Research Article



Heritability Estimates for Maturity and Plant Characteristics in Popcorn

Muhammad Noor^{1*}, Hidayat ur Rahman² and Muhammad Iqbal³

¹Department of Agriculture, University of Swabi, Swabi, Khyber Pakhtunkhwa, Pakistan; ²Department of Plant Breeding and Genetics, The University of Agriculture Peshawar, Khyber Pakhtunkhwa, Pakistan; ³Cereal Crops Research Institute, Pirsabak Nowshehra, Khyber Pakhtunkhwa, Pakistan.

Abstract | Genetic parameters particularly heritability estimates for a trait of interest help plant breeders to plan their long term breeding programs more accurately. This study was conducted to estimate the magnitude of heritability for flowering and maturity attributes along with plant and ear height parameters in four popcorn populations. Broad sense heritability estimates varied from 0.69 to 0.76, while narrow sense ranged from 0.38 to 0.69. Maximum broad sense heritability estimate of 0.84 was observed in cross-II for days to anthesis. Minimum narrow sense heritability of 0.46 was calculated in cross-III for plant height exhibited high estimates of broad sense heritability estimates (0.69 to 0.85). Similarly, narrow sense heritability ranged from 0.52 to 0.69. High broad sense heritability estimates of 0.80 to 0.88 were calculated for days to maturity in cross-III and cross-III, respectively. Similarly minimum heritability estimate of 0.60 was observed in cross cross-III. The mean of F_1 generations was low in almost all crosses from their parents for flowering and plant characters. It is concluded that in all crosses broad and narrow sense heritability estimates were of moderate to high range, indicating that the total variability was mostly of genetic nature and hence, could be effectively utilized in maize breeding programs for developing popcorn varieties having early maturity and accompanied with other desirable attributes. **Received** | April 09, 2017; **Accepted** | May 18, 2017; **Published** | June 18, 2017

*Correspondence | Muhammad Noor, Department of Agriculture, University of Swabi, Swabi, Khyber Pakhtunkhwa, Pakistan; Email: m.noor@uoswabi.edu.pk

Citation | Noor, M., Hidayat ur Rahman and M. Iqbal. 2017. Heritability estimates for maturity and plant characteristics in popcorn. *Sarhad Journal of Agriculture*, 33(2): 276-281.

DOI | http://dx.doi.org/10.17582/journal.sja/2017/33.2.276.281

 $\textbf{Keywords} \mid \textbf{Popcorn, Genetic variability, Heritability, Silking, Anthesis}$

Introduction

Maize (Zea mays L.) is an important cereal crop after wheat and rice in the world as well as in Pakistan. In Pakistan maize was cultivated on an area of 1168.5 mhac with the total production of 4944.2 mtons (PBS, 2015). There are different types of maize including, pop, sweet, white-seeded, high-lysine and high-oil content. These variations are commonly defined according to kernel type which encompass the various types as flint, pop, sweet, dent, flour and pod corn. Such grouping of maize, is due to variation in quantity, quality and composition of endosperm of the grain. As reported variation in endosperm composition arise due to a single gene like, sugary (su) vs starchy (Su), floury (fl) vs flint (FI), waxy (wx) vs nonwaxy (Wx). Similarly recessive genes with modifier action has been extensively utilized in maize breeding for special-purpose types. Popcorn (*Zea mays everta* Sturt.) has the ability to explode on heating at 177°C due to a hard seed coat and starchy endosperm (Hoseney et al., 1983). Popcorn is mainly utilized as



a snacks food in different flavors of popcorn confections. The popping usually takes place at grain moisture content of 12 to 15% (Hoseney et al., 1983).

The pattern and magnitude of genetic variability for parameters of interest in breeding populations provide a platform for long term breeding programs. The genetic parameters greatly influence gene frequencies of desirable alleles that is why they can be entertained in the breeding procedures effectively. Of these, heritability estimates are of great importance as they influence the choice of procedures for selection and subsequent plant breeding manipulations by plant breeders. Plant breeders usually exploit heritability in making decision about breeding method and also in prediction of gain from selection as well (Laghari et al., 2010). Characters with high heritability (narrow sense) can easily be fixed with simple selections indices, resulting in quick progress, as they are usually under additive genetic effects. Broad sense heritability (h_{BS}^2) estimates are calculated as the ratio of total genetic variance to the phenotypic variance, on the other hand narrow sense heritability estimates are calculated as ratio of additive portion of genetic variance to the phenotypic variance (Sujiprihati et al., 2003). Plant breeders mostly prefer narrow sense heritability because it carries the additive portion of total genetic variance, which represent the fixable portion of genetic variation and directly affect selection for desirable traits (Falconer and Mackay, 1997). This study was conducted to estimate broad and narrow sense heritability for maturity and plant characteristics in four popcorn populations.

