosses were made between 5 female lines (P₁-P₅) and 7 male lines (P₆-P₁₂) which were pure

inbred lines and belong to different subspecies or mutations in *B. campestris* L., using North Carolina Design II in 2003. 34 F₁ crosses (D₅₋₉ did not get seeds) and their parent (sterile line replaced by maintainer) was laid out in randomized complete block design with 3 replications, where there were 5 rows per plot, and the row was 2.6m long, and the space between individuals was 0.4m×0.167m. Ten plants with identical performance were sampled from each plot to measure 8 main vegetative traits (NL=Number of leaves, PW=Petiole weight, MLL=Max. leaf length, MLW=Max. leaf width, PL=Petiole length, RL=Root length, RW=Root weight, FWPP=Fresh weight per plant.) before hoar frost descends per year. The other 10 plants were also sampled to determine the main yield traits—siliques per plant (SPP), 1000-seed weight (1000-SW), seeds per siliques (SPS) and seed yield per plant (SYPP) in the mature stage. The type of all parents was listed in Table1.

Table1 Types of parents

Parent	Type of parent	Parent	Type of parent	Parent	Type of parent
P ₁	<i>B. camp. ssp. pekinensis</i> S	P ₅	<i>B. camp. var. oleifera</i> S	P ₉	<i>B. camp. var. oleifera</i> R
P ₂	<i>B. camp. var. Purpuraria</i> S	P ₆	<i>B. camp. var. oleifera</i> R	P ₁₀	<i>B. camp. ssp. chinensis</i> R
P ₃	<i>B. camp. ssp. chinensis</i> S	P ₇	<i>B. camp. var. oleifera</i> R	P ₁₁	<i>B. camp. ssp. pekinensis</i> R
P ₄	<i>B. camp. var. oleifera</i> S	P ₈	<i>B. camp. var. oleifera</i> R	P ₁₂	<i>B. camp. ssp. chinensis</i> R

Note: S: cytoplasmic male sterile line; R: cytoplasmic male sterile restorers

Genetic model and statistical analysis

Based on the diallel model with additive-dominance effects and their interactions with environment, the phenotypic mean of a trait measured for the F₁ cross can be partitioned as $y = \mu + E + A + D + AE + DE + \varepsilon$, where y is the phenotypic value of a trait, μ is the population mean for all entries of mating design, E is the environmental effect, A is the additive effect, D is the dominant effect, AE is the additive × environment interaction effect, DE is the dominance × environment interaction effect, ε is the residual effect. Using mixed line model approaches (Zhu, 1995; Atchley et. al., 1997; Wen et. al., 2005; Zhu, 1997), genetic contribution ratio of vegetative traits to SYPP and yield component traits were estimated. $CR_{A(C \rightarrow T)}$ is the additive contribution ratio of vegetative traits to yield traits, $CR_{D(C \rightarrow T)}$ is the dominance contribution ratio; $CR_{AE(C \rightarrow T)}$ is the interaction contribution ratio of additive × environment, $CR_{DE(C \rightarrow T)}$ is the interaction contribution ratio of dominance × environment; $CR_{P(C \rightarrow T)}$ is phenotype contribution ratio. The genetic effect of yield traits and genetic contribution effects of vegetative traits to yield traits were also predicted (A_i is the additive effect of genes controlling yield traits from parent line i ; $A_{i(C \rightarrow T)}$ is the additive contribution effect of vegetative traits to yield traits from parent line i ; D_{ij} is the dominance effect of genes from the cross $i \times j$; $D_{ij(C \rightarrow T)}$ is the dominance contribution effect of vegetative traits to yield traits from the cross $i \times j$). Jackknifing over genotypes was used to estimate standard errors of estimated genetic variances (Zhu and Weir, 1996). All statistical analysis was conducted by QGAStation software (<http://ibi.zju.edu.cn/software/QGA.htm>).

Results

Contribution analysis of vegetative traits to SYPP

The phenotype contribution ratios of 8 vegetative traits to SYPP were very significant. Only RL had very significant positively additive contribution to SYPP, which showed that improving RL could increase SYPP indirectly. The dominance contribution ratio to SYPP were very significant for all vegetative traits, which indicated that the dominance contribution ratio was greater than additive contribution ratio, and the improvement on SYPP of F₁ cross could be realized by indirect improvement on all these vegetative traits of F₁ cross. The interaction contribution ratios of additive × environment of genes controlling vegetative traits to SYPP were not detected, while these of dominance × environment of all vegetative traits except MLW and FWPP to SYPP got to significant at 0.01 level, especially, that of PW was the greatest (22.3%), which showed that PW could become the major vegetative trait affecting SYPP in a special year (Table2).

for SPP	CR _{AE} (C→T)	—	—	—	—	—	—	—	—
	CR _{DE} (C→T)	0.985**	0.170**	0	0.023**	0.012**	0.084**	0.002**	0.004**
	CR _P (C→T)	0.934**	0.054**	0.045**	-0.037	0.062**	0.037**	-0.044	-0.013

The interaction contribution ratios of dominance × environment of most vegetative traits to yield traits, except for MLL to SPP and RL to 1000-SW, were very significantly different but smaller, however, these of NL to SPP were 98.5%, which showed that NL was major dominance contribution for SPP, that is, in a special year, the crosses with higher SCA in NL had more SPP commonly.

