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Evaluation of the vegetative mass in peanut selection materials

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Abstract

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The study of the vegetative characteristics of peanuts – dimensions of the bush, dimensions and mass of the leaves was carried out in the offspring of the F3 generation from the selection nursery of Semenarska kashta Sadovo. In the breeding improvement work with the collection, the aim is to select materials with reduced vegetative mass, which successfully use solar radiation and economically use the available water resources. A broad base of genetic diversity was established for some of the sign studied, to aid phenotypic selection in the resulting offspring. The test of how effective the selection of material with reduced vegetative mass would be was carried out using the determination of the phenotypic and genotypic coefficient of variation, the genetic progress achieved and the genetic progress relative to the mean. High genetic advance has been achieved in the bush index indicator, where the influence of the genome is higher than the influence of the environment. In the other indicators, the influence of the environment is higher than that of the genotype and the genetic progress in them is lower.

With the help of the factor analysis, progeny sources of variation in the individual indicators were revealed. Breeding work with culture shows high genetic progress in this regard.

Keywords: peanuts; vegetative characteristics; phenotypic and genotypic coefficients; genetic progress

Introduction

Peanuts are considered as one of the most important legumes, not only because of their economic value, but also from a nutritional point of view. Moreover, the crop is widely used in crop rotation, because it is a plant with a short development cycle and its operations are fully mechanized (Grotta et al., 2008; Jiao et al., 2015). Climate change, expressed by increasing temperatures and moisture deficits, leads to reduced yield in peanuts (Porter and Semenov, 2005). The production of peanuts in Bulgaria is carried out under irrigated conditions. Climatic conditions during summer in the country suggest high evaporation, rainfall deficit and offer high potential for irrigation yield. Parameters and functions that are stable in this environment can be accepted as reliable for modeling the selection of the peanut plant. Unlike modeling researchers, however, breeders working to develop improved peanut varieties wish to obtain high variability in desired parameters. Caliskan et al. (2008) indicated that growth and development of peanuts are strongly influenced by environmental factors. All crops produce leaves that capture light and convert biomass into fruit. By better quantifying parameters that describe these processes, peanut models can be developed that accurately simulate leaf area index, biomass, and seed production. Despite the fact that peanut is a known crop species, there is still scarce information to allow the simulation of such models. Reported solar radiation efficiency values for peanuts are lower than for many cereals (Kiniry et al., 1989) and similar to those for rice (*Oryza sativa* L.) (Kiniry et al., 1989, Kiniry et al., 2001). Similar to cotton boxes production (Thornley and Hesketh, 1972; Rosenthal and Gerik, 1991), fruit production in peanut requires more energy than vegetative organ production. Better penetration of light through smaller leaves allows more leaf area to be illuminated. Lower radiation intensity for efficient photosynthesis results in increased carbon exchange rates. Logically, this would increase the efficiency of the solar radiation used. Such a trend was reported by Bell et al. (1993); Williams (2000); Carr (2005); Figuerola and Berlinger (2006). From the point of view of the possibility of reducing evaporation and increasing the efficiency of photosynthesis, the dimensions and shape of the bush are of extreme importance. Awal and Ikeda (2003) noted that bush size correlated with yield. Most peanut breeding programs focus on fruit yield, seed size, quality traits, and foliar disease resistance (Isleib et al., 2001). Because yield has a relatively low heritability, this approach may not be the most efficient (Ntare and Williams, 1998). Furthermore, pod yield can only be accurately measured in later progenies. Measuring vegetative traits in early progenies, before selection lines are fully stabilized, offers an opportunity to select physiologically adapted material before starting yield testing (Asibuo et al., 2008; Gangadhara and Nadaf, 2016; Jakkeral et al., 2013; Pattanashetti et al., 2008; Upadhyaya and Nigam, 1994, 1998, 1999; Nigam and Blummel, 2010; Sheshashayee et al., 2006).

Estimates of genetic progress are more reliable and meaningful than individual parameter readings (Nyquist, 1991). Factor analysis can be understood as a data reduction technique, through covariance (Brejda, 1998). The analysis shows the percentage contribution of traits to each factor (Seiler and Stafford, 1979), and how their expression is influenced by the interaction of genes in the genotype. The advantage of component analysis lies in demonstrating the genetic composition of each factor (Pandya et al., 1996; Ashkani and Pakniyat, 2003; Ashkani et al., 2007).

The aim of the present study is to assess the genetic nature, and to find the sources of variation for reduced vegetative mass in the progeny from the early generations of the peanut selection process.

Material and Method

Place of the experiment

The experiment was conducted in the city of Sadovo, Bulgaria. The region of Sadovo is characterized by a transitional-continental climate, with its characteristic frequent and prolonged droughts. The average temperature sum for the peanut vegetation, recorded for a 120-year period, is 3165.2°C, the maximum of the average daily temperatures of 23.7°C in the month of August. The amount of precipitation in the area is of a non-constant nature and equals 247.3 l/m^2 for the period. Droughts are typical in the months of July-August during active crop vegetation.

