Journal of Fruit and Ornamental Plant Research Vol. 14, 2006: 5-22

PATTERNS OF VARIATION AND CORRELATION AMONG TRAITS IN A STRAWBERRY GERMPLASM COLLECTION (*Fragaria* × *ananassa* Duch.)

Joanna Ukalska[1], Wiesław Mądry[1], Krzysztof Ukalski[1],
Agnieszka Masny[2] and Edward Żurawicz[2]

[1]Department of Biometry, Warsaw Agricultural University
Nowoursynowska 159, 02-776 Warsaw, POLAND
e-mail: joanna.ukalska@agrobiol.sggw.waw.pl

[2]Research Institute of Pomology and Floriculture
Pomologiczna 18, 96-100 Skierniewice, POLAND

(Received January 12, 2006/Accepted May 31, 2006)

ABSTRACT

In this paper evaluating variation of twenty-eight traits in a strawberry collection consisted of 117 accessions (clones), and assessment of phenotypic, genotypic and environmental correlations among these traits have been carried out. The genotypes studied were a part of the strawberry germplasm collection established in the Research Institute of Pomology and Floriculture in Skierniewice, Poland. The evaluated traits include attributes of growth, development, yield, fruit quality and resistance to the most important strawberry diseases. These traits were observed on one plot for each genotype during three fruit-bearing seasons from 2001 to 2003 using a rate scale from 1 to 9 or rarely 1 to 7 (larger scores of each trait determine larger level of its expression according to its definition). The input data were arranged in an incomplete two-way genotype x year classification (some genotypes have been observed only in two years). Variance components were estimated for each trait separately by REML method for a random model of the two-way classification using VARCOMP procedure of the SAS software package. Coefficients of heritability for the three-year phenotypic means were estimated on the basis of the variance components. Genetic and environmental variance and covariance components needed for estimation of different correlation coefficients were evaluated using MANOVA option of the GLM procedure of the SAS package.

Key words: environmental correlations, genotypic correlations, germplasm collection, incomplete data, multivariate analysis of variance, phenotypic correlations, strawberry

INTRODUCTION

Diversity in a germplasm of a given plant species is usually studied using qualitative or quantitative phenotypic traits, especially those which are highly heritable and important for breeding and crop management purposes. This kind of germplasm variability is commonly known as phenotypic diversity or variation (Harrison et al., 1997, 2000; Jahufer et al., 1997; Harch et al., 1997; Catling and Porębski, 1998; Annicchiarico et al., 2000; Mohammadi and Prasanna, 2003; Rotondi et al., 2003; Upadhyaya et al., 2005). Phenotypic variation (variance in statistical sense) of a trait in a population is assumed in quantitative genetics to be a sum of variance of genetic, environmental and genotype by environment interaction effects (Falconer and Mackay, 1996; Muszyński et al., 2000; Toker, 2004; Upadhyaya et al., 2005; Xu et al., 2006).

Parental genotypes to be used in breeding programs are usually selected on the basis of their phenotypical value for important traits. It is required to choose parental genotypes which are not closely related to each other in order to reduce effects of inbreeding. A successful breeding program requires a high degree of genetic (molecular) and phenotypic diversity among the progeny. This can be achieved by using unrelated and diverse parents at both phenotypic and genetic levels. In order to ensure breeding efficiency, it is necessary to design the breeding program using the knowledge about the breeding value of the potential parents. Among various measures of parent's breeding value for a particular trait are General Combining Ability (GCA), Specific Combining Ability (SCA) as the most important (Muszyński et al., 2000; Masny et al., 2005; Shaw and Larson, 2005; Zhang et al., 2005; Żurawicz et al., 2006). To design an efficient breeding program, genetic variance components and heritability coefficients (h^2) in a reference population (breeding material or gene pool, in which selection and mating processes are made) are also very useful.

Heritability coefficient determines how much of the differences in phenotypic expression of a trait on selection units are as due to their genetic effects (Falconer and Mackay, 1996; Souza et al., 1998; Annicchiarico et al., 2000; Muszyński et al., 2000; Bolaños-Aguilar et al., 2002; Holland and Cervantes-Martinez, 2003; Shaw and Larson, 2005). It reflects a relationship between phenotypic and genotypic values of selection units. This measure is usually applied by geneticists and plant breeders to assess in what extent the phenotypic variation of a trait in a population is affected by genetic effects and, then, is explained by their variation. Due to different selection units which are usually used in a breeding program, various heritability coefficients for these units can be defined (Muszyński et al., 2000; Bolaños-Aguilar et al., 2002; Holland and Cervantes-Martinez, 2003; Toker, 2004). Their values depends on magnitude of genetic and environmental variance components.

It is also useful to determine the degree of linear interrelationships (correlations) between individual traits in the breeding material to ensure if studied traits are affected simultaneously by genes and/or environmental conditions in the gene pool and the target environment. This information is useful in predicting how a breeding gain in one trait will affect also a gain in the other traits included in the breeding program (Hortyński, 1989; Falconer and Mackay, 1996; Mądry et al., 2000; León et al., 2004; Shaw and Larson, 2005; Holland, 2006). Phenotypic, genetic and environmental correlations among traits can be defined using respective simple correlation coefficients (Searle, 1961; Lacey, 1973; Souza et al., 1998; Mądry et al., 2000; Muszyński et al., 2000; Shaw and Larson, 2005; Holland, 2006). Estimation of the all correlation coefficients mentioned above is relatively easy and commonly known when using a complete data set (Searle, 1961; Falconer and Mackay, 1996; Mądry et al., 2000; Muszyński et al., 2000; Bolaños-Aguilar et al., 2002). Estimation of the correlation coefficients on the basis of an incomplete classified data set is difficult from both theoretical and numerical points of view (Holland, 2006). Estimation procedures for such cases have recently been suggested by Holland (2006). They use multivariate REML methods and also variance and covariance component estimators for considered effects. Phenotypic, genetic and environmental correlations deliver useful and complementary information on the interrelationships among studied traits for different kinds of effects (at different levels of variation sources affecting traits). Therefore, each of them is recommended to be estimated and interpreted in genetic and breeding researches.

