Research Article

Finding Ranking of Testers in Line × Tester Experiments

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Abstract

Improvement of crop traits, mainly the characteristics of yield and the extension of genetic variability is the goal of many of breeding projects. It can be realized e.g. by using appropriate forms of parental crosses schemes. If we have a large number of inbred lines (genotypes) experiments is carried out with hybrids obtained by crossing a line ×tester (testers). Analyzed the expression of characteristics (usually yield) in F_1 hybrids, we can assess the value of the breeding lines. An important question is the selection of testers (tester), which should diversify in the maximum degree analyzed trait (yield) in hybrids. In this paper we presents a model for obtaining ranking testers. This may be important diagnostic tool in breeding selection to obtained new hybrids with significant transgressive effects. An example of the results of field experiments were of spring rape. In this experiment, general combining ability (GCA) effects was evaluated in the F_1 generation. The results indicate different (depending on the used testers and analyzed traits) evaluate the GCA effects of inbred line. This approach is new to the practice of breeding and may be useful to the effective selection of the best testers.

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Introduction

Breeders must have information about testers used in different methods of plant breeding (in open pollinated species but also self pollinated crops). The line × testers analysis method is used to estimates favorable parents and crosses and their general (GCA) and specific (SCA) combining abilities. In earlier studies, Sprague and Tatum [1] used terms of GCA and SCA to designate the average performance of line, tester and hybrid combinations. Manivannan and Ganesan [2] applied line × tester analysis in sesame. Ahmed et al. [3] used line × tester techinique in Summer squash to calculate the combining ability. Singh and Kumar [4] also identified suitable parents through line × tester analysis in rice.

GCA is the average performance of a line in a series of hybrids and represents additive gene action (fixable genes). The GCA is difference of parent mean from the grand mean. SCA measures the deviation of hybrids from the value expected on the basis of parental performance. It represents epistatic (non additive) gene action which are not fixable [5-10]. SCA is the hybrid mean minus line and testers effects.

The use of testers has been well documented especially in maize [11-18]. These authors concluded that choice of best testers should be based on simplicity of its use, ability to classify the value of line, maximize genetic gain and enhance the expected mean yield of a population generated using selected cultivars. However it is difficult to identify testers having such characteristic.

The use of parental variety as a tester results in some improvement of the mean of the population [13]. Allison and Curnow [14] suggested use low yielding cultivars as testers. Some authors proposed use single cross hybrids [19] or inbred line as testers [20].

Problem connected with identification of best testers was studied by Yan and Hunt [21]. They used the site regression model to analyze a diallel mating database and identify the ideal tester. The biplot of the first two principal components of the site regression model displays the GCA of lines or testers as well as SCA of the line × testers interaction.

In the existing literature the ranking of testers in line × tester crossing systems can be carried out only on the basis of general combining ability (GCA) effects for lines. The aims of this paper are: (a) find statistical method for determining of testers ranking on the basis of generalization combining ability and (b) provide example of algorithm of selection of adequate ranking. The ranking is making on the basis of generalization combining ability, GCA^u, too, considering only influence of chosen testers being. The algorithm for finding adequate ranking of testers has been given in block designs as an example. The above algorithm can be called the mini-max method.

Methods

Let $\gamma = \begin{bmatrix} \gamma_{11}, & \gamma_{12}, & \ldots, & \gamma_{lt} \end{bmatrix}^T$ be the vector of genotype effects, where $\gamma_{ij}\ (i = 1, 2, \ldots, l;\ j = 1, 2, \ldots, t)$ represent of the progeny of i-th line with j-th tester cross.

The linear model of γ_{ij} may be written as:

$$\gamma_{ij} = m + g_i + q_j + s_{ij}, i = 1, 2, \ldots, l;\ j = 1, 2, \ldots, t,$$

where m is general mean, g_i is the GCA effect for *i*-th line, q_j is the GCA effect for *j*-th tester and s_{ij} is the specific combining ability (SCA) effect for *i*-th line and *j*-th tester.