Plant material

The object of the study were 373 self-pollinated progeny from the F3 generation of 4 hybrid combinations.

Experiment design

The selection materials peanuts are sown in a bed with a width of 2 m. Biometric measurements of basic yield elements were made on the hybrid progeny. In the middle of August, when the vegetative growth has stopped, the dimensions of the bush – height and width – were recorded. The resulting index was calculated as a ratio between the width and height of the bush. The leaf area was measured using graph paper and the mass was taken in the fresh state.

Statistical methods

Estimation of components of variation, phenotypic (PCV) and genotypic (GCV) variances were estimated according to the method proposed by Burton and Devane (1953) as follows:

1. Environmental variance ($\sigma 2e$) = Mse

2. Phenotypic variance ($\sigma 2p$) = ($\sigma 2g + \sigma 2e$)

3. Genotypic variance ($\sigma 2g$) = $\frac{\text{Mse} - \text{Mst}}{\text{r}}$,

where Mse – mean square error, Mst – mean square treatment and r – replications

4. Phenotypic coefficient of variation and genotypic coefficient of variation

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sqrt{\sigma^2 px}}{x} \times 100$$

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\sqrt{\sigma^2 gx}}{x} \times 100$$

where: $\sigma^2 p$ – phenotypic variance, $\sigma^2 g$ – genotypic variance, x – grand mean of a character

Factor analysis was conducted using the maximum likelihood method using the statistical program SPSS 19.0 for windows.

Result and Discussion

According to Deshmukh et al. (1986), PCV and GCV values greater than 20% were considered high, while values less than 10% were considered low and values between 10 and 20% were medium. Based on this argument, the high values of PCV (30.3) significantly exceed those obtained for GCV (2.5) in relation to the height of the bush, showing the strong influence of the environment in the formation of this indicator. As a result, the genetic progress achieved in this indicator is low and has a value of 0.226. Genetic progress

Table 1. Component matrix of the significant components

Component	Initial Eigenvalues			Extraction Sums of Squared Loadings			Rotation Sums of Squared Loadings		
	Total	% of Variance	Cumulative %	Total	% of Variance	Cumulative %	Total	% of Variance	Cumulative %
1	1,423	47,435	47,435	1,423	47,435	47,435	1,388	46,257	46,257
2	1,148	38,270	85,705	1,148	38,270	85,705	1,183	39,448	85,705
3	,429	14,295	100,000						

Source: Author' own elaboration

relative to the mean is also low and changes by a factor of 0.737. Bush width is more affected by environmental conditions than genotype. The coefficients are 6.12 for the phenotype and 2.83 for the genotype, respectively. The achieved genetic progress in this indicator is low and has a value of 0.819. Genetic progress relative to the average is also low and changes by a factor of 1.489. The index of the bush, in contrast to its height and width, has a sufficiently high genetic nature. Its variation is dependent on both environmental conditions (PVC = 15.8) and genotype (GVC = 15.3). The genetic progress achieved is of high value (GA = 7.3), and the genetic progress relative to the mean shows extremely high variability, which is indicative of the emergence of new forms in the existing collection. With the help of the covariance possibilities, we found that the studied indicators are divided into two significant factors, explained by Factor 1 – 46.257% and Factor 2 – 85.705% (Table 1).

According to Biabani and Pakniyat (2008), traits located in individual components are determined by nearby genes in the genome. Shrub index was positively related to component 2 and negatively related to component 1. Shrub height and width were positively related to both significant components (Figure 1).

The location of the studied samples relative to the component plane is shown in figure 2. From it is clear that the source of variation in relation to the bush index is progeny 334 (2*11*12). The source of variation in the height and width of the bush are samples 15 (1*6*2), 89, 90 (1*8*1), 147 (1*10*1) and 631 (2*45*1). They represent sources of variation, and are capable of altering genetic progress in a collection. Pattern 886 (3*12*14) would help reduce both the width and height of the bush. The remaining samples make up the heart-shaped collection of genetically stable materials.

The dimensions of the leaf area change to a greater degree than the environmental conditions. This is indicated by the value of the phenotypic coefficient of 12.4 compared to the value of the genotypic coefficient of 7.3. The genetic progress achieved is high and has a value of 19.3. Genetic progress is also high compared to the average, which shows that in the studied collection of samples, there is genetic diversity with regard to this indicator. Leaf mass also changes

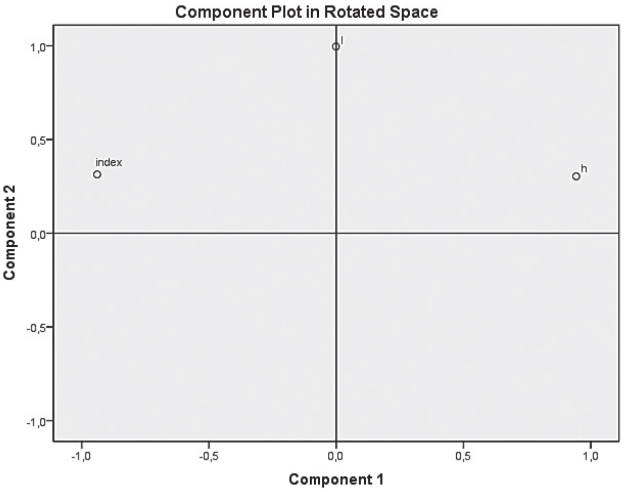

Fig. 1. Location of the investigated indicators in the component plane
Source: Author's own elaboration