Phenotypic and genetic (molecular) diversity in the most important *Fragaria* species has been studied by researchers in the United States and Canada (Lacey, 1973; Shaw, 1991; Harrison et al., 1997, 2000; Catling and Porębski, 1998; Shaw and Larson, 2005). These studies have yielded valuable information which can be used to establish a core strawberry collection in North America. In Poland, strawberries are a widely grown small fruit crop using cultivars developed by Polish breeders and in different countries around the world (Żurawicz and Masny, 2005). Polish strawberry geneticists and breeders have studied variability in their germplasm of the species and developed many cultivars that are well adapted to agro-ecological conditions of Central Europe and very productive in this growing area (Hortyński, 1989; Masny et al., 2005; Żurawicz and Masny, 2005; Żurawicz et al., 2006). In order to increase an extent of diversity available to geneticists and breeders to improve their breeding material a strawberry germplasm collection has been established in the Research Institute of Pomology and Floriculture in Skierniewice, Poland.

The objective of this study was to quantify patterns of phenotypic diversity in a germplasm strawberry collection consisted of 117 accessions (clones). The study was undertaken to assess variability and the phenotypic, genotypic and environmental correlations among twenty-eight important traits.

MATERIAL AND METHODS

Material. The strawberry accessions studied were part of the strawberry germplasm collection belonging to the Research Institute of Pomology and Floriculture in Skierniewice, Poland. The collection consists of 153 cultivars and breeding clones of *Fragaria* × *ananassa* (Duch.). At the beginning of October, 2002, twelve plants of each genotype were planted in the test field 0.25 x 1.0 meters apart in separate beds. The recorded 28 traits include attributes of growth, development, yield, fruit quality and resistance to the most important strawberry diseases. These traits were observed on one plot for each genotype during three fruit-bearing seasons from 2001 to 2003 using a rate scale from 1 to 9 or rarely 1 to 7 (larger scores of each trait determine larger level of its expression according to it definition). Most of these traits were quantitative in nature, being mostly continues. However, from practical reasons, they were observed using a rate scale in which the quantitative expression was respectively approximated. The input data for each trait were arranged in an incomplete two-way genotype x year classification (some genotypes have been observed only in two years). The data set was limited to those genotypes in which the traits under study were observed in at least two of the three years. In rare cases, not all of the traits were observed in each of the genotypes in a particular year. Then, classification of traits x genotype and years combinations was a bit incomplete. The traits chosen to analyses are presented in Table 2.

Statistical methods. Statistical analyses were carried out separately for each the τ-th trait studied ($\tau = 1, \ldots, k$) according to the ANOVA random model (Mądry, 1993; Rotondi et al., 2003; León et al., 2004; Xu et al., 2006):

$$y_{ij} = m + g_i + r_j + e_{ij} \qquad (1)$$

where: y_{ij} is a response trait value observed for the *i*-th genotype ($i = 1, \ldots, a$) in the *j*-th year ($j = 1, \ldots, b$), m is the general mean, g_i is the random main effect of the *i*-th genotype, r_j is the random main environment effect of the *j*-th year, and e_{ij} is the random residual containing the genotype × year interaction effect and the experimental error.

The variance components of the effects in the model (1) were estimated by the REML method using VARCOMP procedure of the SAS software package (Searle, 1987; Littell et al., 1996; SAS Institute, 2002; Holland and Cervantes-Martinez, 2003). Using the variance component estimates, heritability coefficients for the three-year phenotypic mean of clones, h^2, were calculated for each trait according to the general formula in which b denotes the number of years considered (Falconer and Mackay, 1996; Muszyński et al., 2000, Bolaños-Aguilar et al., 2002; Holland and Cervantes-Martinez, 2003; León et al., 2004; Upadhyaya et al., 2005):

$$h^2 = \frac{\hat{\sigma}_g^2}{\hat{\sigma}_p^2} = \frac{\hat{\sigma}_g^2}{\hat{\sigma}_g^2 + \frac{\hat{\sigma}_e^2}{b}}, \qquad (2)$$

where: $\hat{\sigma}_g^2$, $\hat{\sigma}_e^2$ and $\hat{\sigma}_p^2$ are variance components of genotypic effects, the residuals, and the variance of genotypic means across b years.

Statistical analysis was also carried out according to the multivariate linear random model (MANOVA model) for all traits studied (Seber, 1984; Khattree and Naik, 2000; SAS Institute, 2002):

$$\mathbf{Y} = \mathbf{1}_N \mathbf{m}' + \mathbf{XG} + \mathbf{ZR} + \mathbf{E} \qquad (3)$$

where: $\mathbf{Y}$ is the (N×k)-dimensional observation matrix (k is the number of response traits, N is the total number of not empty subclasses in the two-way data set), $\mathbf{m}$ is the k-dimensional vector of the general means, $\mathbf{G}$ is the (a×k)-dimensional matrix of the random genotypic effects, $\mathbf{R}$ is the (b×k)-dimensional matrix of the random year effects, $\mathbf{E}$ is the (N×k)-dimensional matrix of the residuals, $\mathbf{1}_N$ is the (N×1)-dimensional unit vector, $\mathbf{X}$ is the (N×a)-dimensional design matrix for genotypes, and $\mathbf{Z}$ is the (N×b)-dimensional design matrix for years.

The model (3) is a modification of the one-variable model (1) which can be applied to multivariate analysis of variance of the k traits simultaneously in order to estimate the variance components of all effects for each trait and the pairwise covariances among them. These estimates were calculated using the MANOVA option of the GLM procedure in the SAS software package (Khattree and Naik, 2000; Bolaños-Aguilar et al., 2002; SAS Institute, 2002; Shaw and Larson, 2005; Holland, 2006). The least squares method was used, which is based on the expected values of the mean squares and products. The expected values for the mean squares calculated by this method are presented in Table 1.