The above effects are defined as (see e.g. Ceranka and Kaczmarek [22]):

$$
\begin{aligned}
g_i &= \frac{1}{t}\gamma_{i\bullet} - \frac{1}{lt}\gamma_{\bullet\bullet} \\
q_j &= \frac{1}{l}\gamma_{\bullet j} - \frac{1}{lt}\gamma_{\bullet\bullet} \\
s_{ij} &= \gamma_{ij} - g_i - q_j - \frac{1}{lt}\gamma_{\bullet\bullet},
\end{aligned}
\tag{2.1}
$$

where

$$
\gamma_{i\bullet} = \sum_{j=1}^{t}\gamma_{ij}, \; \gamma_{\bullet j} = \sum_{i=1}^{l}\gamma_{ij}, \; \gamma_{\bullet\bullet} = \sum_{i=1}^{l}\sum_{j=1}^{t}\gamma_{ij},
$$

From (2.1) follows that g_i take into consideration influence of each tester (not all testers are a good testing individual line).

Therefore Brzeskwiniewicz and Łuczkiewicz [23] define the values

$$
g_i^u = \frac{1}{t_1}\gamma_{i(\bullet)} - \frac{1}{lt}\gamma_{\bullet\bullet},
\tag{2.2}
$$

where $\gamma_{i(\bullet)} = \sum_{j=1}^{t_1}\gamma_{ij}$ with $t_1 < t$ and g_i^u call the modification of general combining abilities (GCA^u).

GCA^u take into consideration only influence of chosen testers (we assume that these testers have numbers 1, 2, …, t_1).

From (2.1) and (2.2) we have

$$
g_i^u = \frac{1}{t_1}\sum_{j=1}^{t_1}\left(g_i + q_j + s_{ij}\right),
\tag{2.3}
$$

and therefore the estimators of g_i^u can be expressed as

$$
\hat{g}_i^u = \frac{1}{t_1}\sum_{j=1}^{t_1}\left(\hat{g}_i + \hat{q}_j + \hat{s}_{ij}\right),
\tag{2.4}
$$

where $\quad \hat{g}_i = \dfrac{1}{t}\hat{\gamma}_{i\bullet} - \dfrac{1}{lt}\hat{\gamma}_{\bullet\bullet}$, $\quad \hat{q}_j = \dfrac{1}{l}\hat{\gamma}_{\bullet j} - \dfrac{1}{lt}\hat{\gamma}_{\bullet\bullet}$ and $\quad \hat{s}_{ij} = \hat{\gamma}_{ij} - \hat{g}_i - \hat{q}_j - \dfrac{1}{lt}\hat{\gamma}_{\bullet\bullet}$ $\quad$ for

$i = 1, 2, \ldots, l; \; j = 1, 2, \ldots, t.$

From (2.2) we can expressed alternative formulae for $\hat{g}_i^{u}$

$$\hat{g}_i^{u} = \frac{1}{t_1}\hat{\gamma}_{i(\bullet)} - \frac{1}{lt}\hat{\gamma}_{\bullet\bullet}, \tag{2.5}$$

where $\hat{\gamma}_{i(\bullet)} = \displaystyle\sum_{j=1}^{t_1}\hat{\gamma}_{ij}$ and $\hat{\gamma}_{\bullet\bullet} = \displaystyle\sum_{i=1}^{l}\sum_{j=1}^{t}\hat{\gamma}_{ij}.$

Note that $\hat{g}_i^{u}$ given in (2.4) and/or (2.5) is function of subset of all testers. For given t_1 we have $\dbinom{t}{t_1}$ subsets of testers and therefore the numbers of $\hat{g}_i^{u}$ is equal to $2^t - 1$ and with $\hat{g}_i$ is equal to $2^l - 1$. We have also $2^t - 1$ ranking of testers. Multiple comparisons were performed using Tukey's studentized range test using the least square mean for effect feature (Pr > |t|) which must be less than 0.05 to demonstrate that the comparison was statistically significant. Finally we investigate differences between above lines. Firstly we calculate (Brzeskwiniewicz and Łuczkiewicz [24])

$$t = \frac{\max\limits_{i,i'=1,\ldots,l}\left|\hat{g}_i(1) - \hat{g}_{i'}(1)\right|}{\sqrt{\dfrac{2}{\mu_1 t_1} \cdot s^2}},$$