Materials and Methods

This research was conducted at Cereal Crops Research Institute Pirsabak, Nowshera and The University of Agriculture (UOA) Peshawar, Pakistan. A set of four popcorn inbred lines were used as parental material in this study. Two of the four inbred lines were of Bangladeshi origin and the other two were locally developed at Cereal Crops Research Institute, Pirsabak (Table 1). Six basic generations (two Parents, F_1 , F_2 , BC₁ and BC₂) for each cross were developed through manual pollination procedure of crossing and selfing in two growing seasons (Russell and Hallauer, 1980). F_1 hybrids were developed in first growing season (Spring 2012), by crossing four parents. Part of seed from each inbred line and their resultant F_1 hybrid were grown in the field during summer 2012 for the production of F_2 , BC_1 and BC_2 generations. Development of F_2 generations for each cross was assured by selfing each F_1 . In the same growing season (Summer 2012) BC_1 and BC_2 generations were developed by crossing F_1 with their male and female parents, respectively.

The material comprising 20 entries including four each of the parents, F_1 , F_2 , BC_1 and BC_2 were evaluated in randomized complete block (RCB) design with three replications at Cereal Crops Research Institute Pirsabak, Nowshera and The University of Agriculture Peshawar, Pakistan, during summer (July-October) 2013. The plot size varied for different generations where the non-segregating generations (P_1, P_2) and F_1) were planted in four rows while F_2 , BC₁ and BC_2 generations were sown in eight rows each. Row length, row to row and plant to plant distances were kept 5, 0.75 and 0.25m, respectively. Data were recorded in each plot in each replication on forty plants in P_1 , P_2 and F_1 , while 80 plants were used for data recording in F_2 , BC₁ and BC₂. Data were recorded on plot basis for days to 50% tasseling, silking, anthesis and maturity while ten plants were used for the plant and ear height parameters.

Table 1: *Pedigree and maturity of the parental inbred lines.*

S. No	Name	Pedigree	Maturity
1	P-1	PS-POP-1-1-4	Early
2	P-2	PS-POP-29-2-1	Early
3	P-3	BD-POP-1-2-3-3	Moderate
4	P-4	BD-POP-2-1-2	Moderate

Heritability estimates

Both broad sense and narrow sense heritability estimates were calculated from the variances of segregating and non-segregating generations on average data from two locations, using the formula suggested by Warner (1952).

$$h_{BS}^{2} = \frac{VF - \sqrt[s]{(VP_{1})(VP_{2})(VF_{1})}}{VF_{2}}$$

Where:

 VF_1 , VP_1 and VP_2 : The variances of non-segregating generations i.e. parent 1, parent 2 and F_1 , respectively; VF_2 : The variance of F_2 generation.

Heritability in Narrow sense

$$h_{NS}^{2} = \frac{2VF_{2} - (VBC_{1} + VBC_{2})}{VF_{2}}$$

Links

Researchers

Sarhad Journal of Agriculture

Table 2: Broad-sense $(h^2_{(BS)})$ and narrow-sense $(h^2_{(NS)})$ heritability estimates for days to 50% -tasseling, -anthesis, -silking, -maturity, plant and ear height in four maize crosses evaluated at UOA, Peshawar and Cereal Crops Research Institute, Pirsabak Nowshera.

Parameters	Cross-I		Cross-II		Cross-III	Cross-III		Cross-IV	
	(h_{BS}^2)	(h^2_{NS})	(h_{BS}^2)	(h ² _{NS})	(h_{BS}^2)	(h^2_{NS})	(h_{BS}^2)	(h_{NS}^2)	
Days to 50% Tasseling	0.69	0.45	0.76	0.69	0.75	0.57	0.76	0.38	
Days to 50% Anthesis	0.82	0.54	0.84	0.67	0.81	0.46	0.83	0.57	
Days to 50% Silking	0.81	0.48	0.81	0.67	0.79	0.44	0.75	0.58	
Plant Height	0.84	0.52	0.73	0.55	0.79	0.69	0.80	0.54	
Ear Height	0.83	0.68	0.80	0.43	0.82	0.71	0.85	0.74	
Days to 50% Maturity	0.86	0.77	0.88	0.63	0.80	0.60	0.82	0.61	

Cross-I: $PS-Pop-1-1-4 \times BD-Pop-1-2-3-3$, $Cross-II = PS-Pop-1-1-4 \times BD-Pop-2-1-2$; **Cross-III:** $PS-Pop-29-2-1 \times BD-Pop-1-2-3-3$, $Cross-IV = PS-Pop-29-2-1 \times BD-Pop-2-1-2$.

