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ATTEMPT TO ADAPT A STATISTICAL MODEL FOR THE HETEROSIS EFFECT IN MAIZE F_1 HYBRIDS DEPENDING ON THE GENETIC DISTANCE OF PARENTAL FORMS

ABSTRACT

During the recent years traditional tillage techniques and procedures have been successfully used in combination with the modern molecular technologies. This enables the researchers not only to employ more objective methods of parental material selection, but also shortens the time required to breed a new variant. Many researchers tried to surmise the heterosis effect by examining the genetic distance between two parental lines. The main objective of this work was to display the correlation between the heterosis effect among the F1 generation of maize and the genetic distance between the parental components. Furthermore, an attempt was made to predict the future heterosis effect using mathematical functions. Finding a proof of those correlations would make it possible to select the parental material, used to create a new variation, more effectively and thus to reduce the number of lines tested during the experiment. Hence it would reduce the time needed for the experiments and also significantly reduce the overall cost of the research project. The research displayed that the molecular markers AFLP and RAPD are useful for predicting the formula of a new corn hybrid . They can be also used to group lines according to their origin or parentage, including those having incomplete information about their parentage. For both markers: RAPD and AFLP, the functions that best describe the correlation between the heterosis effect and the genetic distance, were: a third degree polynomial y=a+bx+cx^2+dx^3 and a linear function y = a + bx.

Key words: genetic distance, heterosis, maize, ststistical model

INTRODUCTION

Heterosis is a genetic term defining the favourable results of crossing demonstrated by vigour in the first hybrid progeny. Parental forms for heterotic crossings can be selected by different methods, e.g. by the estimation of the genetic distance on the basis of statistical methods (Srivastava, Arunchalam 1977; Węgrzyn *et al.* 1994), by basing on information about the origin of lines designed for crossing, by proteinaceous

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markers (Fabrizius *et al.* 1998), or by molecular markers (Tams *et al.* 2002). Actually, numerous techniques are known permitting the identification of polymorphism, organization and structure of genetic material, both within the coding and the not-coding sequences. Systems of molecular markers permit the analysis of organisms differentiation, independent of their developmental phase and the influence of environmental factors. Furthermore, the molecular methods ensure a high repeatability of results and easiness of application which determines about their high degree of usefulness. The particular techniques of the genetical material variability analyses differ among each others being the result of their specificity, type and polymorphism level which they represent (Sztuba-Solińska 2006). The objective of the presented studies was the determination of the heterosis effect in F1 hybrids, depending on the genetic distance between the parental components defined on the basis of molecular markers RAPD and AFLP using statistical models.

MATERIAL AND METHODS

Plant material used in our studies consisted of parental lines of maize and their F1 hybrids obtained from Plant Breeding Smolice Co. Ltd (Table 1).

Table1

Parental lines and F1 hybrids of maize

No.	Maternal lines	Paternal lines	Hybrids F_1
1	S160	S336A	S160 x S336A
2	S41336	S41324A-2	S41336 x S41324A-2
3	S50668-4	S56125A	S50668-4 x S56125A
4	S56122	S56125A	S56122 x S56125A
5	S245	S41789	S245 x S41789
6	S311	Co255	S311 x Co255
7	S63300	S66208A	S63300 x S66208A
8	S41796	S41324A-2	BLASK CV
9	S41789	S41324A-2	GROM CV
10	S56125A	S41324A-2	BRDA CV

Experiment with parental lines and hybrids was established in 2004 in the Experimental Station of the Department of Genetics and Plant Breeding on the area of the Experimental Farm at Dłoń belonging to Poznań Agricultural Academy (currently the University of Life Sciences in Poznań), on plots of 10 m^2 area in a completely random block design with three replications. Cultivation treatments were carried out according to the standard crop husbandry.

Measurements were carried out in the first half of November and they included the following parameters: cob length, cob diameter, core length, core diameter, number of grain rows, number of grains in a row, weight of thousand seeds (WTS) and grain yield. Measurements were carried out on 10 randomly selected cobs from three replications of each parental line and from hybrid F_1 forms.

Obtaining of molecular markers RAPD (Random Amplified Polymorphic DNA)

Genomic DNA from hybrid forms and parental components of maize were isolated by the modified method of Thompson and Henry (1995).