The least squares estimators of the variance components are as follows:

$$\hat{\sigma}^2_{e(\tau)} = s^2_{e(\tau)} \quad \hat{\sigma}^2_{g(\tau)} = \frac{s^2_{g(\tau)} - s^2_{e(\tau)}}{k_1}, \qquad (4)$$

The estimators for the covariance components can be calculated as follows:

$$\hat{\sigma}_{e(\tau\tau')} = s_{e(\tau\tau')}$$

$$\hat{\sigma}_{g(\tau\tau')} = \frac{s_{g(\tau\tau')} - s_{e(\tau\tau')}}{k'_{1(\tau\tau')}}. \qquad (5)$$

The phenotypic correlation coefficients, r_p, for traits τ and τ' (τ, τ' = 1, 2, ..., k) of genotypes in a reference population were determined as the simple correlation coefficients between across year phenotypic means of the both traits (Searle, 1961; Lacey, 1973; Hortyński, 1989; Falconer and Mackay, 1996; Muszyński et al., 2000). The phenotypic correlation coefficients between three-year means of genotypes were estimated according to the general formula in which b denotes the number of years as in heritability coefficient (2):

Table 1. Expected values for the mean squares and products for one-variable and multi-variable analysis of variance (ANOVA and MANOVA) according to the random model for incomplete genotype × year data set

Source of variance	df	MS	MCP	E(MS)	E(MCP)
Genotypes (G)	a-1	$s^2_{g(\tau)}$	$s_{g(\tau\tau')}$	$\sigma^2_{e(\tau)} + k_1\sigma^2_{g(\tau)}$ [a]	$\sigma_{e(\tau\tau')} + k'_{1(\tau\tau')}\sigma_{g(\tau\tau')}$ [a]
Years (R)	b-1	$s^2_{r(\tau)}$	$s_{r(\tau\tau')}$	[a]	[a]
G×R=E	N-a-b+1	$s^2_{e(\tau)}$	$s_{e(\tau\tau')}$	$\sigma^2_{e(\tau)}$	$\sigma_{e(\tau\tau')}$

[a] k_1 and k_2 represent the coefficients calculated separately for each trait (the incompleteness of the data for each of the traits considered was a bit different); $k'_{1(\tau\tau')} = \frac{1}{2}\left(k_{1(\tau)} + k_{1(\tau')}\right)$

$$\boxed{r_p = \frac{\hat{\sigma}_{p(\tau\tau')}}{\sqrt{\hat{\sigma}^2_{p(\tau)} \cdot \hat{\sigma}^2_{p(\tau')}}} = \frac{\hat{\sigma}_{e(\tau\tau')} + b\hat{\sigma}_{g(\tau\tau')}}{\sqrt{\left(\hat{\sigma}^2_{e(\tau)} + b\hat{\sigma}^2_{g(\tau)}\right)\left(\hat{\sigma}^2_{e(\tau')} + b\hat{\sigma}^2_{g(\tau')}\right)}}. \quad (6)}$$

The genotypic correlation coefficients, r_g, for traits τ and τ' are measures of the simple correlation coefficients between the unobservable genotypic effects for the both traits. Their estimators have the following form (Searle, 1961; Hortyński, 1989; Falconer and Mackay, 1996; Muszyński et al., 2000; Shaw and Larson, 2005; Holland, 2006):

$$r_g = \frac{\hat{\sigma}_{g(\tau\tau')}}{\sqrt{\hat{\sigma}^2_{g(\tau)} \cdot \hat{\sigma}^2_{g(\tau')}}}. \quad (7)$$

The environmental correlation coefficients are measures of the simple correlation between the unobservable residuals for the traits τ and τ'. They were estimated according to the following formula (Searle, 1961; Hortyński, 1989; Falconer and Mackay, 1996; Muszyński et al., 2000):

$$r_e = \frac{\hat{\sigma}_{e(\tau\tau')}}{\sqrt{\hat{\sigma}^2_{e(\tau)} \cdot \hat{\sigma}^2_{e(\tau')}}}. \quad (8)$$

RESULTS AND DISCUSSION

The variance components calculated for the traits studied are presented in Table 2. For most of the traits the values of the genotypic

Table 2. The variance components and coefficients of heritability for each of the twenty-eight traits studied in the strawberry germplasm collection

Trait	$\hat{\mu}$	$\hat{\sigma}_g^2$	$\hat{\sigma}_r^2$	$\hat{\sigma}_e^2$	h^2
Plant habit	5.22	0.27	0.00	1.28	0.39
Plant vigour	4.85	0.57	0.00	1.10	0.61
Plant density	5.36	0.65	0.05	1.00	0.66
Number of flowers per inflorescence	5.36	0.38	0.00	1.37	0.46
Position of inflorescence relative to foliage	4.18	0.43	0.05	0.70	0.65
Type of flower	3.01	0.01	0.00	0.01	0.74
Anther quality of first flower	3.81	0.40	0.37	1.25	0.49
Time of flowering	4.39	1.67	0.11	1.07	0.82
Fruit size	4.65	0.75	0.11	1.13	0.67
Uniformity of fruit size	4.34	0.24	0.02	1.54	0.31
Uniformity of fruit shape	5.06	0.49	0.01	1.90	0.44
Insertion of calyx	5.48	0.78	0.17	1.11	0.68
Calix size	4.97	0.69	0.14	1.01	0.67
Skin color	5.14	0.44	0.01	0.51	0.72
Fruit glossiness	6.05	0.35	0.09	0.94	0.53
Flesh color	4.57	1.30	0.03	1.33	0.75
Uniformity of flesh color	5.53	0.82	0.04	1.54	0.61
Firmness	4.75	3.12	0.00	1.62	0.85
Achene position	3.89	0.33	0.14	0.62	0.62
Achene color	3.84	0.12	0.13	0.51	0.41
Adherence of calyx	5.10	1.73	0.04	1.45	0.78
Fruit flavor	5.02	0.39	0.00	1.66	0.42
Fruit sweetness	5.40	0.27	0.00	1.31	0.38
Fruit acidity	5.77	0.12	0.08	1.26	0.22
Susceptibility to leaf spot	1.90	0.28	0.92	1.49	0.36
Susceptibility to leaf scorch	3.85	0.58	0.40	2.26	0.44
Susceptibility to powdery mildew	4.76	1.12	0.29	1.80	0.65
Fruit yield	4.55	0.94	0.16	1.59	0.64

$\hat{\mu}$ – estimator of the general mean; $\hat{\sigma}_g^2$, $\hat{\sigma}_r^2$, $\hat{\sigma}_e^2$ – estimators of variance components for gentotypic, year and environmental effects, respectively; h^2 – coefficient of heritability variance components, $\hat{\sigma}_g^2$, were several times higher than the values of the variance components of the year effects, $\hat{\sigma}_r^2$. Therefore, the year effects for the considered traits were usually more uniform than the genotypic effects. Achene color and susceptibility to leaf scorch were exceptions to this rule. For anther quality of first flower and susceptibility to leaf scorch the both variance components were similar. It means that in the strawberry germplasm collection genotypic variation for many important traits is substantially large. Then, one may expect that this collection could be a source of valuable genes affecting attributes being an objective of strawberry breeding programs in Poland (Hortyński, 1989; Żurawicz and Masny, 2005) .