Additive effects contribution of parent vegetative traits to SYPP

Predicted additive effects of SYPP (A_i) and contributed additive effects of 8 vegetative traits to SYPP ($A_{i(C→T)}$) were presented in Table 4. There were significantly positive additive effects of SYPP for 4 parents (P_1 , P_4 , P_5 and P_{12}). Except NL of P_6 , the additive contribution effects of all vegetative traits to SYPP were significantly difference at 0.01 level, but their values had great difference. The positive additive effect of SYPP was contributed mainly from MLL and PL of parent P_1 and P_2 , MLW of P_3 and P_{10} , FWPP and PW of P_{11} and P_{12} , RW and RL of P_4 - P_9 . If we classified all vegetative traits into two groups: root-system traits and leaf traits, the SYPP of most vegetable type of parents such as P_1 - P_3 , P_{10} and P_{11} mainly benefited from the positive contribution of leaf traits, on the contrary, parents of *B.camp.var.oleifera*, such as P_4 - P_9 mainly benefited from the contribution of their root system. It was implied that different growth type of parents might have formed different genetic mechanism on seed yield after long course of artificial selection and evolution.

Table 4 Contributed additive effects of vegetable traits to seed yield per plant (SYPP)

Parents	A_i	$A_{i(C→T)}$							
		NL	PW	MLL	MLW	PL	RL	RW	FWPP
P_1	2.55**	0.43**	-0.02**	0.93**	-1.06**	-0.70**	0.33**	-1.34**	0.17**
P_2	-0.90**	0.10**	0.22**	0.57**	0.11**	0.53**	-0.72**	-0.09**	0.06**
P_3	-1.07**	0.53**	0.43**	0.57**	0.73**	0.39**	-1.01**	-0.20**	0.28**
P_4	1.13*	-0.33**	-0.51**	-0.49**	0.21**	-0.28**	0.33**	0.37**	-0.71**
P_5	0.43*	-0.28**	-0.16**	-0.15**	-0.23**	-0.05**	0.26**	0.50**	-0.35**
P_6	-0.05	0.02+	0.18**	-0.10**	-0.11**	-0.02**	0.17**	0.37**	0.27**
P_7	-1.48**	-0.12**	0.31**	0.43**	0.43**	0.44**	0.31**	0.72**	0.39**
P_8	-0.59*	0.16**	-0.14**	0.17**	0.37**	0.11**	0.75**	0.99**	0.04**
P_9	0.10	-0.16**	-0.04**	-0.05**	-0.08**	-0.05**	0.53**	0.64**	0.14**
P_{10}	-0.83*	-0.41**	-0.18**	0.26**	0.37**	0.20**	-0.33**	-0.34*	-0.28**
P_{11}	-1.42**	0.66**	0.79**	0.55**	-0.19**	0.20**	-0.45**	0.28**	0.97**
P_{12}	2.11**	-0.59**	0.88**	-0.83**	-0.54**	-0.75**	0.33**	-0.15**	-0.98**

Dominant effects contribution of vegetative traits to yield traits in every combination

14 F_1 crosses were significant dominance effects of SYPP in 34 F_1 crosses, in which D_{1*9} , D_{1*10} , D_{2*7} , D_{2*8} , D_{2*12} , D_{3*9} , D_{3*10} , D_{5*10} and D_{5*12} had greater positive dominance effects of SYPP (Table was omitted), the dominance contribution effects of most vegetative traits to SYPP in these crosses were significantly different at 0.05 level, however, their dominance contribution value was different. This meant that different crosses with high dominant effects of SYPP had different dominant contribution traits. In 34 F_1 crosses, RW in 7 crosses, MLW in 6 crosses, MLL in 5 crosses, NL, PW and PL in 4 crosses respectively, RL and FWPP in 2 crosses respectively had greater dominant contribution, which indicated that RW was relatively steady and main dominance contribution traits to effects of SYPP in these crosses, MLL and MLW in the next place.

There were 34 crosses in the experiment (the cross D_{5*9} did not get seeds) in all. Among them, 3 of 10 crosses belonging to inter-strains and 16 of 24 crosses belonging to subspecies or mutations had over

zero dominance effect value on SYPP. It was indicated that it was easier to obtain higher yield combinations from inter-subspecies or inter-mutations crosses, and this was also proved by our breeding practice.

Discussion

In crop breeding, breeders can only select phenotypic value, this can influence genetic component of other traits by selecting special trait. In this paper, phenotypic variance of 8 vegetative traits to SYPP were all significant difference, however, only RL was significant additive difference to SYPP. In 8 vegetative traits, RL and MLL to 1000-SW, RL to SPS, PL and MLL to SPP had the greatest positive contribution, which indicated that the higher yield of offspring could obtain by indirectly selecting longer RL and MLL

RW was main dominant contribution trait in vegetative traits to SYPP, MLW and MLL secondly, which showed a good vegetative growth settled a good basis for reproductive growth, the vegetative traits with promoting or restraining effects on SYPP were incompletely uniform. Harmonious and balanced development between leaf traits and root system traits was commonness of higher yield crosses, only from the crosses with a balanced growth between leaf traits and root system traits could easily obtain higher seed yield.

High yield heterosis is difficult to gain due to shortage of genetic diversity within inter-strains cross in many crops. However the hybrids inter-species or inter-subspecies have stronger heterosis in vegetative body and seed yield (Wang et. al., 2007, Zhu et. al., 1997.). This study provided above opinion. It was showed that a farther genetic distance was one of important factor except that different type parents had their unique development characteristics and yield genetic mechanism.

B.camp. var. Purpuraria, *B.camp. ssp. Pekinensis* and *B. camp. ssp. Chinensis* as well as *B. camp. var. oleifera* have same similar origin and chromosome composition(AA=20). They have various genetic mechanism *B.campestris* L. is divided into *B.camp.ssp. Pekinensis* (Chinese-cabbage), *B.camp. ssp. Chinensis* (No-heading Chinese-cabbage) and other variety, so the utilization of vegetable of *B.campestris* will be a new chance in rapeseed *B. Campestris* L breeding.

References Omitted