

HIERARCHIC CROSSING DESIGN IN ESTIMATION GENETIC CONTROL QUANTITATIVE TRAITS OF STRAWBERRY (*Fragaria* × *ananassa* Duch.)

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Abstract. The aim of the research was to assess genetic control, heritability and correlation of some quantitative characters on the basis of hierarchic crossing scheme. In the experiment two systems of classification were applied. In the first one superior classification was made according male forms ($5♂ \times 4♀$) and in the second one female forms were superior ($10♀ \times 3♂$). Genetic control for most analysed traits was the same regardless of classification system. Only in case of yield genetic control was different in paternal than in maternal classification. Additive genetic components were essential in determining the time of flowering, whereas non-additive ones in determining the number of stolons. The high value of broad-sense heritability for most cases suggests large genetic influence on analysed characteristics.

Key words: correlation coefficient, heritability, hierarchic crossing design, quantitative traits

INTRODUCTION

Changing tastes and increasing demands of individual clients as well as processing industry towards both fresh and processed fruits cause the constant need to improve cultivars of this plant species. Nowadays there are about 50 genotypes entered in the Register of Cultivars. 10 new genotypes have been registered recently (years 2008–2009), all of them have been developed by Polish breeders. It indicates the constant breeding progress, which may be realized thanks to better knowledge of genetic factors determining desirable traits. The knowledge concerning ways of genetic control towards some of these traits (quantitative traits) may be acquired through crosses applied in different designs. These crosses are the most often planned according to the diallel cross design [Simpson 1992, Masny et al. 2008]. Whereas, in this paper the hierarchic crossing design was used to evaluate some quantitative traits of strawberries.

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MATERIAL AND METHODS

The experimental material consisted of two hybrid populations of strawberry seedlings F_1 in the first and second year of ripening (years 2000, 2001) obtained as a result of the hierarchic crossing design of cultivars and breeding clones. The first population (I) was classified in a superior way according to male parents. It consisted of 5 male parents ('Selva', 'Tenira', 'Korona', 'Kent', 'clone 1594'). Each of them was crossed with 4 female parents from the group of cultivars such as 'Pegasus', 'Pandora', 'Korona' and breeding clones with numbers 286, 1387, 3387, 2589, 590, 1890, 1594. In general, 20 cross combinations were performed and 600 plants were analysed in this model. In the second population (II) the superior classification was made according to female parents. Each of 10 female forms, which belonged to the genotypes 'Korona', 'Pandora', 'Pegasus', 590, 286, 1387, 1594, 1890, 2589 and 3387 was crossed with 3 male forms belonging to the group of genotypes 'Selva', 'Revada', 'Kent', 'Tenira', 'Korona', 'Pegasus', 1387, 1594, 3387. This model included 30 cross combinations and 900 plants altogether. The plants were individually assessed in terms of the following traits: time of flowering and fruit ripening time, number of inflorescences and flowers per inflorescence, number of stolons and fruits, yield and average fruit weight. The analysis of variations revealed the significant differences between both analysed models. Based on values of the average square deviations, statistical variance components were evaluated for the first population: σ^2_s , $\sigma^2_{D(S)}$ and σ^2_e , and for the second one: σ^2_D , $\sigma^2_{S(D)}$ and σ^2_e . The sum of these evaluations constituted the assessment of phenotypic variation σ^2_p , from which the genetic variation was distinguished and the presence of the variation caused by additive action of genes in it was determined. Coefficients of heritability in broad and narrow sense as well as correlation coefficients for the evaluated characteristics were also estimated.

RESULTS AND DISCUSSION

The results acquired after the analysis of evaluated hierarchic models prove that additive and non-additive genetic effects determine the group of evaluated traits (tab. 1). However, it is worth mentioning that the second ones predominate in determining the evaluated characteristics. Non – additive genetic effects determined mainly forming of stolons, whereas additive effects influenced time of flowering. The high level of non – additive genetic variations for the number of stolons was also obtained in the research conducted by Simpson and Sharp [1988] as well as Lal and Seth [1982]. Such a way of genetic control determines the strategy of breeding programme, in which a considerable amount of cross combinations should be made to detect combinations of high results and then the best combinations should be crossed once again to a greater extent. The majority of evaluated traits demonstrated similar genetic factors regardless of cross classification system. Only yield was subject to different genetic control in male parent model than in female one to a considerable degree. The similar tendency, although at a substantially lower level, has been observed in terms of number of flowers per inflorescence and time of ripening. The researchers do not agree on the genetic factors of

Table 1. Estimates of statistical variance components for analysed traits in hierarchic model classified according male (I) and female (II) parents

Tabela 1. Ocena statystycznych komponentów wariancyjnych dla badanych cech w układzie hierarchicznym sklasyfikowanym według form ojcowskich (I) i matecznych (II)