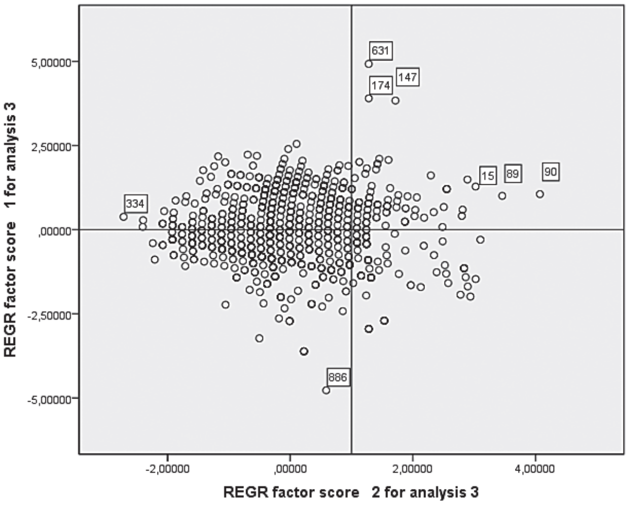

Fig. 2. Location of the tested progeny in the component plane
Source: Author's own elaboration

to a greater degree with environmental conditions than with genotype, coefficients of 9.5 and 7.3, respectively. The genetic progress achieved by this metric is of value (GA = 1.3), but the genetic progress relative to the mean is very high, indicating that high genetic diversity has also been achieved by this metric.

Using the covariance, it was found that the considered indicators relate positively to both significant components (Figure 3).

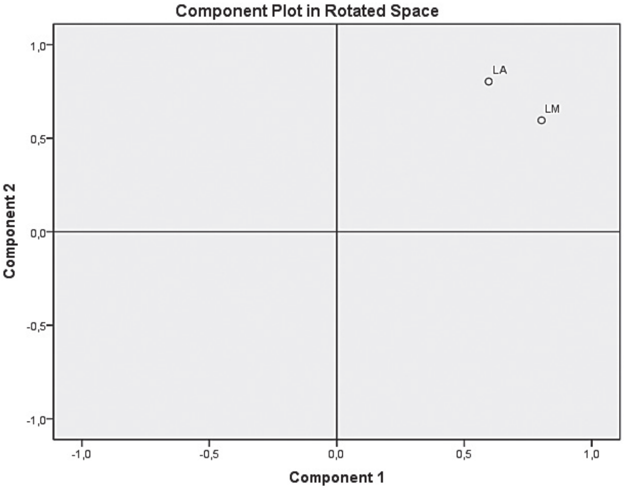

Fig. 3. Location of the investigated indicators in the component plane
Source: Author's own elaboration

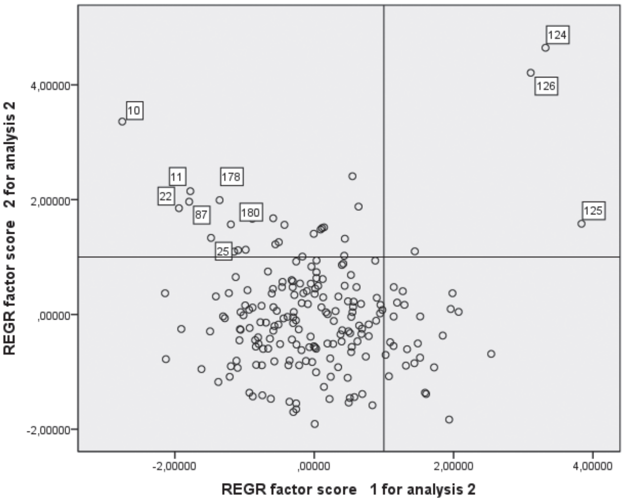

Fig. 4. Location of the tested progeny in the component plane
Source: Author's own elaboration

The location of the samples in the component plane is shown in Figure 4. From it is clear that samples 124, 126 and 125 are carriers of variance in leaf mass and leaf area. Samples 10, 11, 22, 25, 87, 178 and 180 do not relate to leaf area and leaf mass, but are negatively located with respect to component 1, which means that when used in future crosses, they will lead to a decrease in leaf area and the leaf mass. The remaining samples are genetically stable and make up the core collection.

Conclusion

As a result of the breeding improvement work with the peanuts, a great variability was created in terms of the index of the bush, the dimensions and the mass of the leaves, making the selection effective in this direction.

The genetic potential is high and this allows efficient selection of offspring that successfully use solar radiation and available soil water.

Sources of variation in the studied indicators were found in the collection of materials.

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