Table 3: Generation means from the combined analysis for days to tasseling, anthesis and silking evaluated at UOA Peshawar and CCRI during summer, 2013.

Generation	Days to 50% tasseling				Days to 50% anthesis				Days to 50% silking				
	Cross				Cross				Cross				
	Ι	II	III	IV	Ι	II	III	IV	Ι	II	III	IV	
P_1	49.10	49.10	49.53	49.53	52.53	52.53	52.77	52.77	53.60	53.60	54.03	54.70	
P_2	53.00	52.17	53.00	52.17	56.57	55.53	56.57	55.53	57.60	57.13	57.60	57.20	
\mathbf{F}_{1}	47.40	48.03	47.67	48.10	50.93	51.37	51.00	51.70	52.07	52.37	52.20	52.77	
F_2	50.10	51.65	49.55	50.25	53.47	55.35	53.60	53.73	54.75	56.68	54.75	55.85	
BC ₁	48.50	50.12	49.12	49.48	51.28	53.52	52.63	52.93	52.45	54.93	53.88	54.38	
BC ₂	49.42	52.65	49.63	52.17	53.00	56.17	53.30	55.65	54.38	57.40	54.60	56.78	

Cross-I: PS-Pop-1-1-4 x BD-Pop-1-2-3-3, Cross-II = PS-Pop-1-1-4 x BD-Pop-2-1-2; Cross-III: PS-Pop-29-2-1 x BD-Pop-1-2-3-3, Cross-IV = PS-Pop-29-2-1 x BD-Pop-2-1-2.

Where:

 VF_2 : The variation of F_2 generation; VBC_1 : The variation of back cross with parent 1; VBC_2 : The variation of back cross with parent 2.

Yield is the ultimate objective of any breeding program. Also include yield/production with their estimates as well.

RESULTS AND DISCUSSION

Days to mid 50% tasseling

It is revealed from Table 2 that high broad sense heritability estimates were exhibited by all four crosses for days to 50% tasseling. Heritability estimates for tasseling ranged from 0.69 to 0.76. High broad sense heritability estimate (0.76) was observed for both cross-II and cross-IV, followed by cross-III and cross-I with h_{BS}^2 of 0.75 and 0.69, respectively. For days to 50% tasseling moderate narrow sense heritability estimates were observed in four crosses. Narrow sense heritability ranged from 0.38 to 0.69 for cross-II and cross-I, respectively. Minimum (47.40) days to 50% tasseling were observed in F_1 of cross-I (Table 3).

Days to mid 50% anthesis

Heritability estimates presented in Table 2 revealed high level of broad sense heritability for days to 50% anthesis among the four crosses. Broad sense heritability estimate ranged from 0.81 to 0.84. Similarly narrow sense heritability estimates ranged from 0.46 to 0.67. Maximum narrow sense heritability of 0.67 was calculated for the cross-II, while minimum (0.46) was observed for cross-III. Cross-I exhibited minimum (51) days to 50% anthesis for F_1 (Table 3).

Days to mid 50% silking

Heritability estimates for days to 50% silking are presented in Table 2. Maximum broad sense heritability estimate of 0.81 was reported for cross-I and cross-II, followed by 0.79 for cross-III, while minimum broad sense heritability of 0.75 was reported for cross-IV. Narrow sense heritability estimates ranged from 0.44 to 0.67 for cross-III and cross-II, respectively. Minimum (52) days to 50% silking were observed in F_1 of cross-I (Table 3).

Sarhad Journal of Agriculture

Table 4: Generation means from the combined analysis for days to 50% maturity, plant height and ear height evaluated at UOA Peshawar and CCRI during summer, 2013.

Generation	Days to Maturity				Plant he	ight (cm)	Ear height (cm)					
	Cross				Cross		Cross					
	Ι	II	III	IV	Ι	II	III	IV	Ι	II	III	IV
P ₁	93.47	93.47	93.33	93.33	148.98	148.98	140.00	140.00	72.95	72.95	71.80	71.80
P_2	98.33	98.67	98.33	98.67	136.10	139.02	135.55	139.02	63.53	71.40	63.53	71.40
F ₁	93.33	93.27	93.60	93.87	160.13	150.75	148.17	156.23	68.15	69.92	77.35	78.00
F_2	95.93	98.28	95.85	97.07	148.79	147.00	144.77	148.33	65.51	66.77	70.57	70.53
BC ₁	94.12	95.85	94.88	95.35	150.00	149.78	142.68	151.41	70.58	69.45	71.05	71.18
BC ₂	95.37	98.18	95.57	97.67	143.39	148.14	141.07	147.16	69.54	70.25	69.58	69.44

