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Decomposition Method of Genetic Correlation Coefficient Based on NC II Mating Design

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Abstract There are different degrees of correlation between crop traits. The phenotypic correlation is decomposed into genetic and environmental correlation in quantitative genetics. In this paper, according to stochastic model of variance and covariance analysis, we calculate different genetic components, bring up a decomposition method of genetic correlation coefficient based on NC II mating design, and use examples to show analytic steps and interpret results.

Key words Analysis of variance, Analysis of covariance, Stochastic model, Genetic correlation coefficient

1 Introduction

There is a correlation between the crop traits in different degrees, and the simple correlation or phenotypic correlation between the two traits is controlled by both genetic and environmental factors, which can not explain the genetic linkage between traits. Therefore, the theory of crop genetic correlation decomposes the phenotypic correlation into genetic correlation and environmental correlation, and genetic correlation is used to demonstrate the genetic correlation between the two traits, and estimate the degree of correlation in genetic variation among traits[1-2]. Zhu Jun[3] developed a hybrid genetic model based on additive, dominant and environmental interaction, decomposed the genotype correlation coefficient into additive correlation coefficient, dominant correlation coefficient, additive and environmental interaction and dominant and environmental interaction correlation coefficients, and applied the mixed linear genetic model in the genetic breeding[4]. Genetic correlation coefficient is one of the important genetic parameters of quantitative traits. The analysis on genetic correlation coefficient of crop economic traits needs to rely on a lot of specific genetic mating design, and diallel design is the commonly used genetic mating design in the classical quantitative genetics, and widely used in the breeding and quantitative traits of plants and animals. In the study of crop genetics and breeding, based on different genetic mating design, phenotypic correlation coefficient, genetic correlation coefficient and environmental correlation coefficient are often used to describe the variability of correlation between two quantitative traits[2, 5], but traditional genetic breeding theory does not re – decompose the genetic correlation coefficient. Therefore, this paper only focused on exploring and explaining a new method for decomposition of genetic correlation coefficient based on analysis of variance and analysis of covariance about traits under NC II genetic mating design, in order to provide theoretical guidance for crop genetic breeding.

2 General principles

The NC II mating design is constituted by the hybrid descendants of $m+f$ parental lines, that is, m male parental lines and f female parental lines are randomly selected to hybridize and form $m \times f$ combinations. The randomized block design was used, repeated r times.

2.1 Analysis of variance and covariance The analysis is performed based on the plot mean, and the analysis results of variance and covariance and the expected mean squares[5-7] are shown in Table 1.

Table 1 Analysis of variance and covariance of NC II mating design

Source of variation	*df*	X trait		X and Y traits	
		MS	*EMS*	*MP*	*EMP*
Block	$r-1$				
Between male parents	$m-1$	MS_m	$\sigma_e^2+r\sigma_{mf}^2+rf\sigma_m^2$	MP_m	$cov_e+rcov_{mf}+rfcov_m$
Between female parents	$f-1$	MS_f	$\sigma_e^2+r\sigma_{mf}^2+rm\sigma_f^2$	MP_f	$cov_e+rcov_{mf}+rfcov_f$
Male parent × female parent	$(m-1)(f-1)$	MS_{mf}	$\sigma_e^2+r\sigma_{mf}^2$	MP_{mf}	cov_e+rcov_{mf}
Error	$(r-1)(mf-1)$	MS_e	σ_e^2	MP_e	cov_e
Total	$rmf-1$				

2.2 Genetic parameter estimation In NC II design, it is assumed that these test materials constitute a random sample from panmictic population. According to this assumption, we can estimate the variance

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components of parent from Table 1:

$$\left.\begin{array}{llll} \hat{\sigma}_e^2 = MS_e & \hat{\sigma}_{mf}^2 = \dfrac{MS_{mf} - MS_e}{r} & \hat{\sigma}_f^2 = \dfrac{MS_f - MS_{mf}}{rm} & \hat{\sigma}_m^2 = \dfrac{MS_m - MS_{mf}}{rf} \\ c\hat{o}v_e = MP_e & c\hat{o}v_{mf} = \dfrac{MP_{mf} - MP_e}{r} & c\hat{o}v_f = \dfrac{MP_f - MP_{mf}}{rm} & c\hat{o}v_m = \dfrac{MP_m - MP_{mf}}{rf} \end{array}\right\} \tag{1}$$