Traits – Cecha	Hierarchic model Układ hierarchiczny	Variance components* Komponenty wariancyjne*				
		σ^2_S	$\sigma^2_{D(S)}$	σ^2_e	σ^2_P	σ^2_A / σ^2_G
		σ^2_D	$\sigma^2_{S(D)}$			
Time of flowering	I	1.14	1.88	6.50	9.52	0.61
Termin kwitnienia	II	1.92	3.16	8.50	13.58	0.61
Time of ripening	I	0.53	2.86	15.72	19.11	0.18
Termin dojrzewania	II	0.72	1.67	5.24	7.63	0.43
Number of inflorescences	I	4.58	9.42	34.05	48.05	0.49
Liczba kwiatostanów	II	3.20	10.43	38.65	52.28	0.31
Number of flowers per inflorescence	I	0.58	1.13	6.21	7.92	0.51
Liczba kwiatów w kwiatostanie	II	0.50	1.56	6.51	8.57	0.32
Number of stolons	I	0.55	9.14	45.18	54.87	0.06
Liczba rozłogów	II	0.34	11.00	38.32	49.66	0.03
Number of fruits	I	43.28	99.67	883.35	1026.3	0.43
Liczba owoców	II	57.74	170.42	831.78	1059.9	0.34
Yield	I	1741.1	5486.2	51277	58504	0.32
Plon owoców	II	2867.2	3998.5	47505	54370	0.72
Average fruit weight	I	0.48	1.35	8.53	10.36	0.35
Średnia masa owoców	II	0.69	1.72	8.08	10.49	0.40

* σ^2_S – variance between male half-sib family – wariancja pomiędzy półrodzeństwem po formach ojcowskich,
 σ^2_D – variance between female half-sib family – wariancja pomiędzy półrodzeństwem po formach matecznych,

$\sigma^2_{D(S)}$ – variance between female within male – wariancja między matkami w obrębie ojców,

$\sigma^2_{S(D)}$ – variance between male within female – wariancja między ojcami w obrębie matek,

σ^2_e – error variance – wariancja błędu, σ^2_P – phenotypic variance – wariancja fenotypowa,

σ^2_A / σ^2_G – quotient additive to genetic variance – stosunek wariancji addytywnej do genetycznej

fertility. In the series of experiments Shaw [1991] obtained the ratio of additive variation towards genetic one between 0.32–1.00 for the fruit yield. He seeks the causes of such a huge variability in diversity of evaluated material, environmental conditions and statistical assessment methods. After the studies in which considerable amount of non – additive variations for yield has been found, Hortyński [1987] indicates the same factors, which determine the occurring variability. He also informs about significant interactive relationships between genotypes and changeable environmental factors in separate years. Because of that the author proposes to conduct selective research of this species over at least 2 subsequent years of plant yielding. According to Shaw [1991] there is a changeable participation of genetic and environmental variations for this trait within the vegetation period. Environmental variation is more important at the beginning and in the final phase of fruit harvest time, whereas genetic variation affects more the height of harvest. As a result, the values of coefficient of heritability for yield and fruit size are high in the ripening time and they considerably exceed the values for these traits acquired in this paper, which concern 2 – year period (tab. 2). The high level of heritability in narrow sense for the mentioned traits amounting to 0.66 and 0.68 respec-

tively was acquired by Coman and Popescu [1997]. Coefficients of heritability for the rest of traits were similar to those defined before by other researchers [Simpson and Sharp 1988, Simpson 1992, Ukalska et al. 2006].

Table 2. The broad (h^2_1) and narrow (h^2_s) sense heritability of analysed characteristics for hierarchic classification model according male (I) and female (II) forms

Tabela 2. Odziedziczalność w szerokim (h^2_1) i wąskim (h^2_s) zakresie analizowanych cech dla modelu klasyfikacji hierarchicznej według ojców (I) i matek (II)

Heritability Odziedziczalność	Hierarchic model Model hierarchiczny	Characteristic* – Cecha*							
		1	2	3	4	5	6	7	8
h^2_1	I	0.79	0.60	0.78	0.57	0.67	0.39	0.37	0.52
	II	0.93	0.87	0.80	0.73	0.89	0.64	0.29	0.65
h^2_s	I	0.48	0.11	0.38	0.29	0.04	0.17	0.12	0.18
	II	0.56	0.38	0.24	0.23	0.03	0.22	0.21	0.26

* – Analyzed characteristics according table 1

* – Cechy analizowane według tabeli 1

Table 3. Phenotypic correlation coefficients of some strawberry traits for hierarchic classification model according male (I) and female (II) parents