The heritability coefficients were higher than 0.6 for sixteen of the twenty-eight traits studied. The highest heritability coefficients were identified for time of flowering, type of flower, fruit firmness, adherence of calyx, flesh color and skin color. The relatively high heritability coefficients for these traits reflect the close agreement between their phenotypic three-year means and genotypic values for the genotypes in a population of genetically diverse clones represented by this collection. On the other hand, low heritability coefficients were recorded for traits connected with taste and fruit quality, such as flavor, sweetness, acidity and uniformity of fruit size in the same harvest. Low heritability coefficients were also found for susceptibility to leaf spot and leaf scorch. The relatively low heritability coefficients for these traits reflect the weak agreement between their phenotypic and genotypic values for the clones in the collection.

The phenotypic correlation correlations are presented in Table 3. Among the fruit quality traits, the strongest positive correlations were found between flavor and sweetness, between skin color and flesh color, and between flesh color and uniformity of flesh color. On the other hand, strong negative phenotypic correlations were found between fruit firmness and adherence of calyx, and between skin color and fruit glossiness. In an earlier study, there were strong negative correlations between fruit mass and adherence of calyx and between fruit firmness and adherence of calyx (Hortyński, 1989). Yield was positively correlated at the phenotypic level (for the three-year means of genotypes) with both vegetative growth traits and reproductive traits such as plant vigour, plant density, number of flowers per inflorescence, and anther quality of first flower. Yield was also negatively correlated with fruit traits such as size, glossiness and flesh color. In earlier studies, strong positive phenotypic and genotypic correlations were found between fruit yield on the one hand, and plant vigor, plant density, number of flowers per inflorescence, number of flowers, and fruit size on the other (Lacey, 1973; Webb et al., 1974; Guttridge and Anderson, 1981; Nielson and Eaton, 1983; Olsen et al., 1985; Strik and Proctor, 1988).

The genotypic correlation coefficients are presented in Table 4. The values for the genotypic correlation coefficients were similar as for the phenotypic ones. The maximum difference between the absolute values for the phenotypic and genotypic correlation coefficients was never greater than 0.1. Therefore, those pairs of traits which are correlated at the phenotypic level can be presumed to be also correlated at the genotypic level (for genetic effects), although further testing is necessary to confirm this presumption.

The environmental coefficients of correlation are presented in Table 5. The absolute values for these parameters were lower than the absolute values for the phenotypic and genotypic correlation coefficients. The highest absolute values for environmental correlation coefficients were found for those pairs of traits with the highest absolute values for the phenotypic and genotypic coefficients. These results indicate that patterns of simultaneous affecting the considered strawberry attributes by both environmental and genotypic factors (sources of variation) seem to be rather similar.

All pairs of highly heritable traits, except for flavor and sweetness, were also correlated similarly at both phenotypic and genotypic levels. These close consistency of phenotypic and genotypic correlation coefficients result from that the phenotypic means of genotypes for highly heritable traits are close to their unobservable genotypic values (genotypic effects). Therefore, correlations between phenotypic means and genotypic values for highly heritable traits have similar pattern. Our results (Tab. 3 and 4) illustrate well empirically the known genetic and statistical theory (Searle, 1961; Falconer and Mackay, 1996; Annicchiarico et al., 2000; Muszyński et al., 2000)

CONCLUSIONS

In the strawberry germplasm collection studied in the work genotypic variation for many important traits is substantially large. Of the twenty-eight strawberry traits studied, the most heritable were time of flowering, type of flower, fruit firmness, adherence of calyx, flesh color and skin color. The traits with the lowest heritability were fruit flavor, uniformity of fruit size in the same harvest, susceptibility to leafspot, and susceptibility to leaf scorch. Yield was quite highly heritable.

The estimates of three kinds of correlation coefficients were similar for all pairs of the considered traits. These results indicate that patterns of simultaneous affecting the considered strawberry attributes by both environmental and genotypic factors seem to be rather similar. Most pairs of the traits studied were only weakly correlated. The strongest positive phenotypic and genotypic correlations were found between the following pairs of traits: flavor and sweetness; flesh color and uniformity of flesh color; flesh color and skin color; yield and plant vigor; yield and plant density; yield and number of flowers per inflorescence; yield and anther quality of first flower; and yield and fruit size.

Most pairs of highly heritable traits were similarly correlated at both phenotypic and genotypic levels. It illustrates well empirically the known genetic and statistical theory.

Table 3. Phenotypic correlation coefficients for twenty-eight traits in the strawberry germplasm collection consisted of 117 genotypes

	Plant vigour	Plant density	Number of flowers per inflorescence	Position of inflorescence relative to foliage	Type of flower	Anther quality of first flower	Time of flowering	Fruit size	Uniformity of fruit size	Uniformity of fruit shape	Insertion of calyx	Calix size
Plant habit	-0.08	0.19	-0.02	-0.18	0.10	-0.11	-0.12	-0.24	0.04	0.00	0.08	-0.02
Plant vigour		0.47	0.17	0.05	0.04	0.16	0.08	0.25	0.00	-0.13	-0.12	0.04
Plant density			0.15	-0.03	0.07	0.13	-0.09	0.13	0.01	0.08	0.11	0.13
Number of flowers per inflorescence				0.29	0.08	0.11	-0.12	0.12	0.04	0.21	-0.01	0.02
Position of inflorescence relative to foliage					-0.02	-0.07	-0.13	0.00	-0.04	0.07	-0.13	0.06
Type of flower						-0.06	-0.02	-0.07	0.04	0.15	0.06	0.07
Anther quality of first flower							0.02	0.22	-0.03	-0.02	0.04	-0.08
Time of flowering								0.00	0.06	0.08	0.02	-0.07
Fruit size									0.10	-0.01	-0.14	-0.04
Uniformity of fruit size										0.25	-0.07	-0.05
Uniformity of fruit shape											0.12	-0.02
Insertion of calyx												0.09
Calix size												
Skin color												
Fruit glossiness												
Flesh color												
Uniformity of flesh color												
Firmness												
Achene position												
Achene color												
Adherence of calyx												
Fruit flavor												
Fruit sweetness												
Fruit acidity												
Susceptibility to leaf spot												
Susceptibility to leaf scorch												
Susceptibility to powdery mildew												