where $\mu_1 = \left[r(k-1) + \lambda_1\right]/k$ and s^2 is mean root of error which is estimation of unknown variance σ^2. If $t < t_{\alpha,\upsilon}$ then above lines are not statistical differed, what is unusual situation, and if $t \geq t_{\alpha,\upsilon}$ then above lines are statistical differ, what is usual situation, where α = 0.05 (or 0.01). Utilization of the presented method to opinion of usefulness of testers to testing of GCA effects of inbred lines can be particularly useful in situation when we analysed traits for which genetic differentiation of universally applied testers is small.

Algorithm of selection of adequate ranking we present in the next section by example.

Example

In our field experiment with summer rape many quantitative traits were analyzed. One of them was root neck diameter of rape plant. Experiment was performed in incomplete block design with four replications.

In each of 112 plots we measure this trait in the F_1 hybrids which we got after crossing fourteen lines and two testers.

Let us consider an experiment carried out in group divisible (GD) design with parameters $v = 28$, $r = 4$, $k = 8$, $b = 14$, $l = 14$, $t = 2$, $\lambda_1 = 0$ and $\lambda_2 = 4$. These experiment has $v = 28$ hybrids resulting from crossing $l = 14$ inbred lines of summer rape with $t = 2$ testers. Note that GD designs in line × tester experiments are presented by Brzeskwiniewicz and Łuczkiewicz [25]. The hybrids were allocated in $b = 14$ blocks of size $k = 8$ and each hybrid was replicated $r = 4$ times in the experiment.

It is convenient to compile components $\hat{\gamma}_{ij}$ ($i=1, 2, …, 14; j=1, 2$) of the vector $\hat{\gamma}$, which are estimates of the expected values for the hybrids. Table 1 present $\hat{\gamma}_{ij}$ and marginal sums which are elements of vectors $\gamma_{i\bullet}$, $\gamma_{\bullet j}$ and the general sum $\gamma_{\bullet\bullet}$.

Table 1 Estimates of expected values for summer rape hybrids root neck diameter $\hat{\gamma}_{ij}$

Tester (j)	Tester 1	Tester 2	$\hat{\gamma}_{i\bullet}$
L1	0.8654	0.9134	1.7788
L2	1.0283	0.9274	1.9557
L3	0.7285	0.9371	1.6656
L4	0.7641	0.8543	1.6184
L5	0.7984	0.8771	1.6755
L6	0.8345	0.8493	1.6838
L7	0.8967	0.8813	1.7780
L8	1.0878	0.9289	2.0167
L9	0.8640	0.8730	1.7370
L10	0.7483	0.8557	1.6040
L11	0.8049	0.8312	1.6361
L12	0.7627	0.7261	1.4888
L13	0.8102	0.7901	1.6003
L14	0.8405	0.8566	1.6971
$\hat{\gamma}_{\bullet j}$	11.8343	12.1015	23.9358

From (2.4) or (2.5) we can estimate the GCA and GCA^u for lines with subsets of testers presented in Table 2, where $\hat{g}_i^u(1)$ or $\hat{g}_i^u(2)$ is equal $\hat{g}_i^u(1) = \hat{g}_i + \hat{q}_1 + \hat{s}_{i1}$ or $\hat{g}_i^u(2) = \hat{g}_i + \hat{q}_2 + \hat{s}_{i2}$, respectively.

Table 2 Estimates of GCA and GCA^u for lines

i	$\hat{g}_i$	$\hat{g}_i^u(1)$	$\hat{g}_i^u(2)$
L1	0.0345	0.0100	0.0584
L2	0.1230	0.1735	0.0725
L3	-0.0221	-0.2212	0.1770
L4	-0.0456	0.0006	0.0906
L5	-0.0171	-0.0564	0.0222
L6	-0.0130	-0.0204	-0.0056
L7	0.0341	0.0418	0.0264
L8	0.1535	0.2330	0.0740
L9	0.0137	0.0092	0.1777
L10	-0.0529	-0.0876	-0.0182
L11	-0.0368	-0.0490	-0.0237
L12	-0.1104	-0.0920	-0.1288
L13	-0.0547	-0.0446	-0.0648
L14	-0.0063	-0.0143	0.0017