Tabela 3. Fenotypowe współczynniki korelacji kilku cech truskawki dla modelu klasyfikacji hierarchicznej według ojców (I) oraz według matek (II)

Cecha – Trait	Model	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈
Time of flowering X ₁ Termin kwitnienia X ₁	I II	1.00 1.00							
Time of ripening X ₂ Termin dojrzewania X ₂	I II	0.79* 0.75*	1.00 1.00						
Number of inflorescences X ₃ Liczba kwiatostanów X ₃	I II	0.28* 0.18	0.41* 0.32*	1.00 1.00					
Number of flowers per inflorescence X ₄ Liczba kwiatów w kwiatostanie X ₄	I II	-0.30* -0.27*	-0.26* -0.22*	-0.01 0.00	1.00 1.00				
Number of stolons X ₅ Liczba rozłogów X ₅	I II	-0.14 0.00	-0.15 -0.04	-0.05 -0.10	-0.02 -0.04	1.00 1.00			
Number of fruits X ₆ Liczba owoców X ₆	I II	0.05 0.00	0.18 0.12	0.57* 0.57*	0.22 0.22	-0.03 -0.08	1.00 1.00		
Yield X ₇ Plon owoców X ₇	I II	0.37* 0.35*	0.48* 0.47*	0.65* 0.60*	0.03 0.05	-0.05 -0.03	0.73* 0.71*	1.00 1.00	
Average fruit weight X ₈ Średnia masa owocu X ₈	I II	0.49* 0.46*	0.52* 0.51*	0.29* 0.20	-0.18 -0.13	-0.07 0.00	0.08 -0.04	0.58* 0.53*	1.00 1.00

* Significant at the level $\alpha = 0.05$

* Istotne na poziomie istotności $\alpha = 0,05$

Relatively numerous correlation coefficients between the evaluated traits appeared to be significant (tab. 3). The high positive correlation concerned time of flowering and fruit ripening time. Baruzzi et al. [1999] indicates that there is a relatively fixed rela-

tionship between these traits. He highlights at the same time that such a tendency does not concern all the genotypes. Kulesza [1996] points at potential possibility of acquiring higher yields through cultivars with huge number of inflorescences and flowers per inflorescence based on his research of 12 cultivars, in which he obtained low diversity of number of inflorescences and higher diversity of number of flowers per inflorescence. Even so, acquiring such genotypes is not easy because of lack of correlation between these traits. Moreover, the negative influence of number of flowers per inflorescence on fruit weight should be taken into consideration. This characteristic is especially of importance in case of dessert cultivars. The search for genotypes with many fruits, inflorescences, coronas and leaves seems to be more effective because these traits are more correlated with yield [Lal and Seth 1982, Hortyński 1987, Shokaeva 2004, Ukalska et al. 2006].

CONCLUSIONS

1. Applying different cross classification systems did not affect the disclosure of fundamental differences in the way of genetic control of analysed traits. Only in case of yield, the effects of additive action of genes predominated in maternal classification, whereas the effects of non – additive action of genes in paternal classification.

2. The level of heritability in broad sense of the majority of evaluated traits should be perceived as a high one. Numerous higher values of coefficients of heritability for the maternal classification imply the influence of cytoplasm of this parental form.

3. The values of correlation coefficients for the group of analysed characteristics were similar regardless of the direction of crossing model classification.

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HIERARCHICZNY MODEL KRZYŻOWAŃ W OCENIE DZIEDZICZENIA CECH ILOŚCIOWYCH TRUSKAWKI (*Fragaria* × *ananassa* Duch.)

Streszczenie. Celem badań było przeprowadzenie oceny sposobu genetycznej kontroli, odziedziczalności i korelacji niektórych cech ilościowych na podstawie hierarchicznego układu krzyżowania. W doświadczeniu zastosowano dwa układy klasyfikacji krzyżowania. Pierwszy sklasyfikowano nadrzędnie według form ojcowskich ($5\♂ \times 4\♀$), natomiast drugi według form matecznych ($10\♀ \times 3\♂$). Dla większości badanych cech ich genetyczne uwarunkowanie okazało się podobne niezależnie od zastosowanej klasyfikacji krzyżowania. Tylko w przypadku plonu owoców sposób genetycznej kontroli okazał się odmienny w układzie ojcowskim niż matecznym. Addytywne działanie genów okazało się istotne w dziedziczeniu terminu zakwitania roślin, podczas gdy nieaddytywne dotyczyło liczby rozłogów. Wysokie wartości współczynnika odziedziczalności w szerokim zakresie uzyskane dla większości cech wskazują na wysoki poziom ich genetycznej kontroli.

Słowa kluczowe: współczynnik korelacji, odziedziczalność, hierarchiczny układ krzyżowania, cechy ilościowe

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