*, **significant correlations at P=0.05 or 0.01 respectively

Skin color	Fruit glossiness	Flesh color	Uniformity of flesh color	Firmness	Achene position	Achene color	Adherence of calyx	Fruit flavor	Fruit sweetness	Fruit acidity	Susceptibility to leaf spot	Susceptibility to leaf scorch	Susceptibility to powdery mildew	Fruit yield
0.03	0.01	0.05	-0.03	-0.04	0.09	-0.11	0.00	0.03	0.11	0.04	-0.01	0.02	-0.01	0.10
0.02	0.17	0.05	-0.10	0.01	-0.09	-0.17	0.01	0.03	0.07	0.09	0.02	-0.20*	0.14	0.51**
0.12	0.00	0.15	-0.16	-0.09	-0.04	-0.09	0.09	-0.01	0.08	0.08	0.21*	-0.12	0.10	0.47**
0.12	0.00	0.13	-0.02	-0.19*	-0.01	0.01	0.16	-0.01	0.04	0.02	0.12	-0.27**	0.03	0.43**
-0.01	0.13	-0.08	-0.06	-0.04	0.09	0.10	0.04	0.04	-0.06	-0.06	-0.01	0.11	-0.02	-0.08
0.12	0.01	0.10	0.04	-0.05	0.14	0.18*	0.06	0.00	-0.04	-0.04	0.06	0.09	-0.04	0.08
0.04	0.22*	0.08	-0.06	0.09	0.04	-0.17	-0.02	0.12	0.15	0.11	-0.05	-0.04	0.15	0.34**
0.08	0.13	0.07	-0.10	0.34**	0.11	-0.07	-0.28**	-0.09	-0.05	0.10	-0.08	0.05	0.18*	0.14
-0.03	0.36**	0.06	-0.06	0.43**	-0.05	-0.23**	-0.39**	-0.06	-0.12	0.08	0.01	0.16	0.16	0.31**
-0.11	0.20*	-0.05	-0.04	0.16	0.16	-0.09	-0.01	0.01	0.00	0.11	-0.03	0.01	0.14	-0.06
-0.11	0.18*	-0.11	0.01	0.16	0.07	-0.06	0.06	0.18*	0.09	-0.02	-0.11	0.04	0.13	-0.07
-0.13	0.04	-0.10	0.00	-0.03	0.00	-0.10	0.29**	0.25**	0.31**	-0.07	-0.12	0.02	0.07	0.07
0.00	-0.11	0.01	0.05	-0.04	-0.01	-0.05	0.02	0.01	0.00	-0.04	0.03	0.00	-0.08	-0.03
	-0.47**	0.58**	0.12	0.01	0.03	0.08	-0.07	0.05	-0.06	0.11	0.06	0.08	-0.08	0.08
		-0.15	-0.06	0.23**	-0.14	-0.21*	-0.13	-0.01	0.09	0.08	-0.09	-0.01	0.13	0.22*
			0.50**	0.12	-0.17	-0.11	-0.11	0.09	-0.01	0.17	0.11	0.01	-0.09	-0.18*
				-0.01	-0.17	-0.01	0.07	0.06	-0.02	0.04	-0.03	-0.06	-0.11	0.02
					-0.12	-0.31**	-0.64**	-0.12	-0.11	-0.04	-0.07	0.12	0.09	-0.01
						-0.01	0.06	0.01	-0.01	-0.11	-0.18*	0.10	-0.01	-0.10
							0.22*	-0.04	-0.02	-0.11	0.14	0.05	-0.06	-0.26**
								0.18*	0.20*	-0.05	0.03	-0.10	-0.04	-0.03
									0.78**	-0.08	0.00	0.19*	0.00	-0.09
										-0.13	-0.06	0.13	-0.01	-0.04
											0.14	-0.03	0.05	0.13
												0.00	-0.15	0.12
													0.15	-0.16
														0.06

Table 4. Genotypic correlation coefficients for twenty-eight traits in the strawberry germplasm collection consisted of 117 genotypes

	Plant vigour	Plant density	Number of flowers per inflorescence	Position of inflorescence relative to foliage	Type of flower	Anther quality of first flower	Time of flowering	Fruit size	Uniformity of fruit size	Uniformity of fruit shape	Insertion of calyx	Calix size
Plant habit	0.05	0.31	0.08	-0.15	-0.11	0.19	0.08	-0.02	0.15	-0.02	0.01	-0.07
Plant vigour		0.52	0.49	0.07	-0.06	0.38	0.22	0.32	0.05	0.05	0.03	-0.05
Plant density			0.52	-0.10	0.03	0.41	0.29	0.16	0.05	-0.14	0.03	-0.09
Number of flowers per inflorescence				0.19	0.17	0.28	0.00	-0.03	-0.05	-0.17	-0.06	0.10
Position of inflorescence relative to foliage					0.17	0.08	-0.04	0.06	0.10	0.19	0.01	0.11
Type of flower						0.06	0.12	-0.01	0.10	-0.02	-0.05	0.04
Anther quality of first flower							0.27	0.32	0.15	0.09	0.13	0.09
Time of flowering								0.47	0.18	0.14	-0.08	-0.07
Fruit size									0.09	0.06	-0.14	-0.09
Uniformity of fruit size										0.34	0.09	-0.18
Uniformity of fruit shape											0.29	0.11
Insertion of calyx												0.09
Calix size												
Skin color												
Fruit glossiness												
Flesh color												
Uniformity of flesh color												
Firmness												
Achene position												
Achene color												
Adherence of calyx												
Fruit flavor												
Fruit sweetness												
Fruit acidity												
Susceptibility to leaf spot												
Susceptibility to leaf scorch												
Susceptibility to powdery mildew												