Leaf blades of 2 mm^2 surface were regarded with 200 µl of TPS buffer of the following composition : 100 mM Tris HCl with pH 95; 1 M KCl; 10 mM EDTA. Incubation was carried out in Eppendorf's test tubes, in water bath at 95°C for 15 minutes.

Polymerase chain reaction (PCR) was carried out in the volume of 12,5 µl mixture with the following composition: deionized water; 1 M Tris HCl with pH 8.3; 25 mM $MgCl_2$; BSA; 2mM dNTP; starter – 5 pmol/µl; Taq polymerase – 5U/µl, DNA extract – 25 ng/µl.

Taq polymerase originated from MBI-Fermentas Co., the remaining reagents originated from SIGMA Co.

DNA amplification was carried out using thermocycler T3 BIOMETRA of POLYGEN Co. After the removal of samples from the thermocycler, to each sample the following were added: 1 µl of dye (0.25 % of bromophenol blue; 40 % saccharose; deionized water).

Electrophoresis of amplification products was carried out in 1.5 agarose gel composed of: 1.5 agarose; 100 ml of buffer TBE1 x (10.8 g Tris base; 5.5 g boric acid; 4 ml 0.5 M EDTA pH 8.0) 1 µl ethidium bromide.

Obtaining of molecular markers AFLP (Amplified Fragment Length Polymorphism)

Isolation of genomic DNA was carried out by column method. Leaf fragments of 6 mm^2 surface were placed in test tubes with liquid nitrogen and the plant tissue was triturated. To each test tube, 400 µl of API buffer and 3 µl of RNAse were added. Then, the samples were incubated for 30 minutes at room temperature and 30 min. at 65°C, After incubation, 130 µl AP2 buffer was added and it was mixed in vortex. Then, the samples were placed in ice and after 15 minutes, they were rotated for 20 minutes at 14000 rev/min. After rotation, supernatant was collected and it was placed on columns with an addition of 60 µl of AT3 buffer. Samples were rotated for 2 minutes at 8000 rev/min and then, 450 µl of AW buffer and 50 µl of AE

buffer were added. The isolated DNA was stored at the temperature of -20°C.

Digestion of DNA was carried out using restriction enzymes EcoRI and Msell oraz 5x read buffer. To the digested DNA, 24 µl of adapter ligation solution and 1 µl of T4DNA ligase were added and the sample was incubated at 20° for 3 hours. After ligation, 90 µl of TE with pH 8.0 was added to the mixture. Pre-amplification was carried out using thermocycler T3 BIOMETRA of Polygon Co. To the diluted DNA matrix after ligation, 40 µl pre-amplified primer mix, 3.5 µl 10 x PCR buffer, 15 µl $MgCl_2$ and 1 µl Polymerase (5U µl) were added. To the diluted matrices, after amplification, MIX1 was added (starters and dNTP) and MIX2 (Taq polimerase, 10 x PCR buffer and $MgCl_2$). After the termination of the reaction, PCR samples were frozen at -20°C, Electrophoresis was carried out in 5 % acrylamid gel for 2.5 hrs at 60 W, 400 mA and 1400 V. Detection of PCR products followed in result of dyeing with silver.

Statistical estimation and documentation of results

1. Effects of heterosis for the particular features of the yield structure of hybrids was calculated in relation to the mean value of the feature shown by the better parent in relation to the mean feature value of both parents using the Microsoft Excel. The significance of the calculated effects of heterosis at the significance level of $\alpha = 0.05$ was verified using Scheffe's test and employing the statistical program DGH 2.

2. Mathematical models were used for the description of heterosis effect for yield, depending on the genetic distance determined on the basis of molecular markers RAPD and AFLP selected with the use of the statistical program Curve Expert.

3. Documentation of results both in reference to the reaction of RAPD and AFLP includes photographs of the obtained electrophoretic pictures and their elaboration with the use of the computer program UVIMAP in the function of Nei and Li (1979):

$$GS = \frac{2n_{xy}}{(n_x + n_y)}$$

where $2n_{xy}$ denotes the number of band pairs similar in both genotypes, while n_x and n_y indicate the number of all bands for the given genotype. The GS value denotes the similarity index between the two studied genotypes.