In step 1 for finding adequate ranking of lines we calculate values:

$$\min_{i,i'=1,\ldots,l} \left| \hat{g}_i - \hat{g}_{i'} \right| = 0.0004$$

$$\min_{i,i'=1,\ldots,l} \left| \hat{g}_i^u(1) - \hat{g}_{i'}^u(1) \right| = 0.0008$$

and

$$\min_{i,i'=1,\ldots,l} \left| \hat{g}_i^u(2) - \hat{g}_{i'}^u(2) \right| = 0.0007.$$

In step 2 we select situation in which

$$\sqrt{t} \min_{i,i'=1,\ldots,l} \left| \hat{g}_i - \hat{g}_{i'} \right| = \sqrt{2} \cdot 0.0004 = 0.00057$$

$$\sqrt{t_1} \min_{i,i'=1,\ldots,l} \left| \hat{g}_i(1) - \hat{g}_{i'}(1) \right| = 1 \cdot 0.0008 = 0.0008$$

and

$$\sqrt{t_1} \min_{i,i'=1,\ldots,l} \left| \hat{g}_i(2) - \hat{g}_{i'}(2) \right| = 1 \cdot 0.0007 = 0.0007$$

is follows that for tester no. 1 we have the highest number, equal to 0.0008.

Thereby, we obtain the following succession of lines ranking: L8, L2, L7, L1, L9, L4, L14, L6, L13, L11, L5, L10, L12, L3.

For above example we have $\upsilon = v(v-1) - b + 1 = 71$, $\mu_1 = \dfrac{4 \cdot 7 + 0}{8} = 3.5$, $s^2 = 0.0136$, $t_1 = 1$,

$$t = \frac{\left| g_8(1) - g_3(1) \right|}{\sqrt{\dfrac{2 \cdot 8}{28} \cdot 0.0136}} = \frac{0.2330 + 0.2212}{\sqrt{0.00777}} = 5.152 > 1.99 = t_{0.05,71}$$

and therefore line are statistical differ. In above case we can divided lines on the groups. If

$$\left| \hat{g}_i(1) - \hat{g}_{i'}(1) \right| < t_{\alpha,\upsilon} \sqrt{\frac{2}{\mu_1 t_1} \cdot s^2} = T$$ then line i and i' are in the same group and if $\left| \hat{g}_i(1) - \hat{g}_{i'}(1) \right| \geq T$

then line i and i' are in the different groups. In above example $T = 1.99 \cdot \sqrt{0.0068} = 0.1641$ and therefore lines L8 and L2 are in first group, lines L7, L1, L9, L4, L14, L6, L13, L11, L5, L10, L12 are in second group and line L3 is in third group.

Conclusions

Tester no. 1 discriminate a inbred lines in the largest degree.

Utilization of the presented method to opinion of usefulness of testers to testing of GCA effects of inbred lines can be particularly useful in situation when we analysed traits for which genetic differentiation of universally applied testers is small. Combining ability analysis is an important tool for the selection of desirable parents together with the information regarding nature and magnitude of gene effects controlling quantitative traits. The success of the hybridization programme depends on the ability of the parents entering into hybridization to yield desirable segregants/recombinants. Combining ability helps to define the pattern of gene effects in the expression of quantitative traits by identifying potentially superior parents and hybrids.

Presented approach is new for practice of breeding and can be contribute to the effective selection of new genotypes. This may be important diagnostic tool in breeding selection to obtained new hybrids with significant transgressive effects. Breeding strategies based on selection of hybrids require expected level

of heterosis as well as the specific combining ability. In breeding high yielding varieties of crop plant, the breeders often face with the problem of selecting parents and crosses. Combining ability analysis is one of the powerful tools available to estimate the combining ability effects and aids in selecting the desirable parents and crosses for the exploitation of heterosis. Line × tester analysis provides information about general combining ability and specific combining ability effects of parents and is helpful in estimating various types of gene actions.

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