Skin color	Fruit glossiness	Flesh color	Uniformity of flesh color	Firmness	Achene position	Achene color	Adherence of calyx	Fruit flavor	Fruit sweetness	Fruit acidity	Susceptibility to leaf spot	Susceptibility to leaf scorch	Susceptibility to powdery mildew	Fruit yield
0.08	0.01	0.07	-0.03	-0.04	0.12	-0.11	-0.03	0.09	0.19	0.03	-0.02	0.03	-0.02	0.13
-0.03	0.22	0.03	-0.13	0.01	-0.07	-0.23	0.01	0.03	0.10	0.16	0.04	-0.22	0.17	0.53
0.13	0.02	0.16	-0.21	-0.10	-0.02	-0.12	0.12	-0.01	0.12	0.10	0.25	-0.13	0.13	0.50
0.14	0.01	0.15	-0.03	-0.22	0.03	-0.01	0.19	-0.05	0.05	0.00	0.15	-0.32	0.04	0.50
-0.04	0.17	-0.10	-0.09	-0.04	0.18	0.08	0.03	0.06	-0.09	-0.07	-0.04	0.16	-0.01	-0.08
0.16	-0.01	0.13	0.06	-0.06	0.16	0.21	0.06	0.00	-0.05	-0.07	0.09	0.14	-0.04	0.09
0.01	0.26	0.10	-0.11	0.12	0.09	-0.23	0.00	0.12	0.20	0.11	-0.08	-0.03	0.19	0.36
0.11	0.15	0.08	-0.11	0.37	0.11	-0.08	-0.32	-0.11	-0.06	0.09	-0.11	0.05	0.20	0.17
-0.07	0.43	0.06	-0.06	0.48	-0.05	-0.27	-0.44	-0.11	-0.17	0.07	0.03	0.22	0.21	0.32
-0.13	0.24	-0.07	-0.05	0.18	0.23	-0.15	-0.01	0.05	0.02	0.09	-0.06	0.01	0.18	-0.05
-0.13	0.20	-0.13	0.02	0.18	0.10	-0.11	0.04	0.21	0.10	-0.09	-0.19	0.06	0.14	-0.09
-0.12	0.01	-0.09	-0.02	-0.04	-0.01	-0.10	0.32	0.29	0.37	-0.15	-0.15	0.02	0.08	-0.10
0.00	-0.12	0.01	0.06	-0.05	0.02	-0.10	0.02	0.03	0.02	-0.07	0.06	-0.02	-0.09	-0.03
	-0.52	0.62	0.13	0.02	0.03	0.06	-0.07	0.06	-0.06	0.15	0.07	0.13	-0.09	0.06
		-0.18	-0.09	0.27	-0.15	-0.25	-0.19	-0.08	0.05	0.11	-0.07	-0.04	0.17	0.23
			0.53	0.15	-0.20	-0.15	-0.14	0.08	-0.05	0.20	0.15	0.01	-0.11	0.22
				0.01	-0.20	-0.02	0.07	0.07	-0.03	0.05	-0.02	-0.07	-0.11	0.02
					-0.13	-0.36	-0.68	-0.12	-0.12	-0.06	-0.09	0.12	0.11	-0.02
						0.02	0.07	0.00	-0.01	-0.13	-0.20	0.12	0.00	-0.09
							0.27	-0.07	-0.06	-0.07	0.15	0.07	-0.08	-0.29
								0.21	0.23	-0.09	0.03	-0.17	-0.04	-0.02
									0.80	-0.11	0.00	0.25	0.00	-0.12
										-0.18	-0.07	0.15	-0.01	-0.06
											0.20	-0.08	0.06	0.16
												-0.05	-0.18	0.17
													0.13	-0.19
														0.05

Table 5. Environmental correlation coefficients for twenty-eight traits in the strawberry germplasm collection consisted of 117 genotypes

	Plant vigour	Plant density	Number of flowers per inflorescence	Position of inflorescence relative to foliage	Type of flower	Anther quality of first flower	Time of flowering	Fruit size	Uniformity of fruit size	Uniformity of fruit shape	Insertion of calyx	Calix size
Plant habit	-0.08	0.19	-0.02	-0.18	0.10	-0.11	-0.12	-0.24	0.04	0.00	0.08	-0.02
Plant vigour		0.47	0.17	0.05	0.04	0.16	0.08	0.25	0.00	-0.13	-0.12	0.04
Plant density			0.15	-0.03	0.07	0.13	-0.09	0.13	0.01	0.08	0.11	0.13
Number of flowers per inflorescence				0.29	0.08	0.11	-0.12	0.12	0.04	0.21	-0.01	0.02
Position of inflorescence relative to foliage					-0.02	-0.07	-0.13	0.00	-0.04	0.07	-0.13	0.06
Type of flower						-0.06	-0.02	-0.07	0.04	0.15	0.06	0.07
Anther quality of first flower							0.02	0.22	-0.03	-0.02	0.04	-0.08
Time of flowering								0.00	0.06	0.08	0.02	-0.07
Fruit size									0.10	-0.01	-0.14	-0.04
Uniformity of fruit size										0.25	-0.07	-0.05
Uniformity of fruit shape											0.12	-0.02
Insertion of calyx												0.09
Calix size												
Skin color												
Fruit glossiness												
Flesh color												
Uniformity of flesh color												
Firmness												
Achene position												
Achene color												
Adherence of calyx												
Fruit flavor												
Fruit sweetness												
Fruit acidity												
Susceptibility to leaf spot												
Susceptibility to leaf scorch												
Susceptibility to powdery mildew												