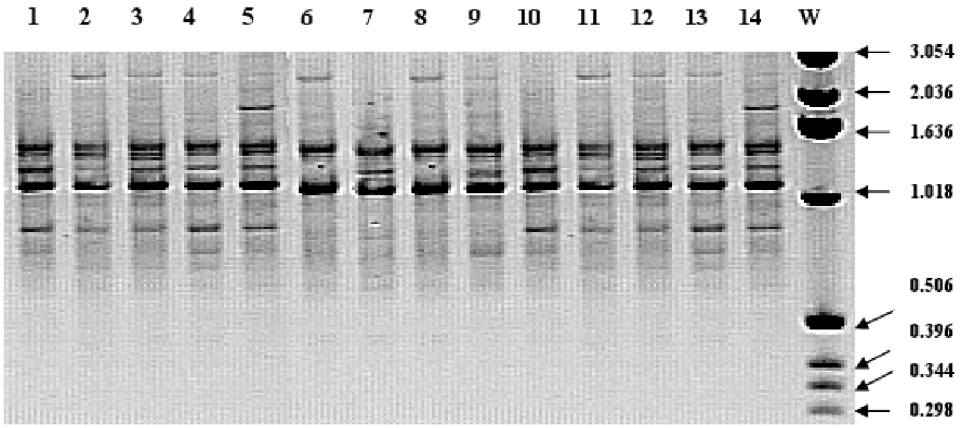

Fig. 1. Electrophoretic distribution of PCR products obtained with the help of molecular markers RAPD using the OPA 07 starter. The successive pathes correspond to the following genotypes: 1-S160, 2-S41336, 3-50668-4, 4-S56122, 5-S245, 6-S311, 7-S63300, 8-S41796, 9-S41789, 10-S56125A, 11-S336A, 12-S41324A-2, 13-Co255,14-S66208A, W-pattern: l Kb Ladder

Table 2

Characteristics of DNA amplification products obtained in result of RAPD-PCR reaction

Starter number	Number of generated fragments DNA	Number of generated polymorphic fragment DNA
OPA 04	9	8
OPA 07	9	6
OPA 10	10	7
OPA 14	10	9
OPB 04	12	8
OPB 17	12	8
OPF 12	10	8
OPG 12	5	3
OPH 20	9	8
OPJ 08	9	7

RESULTS

Genetic distance between the parental lines of maize F1 hybrids determined on the basis of molecular markers RAPD and AFLP.

For the RAPD markers, ten selected starters generated 72 polymorphic bands, on the average, one starter generated from 3 to 9 bands differentiating parental lines (Fig. 1, Table 2). The most effective starter which differentiated most intensively the

studied genotypes was the starter OPA 14 (9 polymorphic bands). Five selected starter combinations, in case of molecular AFLP markers , generated 56 polymorphic bands. One combination of starters generated on the average from 5 to 16 differentiating bands (Fig. 2, Table 3). The greatest polymorphism was obtained with the application of starter combinations E-ACG, M-CAC (16 polymorphic bands). The value of genetic distance between the parental lines of maize F1 hybrids, determined with the application of RAPD markers, was within the range from 64 % between parental lines of the hybrid S 50668-4 X S 56125 a to 93 % between the parental lines of the hybrids S311 x S CO 255 and GROM (Table 4). Molecular markers AFLP permitted to define the genetic distance which was within the range from 78 % between the parental lines of the hybrid BLASK to 96 % between the parental lines of the hybrid BRDA (Table 4).

