PLANT INDUSTRY

Problems of Breeding Identification of Plant Genotypes by Their Phenotypes (Quantitative Traits) at Early Breeding Stages

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Abstract—A solution to problems of breeding identification of the best genotypes in plant populations is proposed. It is shown that breeding identification is possible in a very broad range of trait combinations with rather weak requirements imposed on the background trait. During breeding identification, the value of genetic variance has almost no effect on the quality of identification.

The principle of background traits created by Dragavtsev [1] changed the existing opinion [2, 3] that, without succession of generations (without studying parent–progeny correlation), it is impossible to demarcate the contributions of heredity and environments to the level of a complex quantitative trait by investigating only the individual's phenotype [4]. The logic of the principle of background traits (BgTs) is rather simple: if a trait with zero genetic variance is found in any plant population (wild or F_2), its variation will be only ecological. Then an individual having a positive deviation of this trait from its average population value is a modification that ended up in a better microecological niche (background trait). If the breeding trait (BrT) is shifted in this individual toward the plus side in accordance with the background trait, this plant is a modification and it should not be selected. If the BgT of an individual is expressed at the level of the average population value and the BrT is shifted toward the plus side, this is a recombination or mutation needed by the breeder. The principle of BgTs even with such simplification "works" well in pair-cross systems widely used in breeding, for which it is sufficient to find the same quantitative trait in both parents.

Breeding can be successful if the breeder has methods of identification even without information about the genetics of quantitative productivity traits. V. S. Pustovoit's unique results on increasing the yield of oil from sunflower seeds can be an example.

If the ideal BgT, the genotypic variability of which in the population is close to zero and the ecological correlation with the BrT is close to one, is known, the genotypic value of BrT of any individually taken plant of the population can be identified. We will call such identification of the genotype by the phenotype ideal. However, for breeding problems it is necessary to identify not any plant in the population but only the most outstanding genotypes. Such a statement of the prob-

lem greatly weakens the requirements imposed on the BgT in the case of ideal identification.

Dragavtsev and D'yakov [5] formulated the principle of orthogonality, according to which a trait sensitive to N factors shifting it along the positive regression line is selected as the BgT and a trait sensitive to $N + 1$ factors is chosen as the BrT, and an additional factor is the diversity of polygenes of the BrT shifting it orthogonally toward the reaction to N factors; that is, along the negative regression line. Gerasimenko [6] showed that if the BgT has a large genotypic variance but the genotypic and ecological correlation with the BrT has different signs, the BgT principle markedly increases the resolving power of identification of the genotype by the phenotype.

We will formulate the principles of breeding identification of only the best genotypes:

(1) For breeding identification it is necessary and sufficient to assess the falling of a given point (genotype) outide the contour of the ecological ellipse of concentration in the BgT–BrT system. Points inside the contour of interest are not shown (figure).

(2) In the case of a significant excess of the distance from the center of the ellipse to the point of the genotype being identified above the minor axis of the ecological ellipse, the probability of identifying the genotype by the phenotype is equal to one.

We will explain these principles. Let us assume that, in the BgT–BrT system (figure), BrT has heritability $H^2 = 0.3$; consequently, the genotypic variance of BrT is 1/3 of the phenotypic; BgT also has a certain genotypic range (R_{gBgT}), and $r_g(\text{BgT–BrT})$ can take on values from –1 to1. We will ascertain under what conditions $r_e(\text{BgT–BrT})$ a reliable identification of genotypes by phenotypes is possible.

It is known from analytical geometry that if a is the major and b is the minor radius of the ellipse, $b/a = k$, where k is the oblateness of the ellipse. Then $\alpha = 1 - k$,

where α, the oblateness of the ellipse, is homologous to the modulus of r, the correlation coefficient; that is, $r \approx 1 - k$, then $b/a = 1 - r$, from which $b = a(1 - r)$, $b^2 = a^2(1 - r)^2$.

From the triangle ABC follows:

$$a^2 = R^2_{g\mathrm{BrT}}/4 - R^2_{g\mathrm{BgT}}/4. \qquad (1)$$

Then for the genotypic ellipse $b_g = a_g(1 - r_g)$, for the ecological $b_e = ma_g(1 - r_e)$, where m is the excess of the major radius of the ecological ellipse over the major radius of the genotypic ellipse. For the case $H^2_{\mathrm{BrT}} = 1/3 = 0.33$, $a_e = 2a_g$, $m = 2$, since the range of ecological variability is twice greater than the range of genotypic variability. Thus, $b_g = a_g(1 - r_g)$, $b_e = 2a_g(1 - r_e)$, The best genotypes are easily identified if $b_g > b_e$.

Let us examine various combinations of $r_{g(\mathrm{BgT-BrT})}$ and $r_{e(\mathrm{BgT-BrT})}$ for which a reliable identification of the best genotypes in the population is possible (for the case $H^2_{\mathrm{BrT}} = 0.33$).

(1) $r_{g(\mathrm{BgT-BrT})} = 0$, $r_{e(\mathrm{BgT-BrT})} = 0.5$. Then $b_g = a_g(1 - 0) = a_g$, $b_e = 2a_g(1 - 0.5) = 2a_g \times 1/2 = a_g$. Hence when $r_g(\mathrm{BgT-BrT}) = 0$, $b_g > b_e$, if $r_{e(\mathrm{BgT-BrT})} > 0.5$. Reliable identification of genotypes is accomplished under the condition $r_{e(\mathrm{BgT-BrT})} > 0.5$.