Skin color	Fruit glossiness	Flesh color	Uniformity of flesh color	Firmness	Achene position	Achene color	Adherence of calyx	Fruit flavor	Fruit sweetness	Fruit acidity	Susceptibility to leaf spot	Susceptibility to leaf scorch	Susceptibility to powdery mildew	Fruit yield
-0.18	0.01	-0.07	-0.02	-0.05	-0.02	-0.13	0.16	-0.12	-0.10	0.07	0.02	-0.01	0.06	-0.04
0.26	-0.04	0.13	0.05	0.02	-0.17	0.07	-0.01	0.01	0.00	-0.10	-0.06	-0.11	-0.02	0.39
0.07	-0.09	0.08	0.12	0.00	-0.14	0.01	-0.06	-0.02	-0.05	0.02	0.07	-0.08	-0.10	0.27
0.04	-0.04	0.03	0.05	-0.03	-0.19	0.08	0.04	0.11	0.01	0.07	0.01	-0.11	0.01	0.14
0.17	-0.07	0.04	0.09	-0.03	-0.31	0.21	0.11	0.00	0.02	-0.05	0.08	-0.05	-0.02	-0.04
-0.10	0.08	-0.07	-0.06	0.05	0.05	0.05	0.02	-0.01	-0.01	0.04	-0.06	-0.08	-0.01	0.02
0.16	0.05	0.01	0.11	-0.05	-0.16	0.03	-0.11	0.11	0.01	0.09	0.03	-0.09	-0.03	0.26
-0.09	0.03	-0.05	-0.08	0.00	0.10	-0.02	0.10	-0.02	0.01	0.16	0.05	0.04	-0.01	-0.05
0.20	0.06	0.07	-0.05	0.03	-0.03	-0.10	-0.09	0.14	0.06	0.10	-0.08	-0.06	-0.15	0.28
-0.07	0.06	0.06	0.00	0.08	-0.08	0.10	0.00	-0.08	-0.06	0.17	0.07	-0.01	0.01	-0.13
-0.03	0.11	-0.02	0.00	0.06	-0.07	0.08	0.12	0.09	0.06	0.18	0.13	-0.02	0.05	-0.02
-0.20	0.17	-0.14	0.07	0.08	0.03	-0.12	0.10	0.12	0.08	0.18	-0.04	0.00	-0.03	0.06
0.04	-0.04	-0.02	0.00	0.04	-0.12	0.10	0.03	-0.02	-0.05	0.06	-0.05	0.08	-0.01	-0.01
	-0.20	0.29	0.06	-0.07	0.02	0.16	-0.08	0.04	-0.06	-0.01	0.03	-0.12	0.04	0.16
		-0.03	0.09	-0.03	-0.07	-0.09	0.21	0.19	0.25	0.02	-0.16	0.11	-0.09	0.16
			0.34	-0.19	-0.01	0.03	0.14	0.14	0.12	0.04	-0.02	0.03	0.03	0.01
				-0.22	-0.05	0.01	0.06	0.03	0.05	0.00	-0.06	-0.01	-0.06	0.00
					-0.07	-0.08	-0.18	-0.14	-0.12	0.06	0.08	0.13	-0.05	0.07
						-0.10	-0.03	0.02	0.01	-0.03	-0.12	0.02	-0.04	-0.17
							-0.02	0.07	0.12	-0.22	0.09	0.00	0.05	-0.15
								0.07	0.09	0.10	0.06	0.26	0.00	-0.08
									0.72	-0.01	-0.01	0.01	-0.03	0.00
										-0.01	-0.03	0.08	-0.02	0.02
											0.00	0.10	-0.01	0.03
												0.16	-0.02	-0.04
													0.22	-0.05
														0.07

REFERENCES

Annicchiarico P., Pecetti L., Boggini G., Doust M.A. 2000. Repeatability of large-scale germplasm evaluation results in durum wheat. CROP SCI. 40: 1810-1814.

Bolaños-Aguilar E.-D., Huyghe C., Ecalle C., Hacquet J., Julier B. 2002. Effect of cultivar and environment on seed yield in alfalfa. CROP SCI. 42: 45-50.

Catling P.M., Porębski S. 1998. An ecoregional analysis of morphological variation in British Columbia coastal strawberries (*Fragaria*) for germplasm protection. CAN. J. PLANT SCI. 78: 117-124.

Falconer D.S., Mackay T.F.C. 1996. Introduction to quantitative genetics. 4th. ed. Longman, Essex, England.

Guttridge C.G., Anderson H.M. 1981. Assessing fruit yield characteristics and potential in strawberry. HORT. RES. 21: 83-98.

Harch B.D., Basford K.E., DeLacy I.H., Lawrence P.K. 1997. The analysis of large scale data taken from the world groundnut (*Arachis hypogaea* L.) germplasm collection. I. Two-way quantitative data. EUPHYTICA 95: 27-38.

Harrison R.E., Luby J.J., Furnier G.R., Hancock J.F. 1997. Morphological and molecular variation among populations of octoploid *Fragaria virginiana* and *F. chiloensis* (Rosaceae) from North America. AMER. J. BOT. 84: 612-620.

Harrison R.E., Luby J.J., Furnier G.R., Hancock J.F. 2000. Differences in the apportionment of molecular and morphological variation in North American strawberry and the consequences for genetic resource management. GENET. RES. CROP EVOL. 47: 647-657.

Holland J.B., Cervantes-Martinez C.T. 2003. Estimating and interpreting heritability for plant breeding. PLANT BREEDING REV. 22: 9-112.

Holland J.B. 2006. Estimating genotypic correlations and their standard errors using multivariate restricted maximum likelihood estimation with SAS Proc MIXED. CROP SCI. 46: 642-654.

Hortyński J.A. 1989. Correlations in strawberry breeding programs. ACTA HORT. 265: 169-173.

Jahufer M.Z.Z., Cooper M., Harch B.D. 1997. Pattern analysis of the diversity of morphological plant attributes and yield in a world collection of white clover (*Trifolium repens* L.) germplasm characterised in a summer moisture stress environment of Australia. GENET. RES. CROP EVOL. 44: 289-300.

Khattree R., Naik D.N. 2000. Multivariate data reduction and discrimination with SAS software. SAS. Institute Inc., Cary, NC.

Lacey C.N.D. 1973. Phenotypic correlations between vegetative characters and yield components in strawberry. EUPHYTICA 22: 546-554.