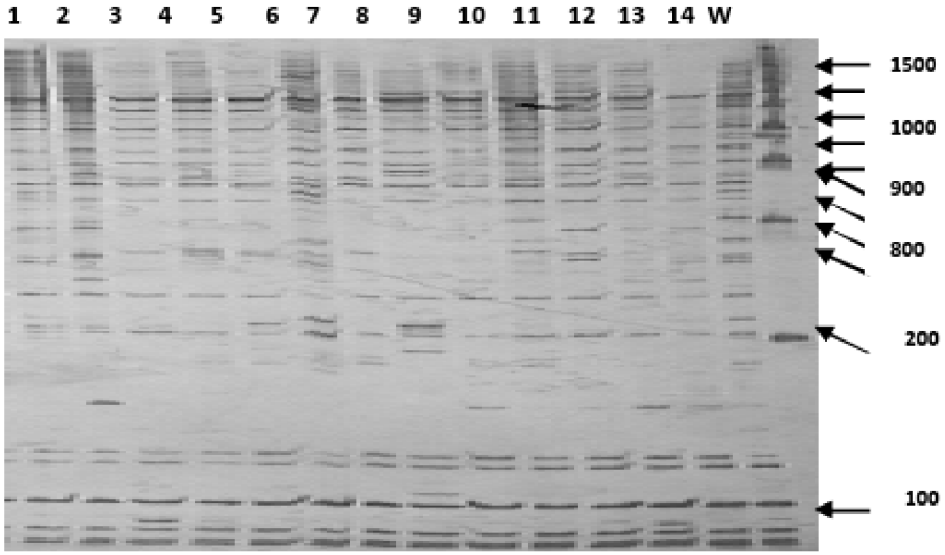

Fig. 2. Electrophoretic distribution of AFLP products obtained with the E-ACC, M-CAG starters. The successive paths correspond to the following genotypes: 1-S160, 2-S41336, 3-50668-4, 4-S56122, 5-S245, 6-S311, 7-S63300, 8-S41796, 9-S4178 10-S56125A, 11-S336A, 12-S41324A-2, 13-Co255, 14-S66208A, W – pattern: 1 Kb Ladder

Table 3

Characterstics of DNA amplification products obtained with the use of AFLP markers

Starter number	Number of generated fragments DNA	Number of generated polymorphic fragment DNA
E-AAC M-CAC	16	12
E-ACG M-CAC	25	16
E-ACC M-CAG	15	11
E-AGG M-CAG	15	12
E-AAC M-CTCT	9	5

Table 4

Genetic distance between parental lines of F_1 maize hybrids

F_1 hybrids	Parental lines		Genetic distance	
	Maternal	Paternal	RAPD [%]	AFLP [%]
S 160 X S 336A	S 160	S 336A	91	92
S 41336 X S 41324A-2	S 41336	S 41324A-2	76	86
S 50668-4 X S 56125A	S 50668-4	S 56125A	64	83
S 56122 X S 56125A	S 56122	S 56125A	73	89
S 245 X S 41789	S 245	S 41789	78	90
S 311 X CO 255	S 311	Co255	93	90
S 63300 X S 66208A	S 63300	S 66208A	78	89
BLASK CV	S 41796	S 41324A-2	91	78
GROM CV	S 41789	S 41324A-2	93	92
BRDA CV	S 56125A	S 41324A-2	89	96

Heterosis effect on yield structure traits of maize F_1 hybrids calculated in relation to the mean value of the feature belonging to the better parent.

Hybrids in which the highest heterosis effect was observed regarding the analysed traits of yield structure included: S160XS336A, S245XS411789, GROM abd BRDA (Table 5).

Table 5.

Size of heterosis effect expressed in percentages

Hybrids F_1	Cob length	Cob diameter	Cob core length	Cob core diameter	Number of grain rows	Number of grains in row	Weight of grains cob	Weight of 1000 seeds	Yield of grain
S 160 X S 336A	155*	137*	146*	131*	131*	167*	242*	115*	117*
S 41336 X S 41324A-2	109*	106*	111*	85	111*	126*	222*	102*	94
S 50668-4 X S 56125A	108*	95	107	84	65	113*	140*	82	92
S 56122 X S 56125A	121*	111	118*	100	114*	144*	243*	104	104
S 245 X S 41789	139*	120*	136*	130*	115*	163*	247*	118*	115*
S 311 X CO 255	131*	119*	134*	103	116*	161*	246*	106	108*
S 63300 X S 66208A	117*	108*	105	97	113*	161*	200*	104	96
BLASK	96	93	101	72	96	129*	207*	93	115*
GROM	147*	138*	150*	128*	131*	173*	269*	123*	130*
BRDA	162*	166*	168*	144*	155*	178*	344*	160*	166*

* significant at $\alpha = 0.05$

Regarding all analysed yield - components and the grain yield, the above mentioned hybrids significantly surpassed the parental lines. a particular attention was deserved by both cultivars, i.e. the hybrid BRDA in which the effect of heterosis ranged from 144 % for the core diameter to 344 % for the grain weight in cob; and the hybrid GROM, for which the heterosis effect was within the range from 123 % for WTS to 269 % for the weight of grain from one cob.The hybrids showing the lowest yields included: S50668 – 4 X S56125A which did not show any heterosis effect for grain yield and for the following traits: cob diameter, cob core diameter, number of grain rows, WTS - and the hybrid BLASK in which heterosis did not occur for the cob length, cob diameter, cob core diameter, number of grain rows and WTS.