2.3 Decomposition of correlation coefficient The hybrid parents are inbred line populations, and based on the principles of quantitative genetics[7-8], several correlation coefficients of two traits can be obtained:

$$\left.\begin{array}{l} \text{Male parent genetic correlation coefficient}: r_m = \dfrac{c\hat{o}v_m}{\sqrt{\hat{\sigma}_{m(X)}^2 \cdot \hat{\sigma}_{m(Y)}^2}} \\ \text{Female parent genetic correlation coefficient}: r_f = \dfrac{c\hat{o}v_f}{\sqrt{\hat{\sigma}_{f(X)}^2 \cdot \hat{\sigma}_{f(Y)}^2}} \\ \text{Parental interaction genetic correlation coefficient}: r_{mf} = \dfrac{c\hat{o}v_{mf}}{\sqrt{\hat{\sigma}_{mf(X)}^2 \cdot \hat{\sigma}_{mf(Y)}^2}} \\ \text{Total genetic correlation coefficient}: r_g = \dfrac{c\hat{o}v_m + c\hat{o}v_f + c\hat{o}v_{mf}}{\sqrt{(\hat{\sigma}_{m(X)}^2 + \hat{\sigma}_{f(X)}^2 + \hat{\sigma}_{mf(X)}^2) \cdot (\hat{\sigma}_{m(Y)}^2 + \hat{\sigma}_{f(Y)}^2 + \hat{\sigma}_{mf(Y)}^2)}} \\ \text{Environmental correlation coefficient}: r_e = \dfrac{c\hat{o}v_e}{\sqrt{\hat{\sigma}_{e(X)}^2 \cdot \hat{\sigma}_{e(Y)}^2}} \\ \text{Phenotypic correlation coefficient}: r_p = \dfrac{c\hat{o}v_m + c\hat{o}v_f + c\hat{o}v_{mf} + c\hat{o}v_e}{\sqrt{(\hat{\sigma}_{m(X)}^2 + \hat{\sigma}_{f(X)}^2 + \hat{\sigma}_{mf(X)}^2 + \hat{\sigma}_{e(X)}^2) \cdot (\hat{\sigma}_{m(Y)}^2 + \hat{\sigma}_{f(Y)}^2 + \hat{\sigma}_{mf(Y)}^2 + \hat{\sigma}_{e(Y)}^2)}} \end{array}\right\} \tag{2}$$

Table 2 Analysis of variance and covariance about NC II mating design of cotton hybridization

Source of variation	*df*	X trait		Y trait		X and Y traits	
		SS	*MS*	*SS*	*MS*	*SP*	*MP*
Block	1	122.9312		0.0162		1.4112	
Between male parents	4	743.1028	185.7757	3.9340	0.98350	17.9660	4.4915
Between female parents	4	1383.8268	345.9567	27.2540	6.81350	125.3130	31.3283
Male parent × female parent	16	555.6532	34.7283	11.9320	0.74575	2.8540	0.1784
Error	24	760.0988	31.6708	12.3688	0.51540	-15.5362	-0.6473
Total	49	3565.6128		55.5050		132.0080	

Table 3 The estimated values of parameters under stochastic model of NC II mating design

Variance components	X trait	Y trait
Genetic variance of sea island cotton($\hat{\sigma}_m^2$)	15.1047	0.0238
Genetic variance of upland cotton($\hat{\sigma}_f^2$)	31.1228	0.6068
Genetic variance of sea - land interaction($\hat{\sigma}_{mf}^2$)	1.5288	0.1152
Environmental variance($\hat{\sigma}_e^2$)	31.6708	0.5154
Genetic covariance of sea island cotton($c\hat{\sigma}v_m$)	0.4313	
Genetic covariance of upland cotton($c\hat{\sigma}v_f$)	3.1150	
Genetic covariance of sea - land interaction($c\hat{\sigma}v_{mf}$)	0.4129	
Environmental covariance($c\hat{\sigma}v_e$)	-0.6473	