León L., Rallo L., Del Río C., Martín I.M. 2004. Variability and early selection on the seedling stage for agronomic traits in progenies from olive crosses. PLANT BREEDING 123: 73-78.

Littell R.C., Milliken G.A., Stroup W.W., Wolfinger R.D. 1996. SAS system for mixed models. SAS Institute Inc., Cary, NC.

Masny A., Mądry W., Żurawicz E. 2005. Combining ability analysis of fruit yield and fruit quality in ever-bearing strawberry cultivars using an incomplete diallel cross design. J. FRUIT ORNAM. PLANT RES. 13: 5-16.

Mądry W. 1993. Studia statystyczne nad wielowymiarową oceną zróżnicowania cech ilościowych w kolekcjach zasobów genowych zbóż. Monografie i rozprawy, SGGW.

Mądry W., Pluta S., Żurawicz E. 2000. Genetic and environmental correlation and path coefficient analysis of fruit yield per bush and other traits in black currants (*Ribes nigrum* L.). J. APPL. GENET. 41: 221-236.

Mohammadi S.A., Prasanna B.M. 2003. Analysis of genetic diversity in crop plants-Salient statistical tools and considerations. CROP SCI. 43: 1235-1248.

Muszyński S., Mądry W., Tomaszewski M., Sowa A., Zimny J. 2000. Genetyka dla rolników. Fundacja „Rozwój SGGW", Warszawa.

Nielson B.V., Eaton G.W. 1983. Effects of boron nutrition upon strawberry yield components. HORTSCIENCE. 18: 932-934.

Olsen J.L., Martin L.W., Breen P.J. 1985. Yield component analysis of 'Benton' and OR-US 4356 strawberries. HORTSCIENCE 20: 74-76.

Rotondi A., Magli M., Ricciolini C., Baldoni L. 2003. Morphological and molecular analyses for the characterization of a group of Italian olive cultivars. EUPHYTICA 132: 129-137.

SAS/STAT User's Guide, Version 8.2. 2002. SAS Institute, Cary NC.

Searle S.R. 1961. Phenotypic, genotypic and environmental correlations. Biometrics 17: 474-480.

Searle S.R. 1987. Linear models for unbalanced data. J. Wiley & Sons, New York.

Seber G.A.F. 1984. Multivariate observations. J. Wiley & Sons, New York.

Shaw D.V., 1991. Genetic variation for objective and subjective measures of fresh fruit color in strawberries. J. AMER. SOC. HORT. SCI. 116(5): 894-898.

Shaw D.V., Larson K.D. 2005. Genetic variation and response to selection for early season fruit production in California Strawberry Seedling (*Fragaria x ananassa* Duch.) Populations. J. AMER. SOC.HORT. SCI. 130(1): 41-45.

Souza V.A.B., Byrne D.H., Taylor J.F. 1998. Heritability, genetic and phenotypic correlations, and predicted selection response of quantitative traits in peach. II. An analysis of several fruit traits. J. AMER. SOC. HORT. SCI. 123(4): 604-611.

Strik B.C, Proctor J.T.A. 1988. Yield component analysis of strawberry genotypes differing in productivity. J. AMER. SOC. HORT. SCI. 113(1): 124-129.

Toker C. 2004. Estimates of broad-sense heritability for seed yield and yield criteria in faba bean (*Vicia faba* L.). HEREDITAS 140: 222-225.

Upadhyaya H.D., Mallikarjuna Swamy B.P., Kenchana Goudar P.V., Kullaiswamy B.Y., Singh S. 2005. Identification of diverse groundnut germplasm through multienvironment evaluation of a core collection for Asia. FIELD CROPS RES. 93: 293-299.

Webb R.A., Purves J.V., White B.A., Ellis R. 1974. A critical path analysis of fruit production in strawberry. SCI. HORT. 2: 175-184.

Zhang Y., Kang M.S., Lamkey K.R. 2005. DIALLEL-SAS05: A comprehensive program for Griffing's and Gardner-Eberhart analyses. AGRON. J. 97: 1097-1106.

Żurawicz E., Masny A. 2005. Uprawa truskawek w polu i pod osłonami. Plantpress Sp. z o.o., Kraków.

Żurawicz E., Mądry W., Masny A. 2006. Usefulness of some strawberry (*Fragaria* x *ananassa*) genotypes for breeding of late ripening cltivars. ACTA HORT. 708: 501-505.

Xu H., Mei H., Hu J., Zhu J., Gong P. 2006. Sampling a core collection of Island cotton (*Gossypium barbadense* L.) based on the genotypic values of fiber traits. GENET. RESOUR. EVOLUTION 53: 515-521.

ZMIENNOŚĆ I WSPÓŁZALEŻNOŚĆ CECH UŻYTKOWYCH W KOLEKCJI ZASOBÓW GENOWYCH TRUSKAWKI (*Fragaria* × *ananassa* Duch.)

Joanna Ukalska, Wiesław Mądry, Krzysztof Ukalski,
Agnieszka Masny i Edward Żurawicz

STRESZCZENIE

Badano zmienność i współzależność 28 cech użytkowych truskawki na podstawie obserwacji 117 genotypów w kolekcji truskawki zgromadzonej w Instytucie Sadownictwa i Kwiaciarstwa w Skierniewicach. Rozpatrywano zarówno cechy wegetatywne, opisujące wzrost roślin, jak i generatywne, opisujące jakość i wielkość plonu, a także cechy odporności na najważniejsze choroby truskawki. Dla obserwacji badanych cech wykonano wielowymiarową analizę wariancji według modelu losowego klasyfikacji genotypy × lata. Oszacowano komponenty wariancyjne dla wszystkich cech i kowariancyjne dla ich par, dotyczące zarówno efektów genotypowych, jak i reszt (błędu). Wyznaczono współczynniki korelacji fenotypowej (średnich cech genotypów obliczonych z *b* lat) oraz korelacji genotypowej i reszt (środowiskowych).

Słowa kluczowe: korelacje fenotypowe, korelacje genotypowe, korelacje środowiskowe; truskawka, wielowymiarowa analiza wariancji, zasoby genowe, zróżnicowanie fenotypowe