Table 6

Size of heterosis effect expressed in percentages

Hybrids F_1	Cob length	Cob diameter	Cob core length	Cob core diameter	Number of grain rows	Number of grains in row	Weight of grains cob	Weight of 1000 seeds	Yield of grain
S 160 X S 336A	162*	141*	151*	134*	134*	172*	268*	121*	126*
S 41336 X S 41324A-2	115*	109	116*	90	113*	137*	230*	106*	100
S 50668-4 X S 56125A	112*	97	108	88	95	127*	177*	88	97
S 56122 X S 56125A	126*	114*	118*	103	115*	169*	257*	105*	111*
S 245 X S 41789	150*	125*	138*	133*	120*	165*	265*	111*	117*
S 311 X CO 255	133*	120*	135*	106*	117*	164*	263*	111*	113*
S 63300 X S 66208A	125*	112*	116*	102	115*	162*	215*	111*	104
BLASK	100	97	103	75	101*	137*	211*	97	120*
GROM	151*	152*	153*	138*	136*	180*	293*	130*	133*
BRDA	174*	172*	170*	155*	158*	193*	367*	162*	173*

* significant at $\alpha = 0.05$

Effect of heterosis on the traits of the yield structure of F_1 hybrids calculated in relation to the mean value of the trait belonging to both parental forms.

The greatest vigour in reference to the analysed characters of yield structure was observed in the following hybrids: S160XS336A, S245XS41789, GROM and BRDA (Table 6). These hybrids surpassed significantly the parental lines in all analysed yield-components as well as in the yield of grain. Among them, the highest evaluation was deserved by both cultivars, i.e. by the hybrid BRDA where the heteresis effect ranged from 155 % for the core diameter to 367 % for the weight of grain in cob, as well as the hybrid GROM where the heterosis effect was within 130 % for WTS to 293 % for the grain weight cob. The lowest

yield ers were hybrids: S50668-4X556125A which did not show any heterosis effect for the yield of grain and for the following traits: cob diameter, diameter of cob core, number of grain rows, WTS; and the hybrid BLASK where heterosis did not occur for: cob length, cob diameter, diameter of cob core and WTS (weight of 1000 seeds).

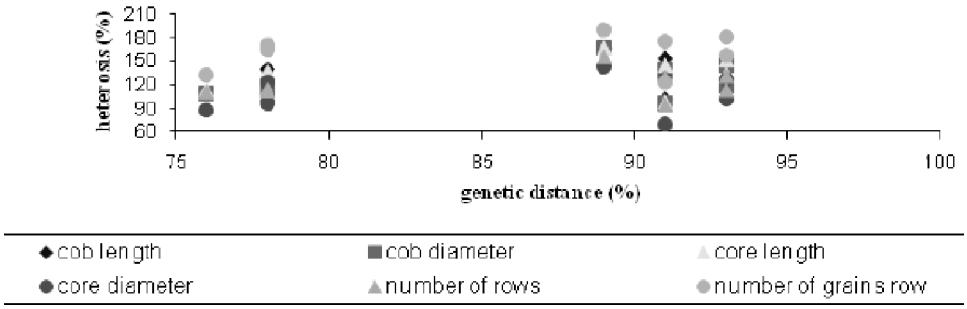

Fig. 3. Heterosis effect in hybrids calculated in relation to the mean value of the better parent depending on the genetic distance between the parental forms determined on the basis of RAPD markers

