

Short Review

Importance of BLUP method in plant breeding

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Abstract

Introduction: The most desirable linear neutral prediction (BLUP) is a standard method for estimating the random effects of a hybrid model. This approach was originally developed in animal breeding to estimate breeding values and is now widely used in many fields of research.

The main practical advantages of using REML/BLUP are:

It allows the comparison of individuals or species over time (generation, year) and space (location, block). Possibility of simultaneous correction of environmental effects, estimation of variance components, and prediction of genetic values.

The best BLUP prediction method, which estimates the averages with high accuracy, especially in mixed models, is also used to evaluate multi-environment experimental data (MET).

Blup is one method is statistical. Pedigree-based blup method.

Materials and methods: The BLUP method achieves this goal by combining phenotypic data and information on pedigree relationships through an index, known as family index selection. This index, which is estimated based on the coefficient of intra-class correlation, exploits the relationships of individuals within a family compared to other families in the population.

Results: The results: show that BLUP has good prediction accuracy compared to other methods. Pedigree-based BLUP method can increase selection yield in production-related traits in *P. zonale* or shelf life of *D. caryophyllus* L.

Introduction

Nowadays, researchers are looking for crop breeding, combining stability with a yield to achieve stable and high-yield genotypes in which both traits of yield and stability are considered simultaneously in addition to reducing genotype interaction. In the environment, high-yield genotypes should be selected [1].

Both the development of new cultivars and the recommendation of newly released varieties require a choice between a wider range of Candida genotypes, so estimating genotypic values is at the heart of any breeding effort. Analysis of metric data from different plant breeding and various experiments can usually be based on a hybrid linear model of the figure.

$$y - X\beta - Zu + e$$

Where y is the observation vector, β and u are fixed and random effect vectors, X and Z are related design matrices, and e is a random residual vector. Fixed effects can be estimated

with the best linear neutral estimation (BLUE), while random effects can be estimated with the best linear neutral prediction (BLUP). In practice, BLUE and BLUP must be substituted experimentally for BLUE and BLUP, respectively, meaning that the components of variance in G and R must be replaced by their estimation [2]. Pedigree-based BLUP method is currently the most promising method used in the absence of marker data. Using this method, useful information can be obtained about the dependence or non-dependence of this feature on family history. This information is very important for selecting individuals for genotype because the purpose of creating diversity panels is to show the total genetic diversity of the parent population, ie individuals must be selected with biocompatibility or non-biocompatibility requirements or photoperiods [3].

The best BLUP prediction method, which estimates the averages with high accuracy, especially in mixed models, is also used to evaluate multi-environment experimental data (MET). At present, little research has been reported on the

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estimation of genotypic values in experiments with multiple environments with BLUP [1].

BLUP is the optimal selection method for additive genetic effects (a), dominant effects (d), and genotypic effects (g), depending on the situation. BLUP maximizes selective accuracy and allows multiple sources of information to be used simultaneously. Individual BLUP uses all the effects of the statistical model, eliminates the imbalance, and considers the genetic relationship between the studied plants and the synchronization between the selected units and the recombination [4]. The main practical advantages of using REML/BLUP are: It allows the comparison of individuals or species over time (generation, year) and space (location, block). Possibility of simultaneous correction of environmental effects, estimation of variance components, and prediction of genetic values. The possibility of dealing with complex data structures (repeated measurements, different years, locations, and design) may be used for unbalanced data and orthogonal designs [4].

The traditional best linear neutral prediction (BLUP) method uses genealogical information. Recently, The BLUP genomic method (GBLUP) modified the BLUP method to combine with single nucleotide polymorphism (SNP) data in the form of a genomic relationship matrix that introduced additive genetic covariance among individuals [5].

GBLUP contains genomic information in estimating breeding value and is used for genomic selection. Therefore, genetic effect modeling is expected to improve GBLUP predictability by inserting print effects. Therefore, the objectives of this study were two: (1) to develop the GBLUP method including printing effects (hereinafter referred to as GBLUP-I), and (2) to estimate genetic variance and to assess the accuracy and neutrality of genomic predictions using Simulated data with different degrees of printing [5].

Materials and methods

BLUP No pedigree information

The simplest case of BLUP occurs when a single genotypic effect in a linear model is considered as an independent random variable without any genealogy correlation. Therefore, genotypes are considered independent and pedigree information is not used. Thus, accuracy compared to BLUE is mainly due to the property of contraction, while genetic covariance between related genotypes has no role. In multivariate experiments, genetic correlations between the functions of a similar genotype in different environments may be used [2].

Selegen-REML/BLUP software

Breeding programs have been developed to meet the needs and include the following categories of plants: allogamy, autogamy, mixed mating system, and clonal propagation.

This different experimental design considers several mating schemes, genotype x cross-environment, repeated field experiments, repeated measurements, offspring of several populations, and other factors. This software not only fits the effects but also provides the components of variance [4] (Figure 1).



Figure 1: Selegen-REML/BLUP.

Genetic model First, a quantitative genetic model of two standard alleles of a resource is developed for printing. An autosomal dimension is considered at the bio-like site with alleles A1 and A2 at frequencies 1-q and q in the population, respectively. The allelic frequency of men and women is assumed to be the same and under Hardy-Weinberg equilibrium. One genotype, AiAj, Ai, and Aj are shown to be paternal and maternal alleles, respectively. Genotypic values of genotypes A1A1, A1A2, A2A1, and A2A2 are represented by a, d1, d2, and -a, respectively [5].

Formula

$$\delta = \frac{d_1 + d_2}{2}$$

and

$$\varepsilon = \frac{d_1 + d_2}{2}$$

Conclusion

BLUP method is a statistical analysis method that has a combination of traditional and modern methods. The traditional method is based on genealogy. BLUP Concept: The best neutral linear prediction. The pedigree-based BLUP method is used when marker data is not available. The BLUP method maximizes the accuracy of selection and allows the simultaneous use of multiple information sources. The new BLUP method is the BLUP genomic method (GBLUP), which modifies the BLUP method to combine with single nucleotide polymorphic data (SNP) in the form of a matrix of genomic relationships that introduces incremental genetic covariance between individuals. The best linear neutral prediction, or BLUP, is a technique for estimating genetic competence. In general, it is a solution for estimating random effects.

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