If the point lies not far beyond the limits of the contour of the ecological ellipse, it is very easy to check its belonging to the contour by using the canonical equation of an ellipse:

$$x^2/a^2 + y^2/b^2 = 1,$$

where x and y are respectively the levels of BgT and BrT. The probability of the point belonging to the contour is determined completely by the confidence intervals of the ellipse, which are not difficult to estimate in each specific case.

(2) $r_{g(\mathrm{BgT-BrT})} = 0.5$, $r_{e(\mathrm{BgT-BrT})} = 0.75$. Then $b_g = a_g(1 - 0.5) = 0.5a_g$, $b_e = 2a_g(1 - 0.75) = 2a_g \times 1/4 = 0.5a_g$. Thus, reliable identification of genotypes is accomplished under the condition $r_{e(\mathrm{BgT-BrT})} > 0.75$.

(3) $r_{g(\mathrm{BgT-BrT})} = -0.5$, $r_{e(\mathrm{BgT-BrT})} = 0.25$. Then $b_g = a_g(1 + 0.5) = 1.5a_g$, $b_e = 2a_g(1 - 0.25) = 2a_g \times 3/4 = 1.5a_g$. In this case (when $r_{g(\mathrm{BgT-BrT})} = -0.5$), the condition of reliable identification is possible when $r_{e(\mathrm{BgT-BrT})} > 0.25$.

Consequently, with a negative average genetic BrT–BgT correlation, the requirements imposed on the value of the ecological correlation are very weak ($r_e > 0.25$); therefore, almost any trait having a negative genotypic correlation with BrT can be used as the background trait.

We note that when $r_{g(\mathrm{BgT-BrT})} = -1$, the value of r_e should be very slightly greater than zero for successful identification.
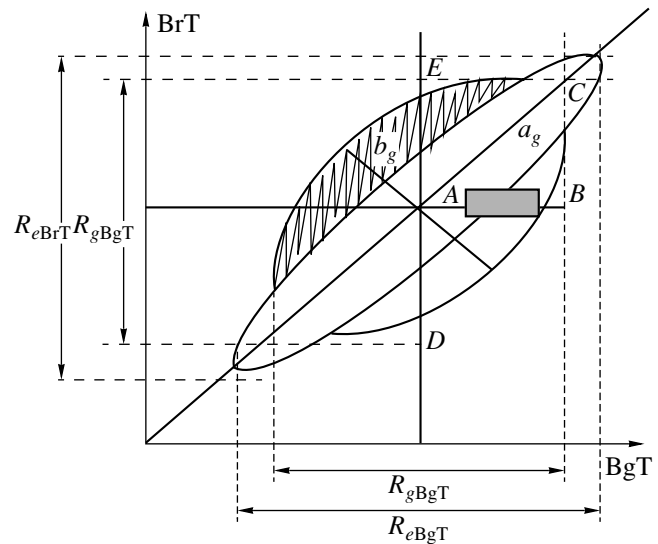
Genotypic (wide) and ecological (narrow) ellipses of concentration of individuals in BgT–BrT coordinate system; identification of the best breeding genotypes is possible in the shaded zone with a certain probability; explanations in text.

Let us examine the relation of genotypic ranges (or, what is almost the same, the genotypic variances) of BgT and BrT.

From formula (1) we can see (figure) that

$$a_g = \sqrt{R^2_{g\mathrm{BrT}}/4 + R^2_{g\mathrm{BgT}}/4}.$$

If $R_{g\mathrm{BgT}} = 0$, that is, BgT is ideal, then the genotypic ellipse disappears, being transformed into straight line DE, in which case

$$a_g = \sqrt{R^2_{g\mathrm{BrT}}/4} = R_{g\mathrm{BrT}}/2,$$

and a_g is transformed into half of the genetic range of BrT. Identification of genotypes changes from breeding identification to ideal identification; therefore, the genotypic value of any individual in the population can be identified $b_g = a_g(1 - 0) = a_g$; that is, b_g and a_g merge and they can be expressed by the segment $DE/2 = AE = AD$.

For constant $r_{g(\mathrm{BgT-BrT})}$ a decrease of $R_{g\mathrm{BgT}}$ will increase genotypic regression:

$$\beta_{g\mathrm{BrT/BgT}} = \mathrm{cov}_g(\mathrm{BrT} - \mathrm{BgT})/\sigma^2_{g\mathrm{BgT}},$$

or will turn the ellipse to the left, shortening respectively a_g and b_g. In this case a_e and b_e (Fig.) will shorten accordingly; that is, the quality of identification will not change. When $R_{g\mathrm{BgT}} \gg R_{g\mathrm{BrT}}$, the value of $\beta_{g\mathrm{BrT/BgT}}$ will decrease (the ellipse increases a_g, b_g and turns to the right). In this case a_e and b_e increase; consequently, the quality of identification in principle will not change. Thus, during breeding identification the value of the genotypic range of BgT does not play a special role. Everything is determined by the level and direction of $r_{g(\mathrm{BgT-BrT})}$.

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