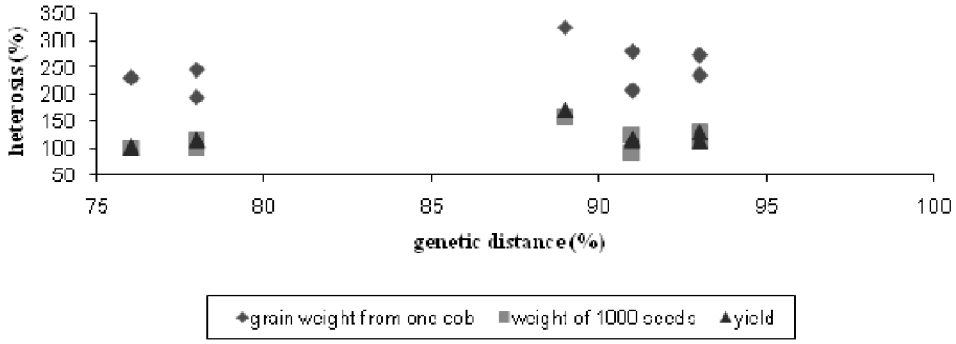

Fig. 4. Heterosis effect of hybrids calculated in relation to the mean value of the feature belonging to the better parent depending on the genetic distance between the parental forms determined on the basis of RAPD markers

Predicting of heterosis effect for the yield and the analysed traits of yield structure depending on the genetic distance, on the basis of molecular markers RAPD and AFLP with the use of mathematical models

The function characterizing the heterosis effect estimated both in reference to the value of the trait represented by the better parent, as well as in reference to the value of the traits of both parents, depending on the distance determined by the RAPD markers was the polynomian of the third degree: $y = a+bx+cx^2+dx^3+ ...; (r^2 = 0.57)$. (Figs 3 and 4). Using this function, one can try to predict the heterosis effect on the basis of the genetic distance between the parental lines which will be contained within the range of 64 – 93 %. The coefficient of the adjustment of the function for RAPD markers was $r^2 = 0.57$.

The function: $y = a+bx+cx^2$ (Figs 5 and 6) characterized the heterosis effect estimated both in relation to the mean value of the trait belonging to the better parent as well as in relation to the mean value of the trait in both parents, depending on the distance determined by AFLP markers. Basing on this function, one can try to predict the heterosis effect for the yield and for the analysed trais of yield structure using the value of the genetic disance between the parental forms contained within the range from 78 % to 96 %. The coefficient of the adaptation of function $r^2 = 0.94$ was higher than the coefficient of function adaptation to RAPD markers $r^2 = 0.57$ and it described this dependance with a higher precision.

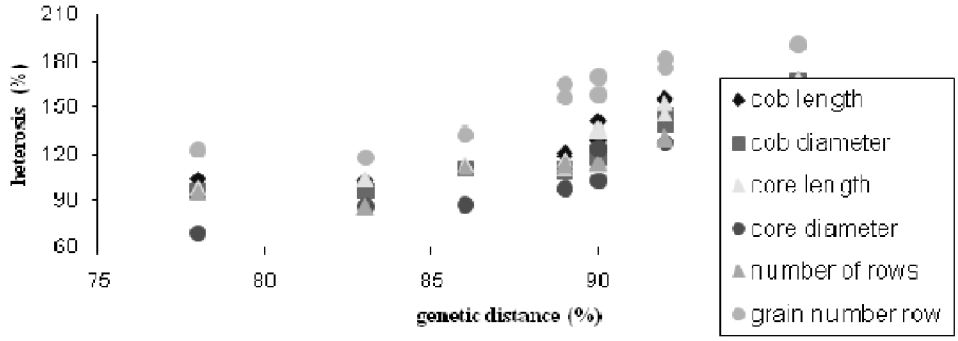

Fig.5. Heterosis effect calculated in relation to the mean value of the better parent depending on the genetic distance between the parental forms determined on the basis of AFLP markers