3 Case study

From the conventional varieties in Henan and Xinjiang, 5 upland cotton varieties and 5 sea island cotton varieties are randomly selected as parent, respectively, and the NC II genetic mating design makes $5 \times 5 = 25$ hybridized combinations F_1. The randomized block design is used and test data are repeated twice. In each combination, 5 normal plants with no obvious phenotypic differences are selected as samples, and their main agronomic traits and cotton fiber quality traits are investigated. Here only plant height (X) and node (Y) are selected for analysis, and the analysis of variance and covariance about two traits can be shown in Table 2. Based on the results in Table 2, according to the expected mean square and expected covariance decomposition method in the stochastic model of analysis of variance, we use equation (1) to calculate the variance and covariance components (Table 3). Based on the estimation of variance and covariance components with various sources of variation in Table 3, we use equation (2) to calculate the correlation coefficients (Table 4). By the approximation test[8] of the correlation coefficients in Table 4, it is found that both genetic correlation coefficient of male parent (r_m) and genetic correlation coefficient of female parent (r_f) are not significant, and it is the genetic correlation of additive genetic effects; genetic correlation coefficient of male and female parent interaction (r_{mf}) is 0.9838, reaching a highly significant level, and it is the genetic correlation of dominant genetic effects, playing a leading role in the genetic correlation; total genetic correlation coefficient (r_g), as the comprehensive genetic correlation coefficient of plant height and node, is 0.6634, reaching a highly significant level, showing

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period (June 25) and culmination period (July 12) of taro blight; the control effect 23 d after the last application reached 79.28%. Applying 1∶1000 70% thiophonate-methyl WP and 1∶1000 70% dimethomorph · cymoxanil WDG one time had poor control effect (only 17.62%) at the early and culmination stages of taro blight. Moreover, at the early stage of taro blight, if we applied 1∶1500 250 g/l mandipropamid suspension for control once again, the control effect on taro blight could be increased by 5.26%. At the same time, the field observation showed that in the 250 g/l mandipropamid suspension treatment area, the taro leaves and stalks were fresh and the upper functional leaves were largely intact and green; in the local conventional fungicide treatment area, the taro blight was serious; in the water control area, the upper functional leaves were basically necrotic and withered. Therefore, 250 g/l mandipropamid suspension had good prospects for the development and application in production. In mid-June, there were many consecutive rainy days in the city and then it entered the rainy season during which the temperature was suitable and humidity was high, and the early stage of taro blight was around mid-June, so it was very conducive to the occurrence and spread of taro blight. It was recommended to apply fungicide after earthing up taro for the first time (late May to early June), apply fungicide at the early stage of taro blight for the second time (late June), and apply fungicide for the third time (early July) according to the disease progress and rain situation. We could spray 1∶1500 250 g/l mandipropamid suspension evenly on the taro plant until the taro leaves and stems were wet, to ensure that the lower taro leaves and stems were fresh and upper functional leaves were intact, so as to achieve high quality, high yield and high efficiency.

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that the combination with great height generally has high node; environmental correlation coefficient (r_e) is -0.1602, not significant; phenotypic correlation coefficient (r_p) is 0.3309, reaching a highly significant level; r_g and r_p have consistent sign and are highly significant, showing that the phenotypic correlation and genetic correlation of plant height and node are consistent.

Table 4 Estimation of correlation coefficients

Correlation coefficients	Estimated values
Genetic correlation coefficient of male parent (r_m)	0.7198
Genetic correlation coefficient of female parent (r_f)	0.7168
Genetic correlation coefficient of male and female parent interaction (r_{mf})	0.9838^{**}
Total genetic correlation coefficient (r_g)	0.6634^{**}
Environmental correlation coefficient (r_e)	-0.1602
Phenotypic correlation coefficient (r_p)	0.3309^{*}

Note: *, ** indicate significance at the 0.05 and 0.01 levels, respectively.

4 Discussions

In this paper, according to stochastic model of variance and covariance analysis, we calculate different genetic components, and further decompose the genetic correlation coefficient into genetic correlation coefficient of male parent, genetic correlation coefficient of female parent and genetic correlation coefficient of male and female parent interaction, with simple meaning, easy to accept. However, the correlation coefficients exactly distributed in this paper are not truly obtained, so in theory, we can not perform the corresponding hypothesis test on the significance of difference. In the practical application, we can do approximation test. The mixed linear genetic model developed by Zhu Jun[3] makes detailed decomposition of genetic correlation coefficient, which is feasible in theory, but it seems to be questionable in practice. For example, the additive and environmental interaction correlation coefficient, or the dominant and environmental interaction correlation coefficient between traits may be generally small[4], which may be of little practical significance in the actual genetic breeding.

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