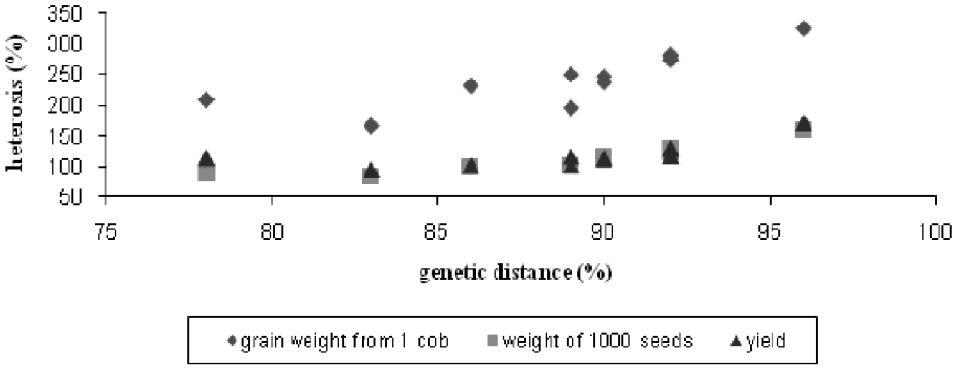

Fig. 6. Heterosis effect of hybrids calculated in relation to the mean value of the better parent depending on the genetic distance between the parental forms determined on the basis of AFLP markers

DISCUSSION

Maize (*Zea mays* L.) is to the most productive cereal plant. It is grown on significant areas (Dubas 1999).

Currently many techniques are known which permit the identification of the polymorphism of the organization and structure of genetic material within the

coding and the not- coding sequences. The systems of molecular markers permit the analysis of organisms differentiation, independent of their developmental phase and the effect of the environmental factors. Furthermore, molecular methods ensure a high repeatability of results and an easy application which are an important value concerning their usefulness. The particular techniques of variability analysis of the genetic material differ among each others resulting from their specificity, type and polymorphism level represented by them (Sztuba-Solińska 2006).The most commonly used techniques for the obtaining of molecular markers are the methods utilizing the chain reaction of DNA polymerase (PCR). The most frequently used techniques include RAPD (Random Amplified Polymorphic DNA), AP-PCR (Arbitrally Primed PCR) and DAF (DNA Amplification Fingerprinting). They are included in the group of MAAP markers (Multiple Arbitrary Amplification Profiling). The chain reaction of polymerase is also utilized in the analysis of microsatellitary sequences by the STM technique (Sequence Tagged Microsatellite Sites) as well as to obtain AFLP (Amplified Fragment Length Polymorphism) markers. One pf the oldest techniques is the RFLP (Restriction Fragment Length Polymorphism) technique.

In the recent years, in the modern breeding programs, traditional breeding methods are used in combination with the molecular techniques. This gives possibilities to introduce more effective criteria for the selection of parental material and it also permits to significantly reduce the time necessary for the breeding of a new cultivar. Many scientists have attempted to draw conclusions referring to heterosis effect by studying the genetic distance between the parental lines.

In the studies presented in this paper, two types of molecular markers RAPD and AFLP have been utilized. The RAPD markers started to be used in the early 1990-ies. They utilize the PCR (Polymerase Chain Reaction) to the generation of bands. They show a dominating character of heredity which permits to distinguish homozygotes from heterozygotes. The applied 9-11 nucleotidic starters are randomly combined starting an application in many regions of genome at the same time.

The AFLP techniques combines the restriction enzymes digestion with the PCR reaction. Both enzymes generate the so called sticky ends to which 20-30 nucleotidic fragments (called adapters) are joined. Then, there follows a pre-amplification reaction which leads to specific amplifications. The distribution of PCR products follows on polyacrylamidic gel and the detection takes place by dyeing with silver or autographical dyeing. These markers show a wide polymorphism, sometimes it is possible to differentiate homo- and heteozygotes by estimating the intensity of the band..

In the present paper, selected combinations of starters, in case of AFLP molecular markers, generated more bands differentiating the analysed

genotypes than it was done by the starters used in case of RAPD permitting a more precise estimation of the genetic distance between the parental components. The number of the generated polymorphic bands was 5 to 16. In case of RAPD markers, the genetic distance between the parental components ranged from 64 % to 93 %. while in case of AFLP markers, the range was 78% – 96 %.

Combining ability is estimated using mainly the experimental methods, but also statistical and genetical parameters (Hoffman *et al.* 1979) can be used. These parameters include the general combining value (GCA) and the specific combining value (SCA). The general combining value represents the mean value of the qualitative form of hybrids obtained by crossing the studied form in numerous combinations. Therefore, the estimation refers to a single parental form crossed with a certain number of partners and it is the meaure of the mean value of the gametes from one parent and the force of their additive action. Additive action of genes has a fixed character and it decides about the genetic conditioning of the trait. The higher is the additive part of the variance, the higher is the GCA variance (Kuriata, Topolski 2003). The specific combination value expresses the difference between the expected general combining value and the real value of the definite crossing combination. Thus, it refers to single crossing combination whose value may be lower or higher than the general value of the combination and it constitutes part of the not-additive force of genes action (Węgrzyn 1996), Ubysz-Bonacka *et al.* 19985; Griffing 1956). Component of not-additive variance (SCA), dominance and interaction (epistasis) are to a high degree unstable. Thus, the magnitude of the GCA to the SCA ratio gives a possibility to estimate the method of the action of genes which conditions the given trait (Adamczyk 1999; Lipińska 1985). In the case of maize, in our own studies, all hybrids, with the exception of the hybrid S50668-4xS56125A , were characterized by a signficant heterosis for the yield. Heterosis estimated both in relation to the mean value of the better parent, as well as, in relation to the mean value of this trait in both parents, occurred in all F1 hybrids, also in case of such traits as the number of grains row and the weight of grains cob.

Selection of adequate inbred lines is the basic element in the hybrid breeding. The number of lines included in the formula of the registered maize hybrids is expressed in hundreds and even in thousands, but only more than ten of them have played an important role (Adamczyk 1998).

Rafalski *et al.* (1998) used two methods based on a chain reaction of polymerase (PCR), in the estimation of genetic similarity of inbred lines. Experiments were carried out by RAPD system and with the use of starters with sequences partially complementary to the in *intron-exon* sequence contact. They showed that the application of starters with partially complementary sequences to the *intron-exon* sequence permit an exact

calculation of the genetic distance, even between genotypes with a high degree of kinship.

Melchinger (1999) found in his work that prognozing of the heterosis effect between groups showing genetic similarity of the embrionic plasma is not possible on the basis of the genetic distance defined when using DNA markers, but it should be defined in field experiments. On the basis of experimental data,the author showed that the division of the embrionic plasma into differentiated genic pools is favourable for the optimal utilization of heterosis.

In the presented paper, an attempt has been made to predict the heterosis effect for the analysed traits of the yield structure and the grain yield basing on the values of the genetic distance between the analysed parental lines, and for this purpose, mathematical functions have been utilized.. The dependence of heterosis effect for the yield on the genetic distance on the basis of AFLP markers has been described in a most precise way by the polynomian of the third degree because the coefficient of the adaptation to this function was $r^2 = 0.94$. The same function described the heterosis effect for yield depending on the genetic distance determined on the basis of RAPD markers, however, the coefficient of the function adaptation was lower and showed the value $r^2 = 0.57$. These differences may have result from the random character of RAPD molecular markers and from the fact that the genetic distance was less precisely defined.

CONCLUSIONS

1.Selected starter combinations in case of AFLP molecular markers generated more bands differentiating the analysed genotypes which permitted a more precise estimation of the genetic distance between the parental forms. The number of the generated polymorphic bands ranged from 5 to 16, while for the RAPD markers, there were 3 to 9 bands.

2.In case of RAPD markers, the genetic distance between parental components ranged from 64 % to 93 %, and in case of AFLP markers, the range was from 78 % to 96%

3.AFLP and RAPD molecular markers can be useful in the selection of parental forms for maize crossing taking at the same time into consideration the origin of these components.

4.Utilizaing statistical functions, an attempt was undertaken to predict the heterosis effect for the analysed traits of the yield structure and grain yield. For the RAPD molecular markers, the function which described in the best way that the heterosis effect for yield and for the particular traits of yield structure depended on the genetic distance was the polynomial of the third degree: $y = za+bx+cx\Delta 2+dx\Delta 3$, while for the AFLP molecular markers, it was a linear function : $y = a + bx$.

ACKNOWLEDGEMENTS

We may accept the thesis that the AFLP and RAPD molecular markers are useful for predicting the formula of a new hybrid, as well as for grouping maize lines according to their origin or parentage, including those having incomplete information about their parentage. For both markers: RAPD and AFLP, the functions that best describe the correlation between the heterosis effect and the genetic distance, were: a third degree polynomial $y=a+bx+cx^2+dx^3$ and a linear function $y = a + bx$.

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