Cross-I: *PS-Pop-1-1-4 x BD-Pop-1-2-3-3, Cross-II = PS-Pop-1-1-4 x BD-Pop-2-1-2;* **Cross-III:** *PS-Pop-29-2-1 x BD-Pop-1-2-3-3, Cross-IV = PS-Pop-29-2-1 x BD-Pop-2-1-2*

Plant height

Cross-III exhibited minimum (136.10 cm) plant height for P_2 (Table 4). Estimates of heritability for plant height are provided in Table 2. High level of broad sense heritability was observed for plant height in all four crosses. Broad sense heritability varied from 0.73 to 0.84. Maximum broad sense heritability of 0.84 was found for cross-I, followed by cross-IV with h_{BS}^2 of 0.80. The narrow sense heritability estimates showed a range of 0.52 to 0.69 for cross-I and cross-III, respectively for this parameter. Narrow sense heritability of 0.69 and 0.52 was observed for cross-I and cross-III, respectively.

Ear height

Broad sense heritability estimates in all four crosses were high for ear height, ranging from 0.80 to 0.85 (Table 2). Similarly narrow sense heritability estimates ranged from moderate to high for ear height. Maximum (0.74) estimate of narrow sense heritability was observed for the cross-IV while, minimum (0.43) estimates of heritability in narrow sense was noticed in the cross-II for this trait. Both cross-I and cross-III exhibited minimum (63.53 cm) ear height for P₂ (Table 4).

Days to 50% maturity

Minimum (93.27) days to 50% maturity were observed in cross-II for F1 (Table 4). Broad and narrow sense heritability estimates for days to maturity are provided in Table 2. High levels of broad sense heritability were calculated for days to 50% maturity in all four crosses. Broad sense heritability varied from 0.80 to 0.88 for days to maturity. Maximum broad sense heritability of 0.88 was found for cross-II, followed by cross-I with h_{BS}^2 of 0.86. Minimum broad sense heritability of 0.80 was observed for days to 50% ma-

turity in cross-III. Similarly narrow sense heritability estimates varied from moderate to high range. Maximum (0.77) narrow sense heritability was noticed for cross-I, followed by cross-II with $h_{\rm NS}^2$ 0.63. Likewise, minimum narrow sense heritability estimates of 0.60 were observed for cross-III.

Days to 50% mid tasseling

High heritability estimates of broad sense were observed for days to 50% tasseling in all the four crosses, showing that selection in these crosses for this trait will be effective due to high genetic variances. Our result of high broad sense heritability were in line with those observed by Al-Falahy (2015) while, Bekele and Rao (2014) reported moderate heritability of broad sense in their studies for days to tasseling in maize. Narrow sense heritability estimates ranged from moderate to high in all four studied crosses for days to 50% tasseling. This exhibit that parents could be easily utilized for both direct selection and hybrid development. However, low narrow sense heritability was observed by Moradi (2014), while Al-Falahy (2015) reported moderate estimates for days to 50% tasseling.

Days to 50% mid anthesis

High estimates of broad sense heritability were observed for days to 50% anthesis in all four crosses. On the other hand, moderate level of narrow sense heritability was estimated for days to 50% anthesis in three of the four crosses, while high level of narrow sense heritability was calculated for only one cross. As moderate to high level of narrow sense heritability is indicative of the predominant role of additive gene action, therefore these parents can be effectively utilized for enhancing early maturity through selection. Such a selection will be effective because in such case



phenotype will be true picture of genotype due to the relative small contribution of the environment to the phenotype. High broad sense heritability was also reported by Shukla et al. (2014) for days to anthesis in maize. In contrast low broad sense heritability estimates were observed by Dorri et al. (2014) for days to anthesis. Our results of high and low estimates of narrow sense heritability are in line with Majidi et al. (2009) and Dorri et al. (2014), respectively.

Days to 50% mid silking

Days to 50% silking showed high broad sense heritability estimates in all the four crosses, while narrow sense heritability ranged from moderate to high in these crosses for this maturity character. Due to high estimates of heritability phenotype will be a clear picture of genotype and hence selection will be more effective for earliness in silking. Earlier researchers like, Bello et al. (2012) also observed high broad sense heritability estimates for days to silking in their studies while estimating heritability and other genetic parameters in maize. Moderate to high narrow sense heritability can easily be utilized for promoting earliness in these germplasm. Our high heritability estimates for broad sense and moderate for narrow sense are in conformity with those of Abadi et al. (2011).

Plant height

Broad sense heritability estimates calculated for plant height in all four crosses were of high magnitude, while narrow sense heritability estimated for plant height were of moderate level. Estimates of both broad and narrow sense heritabilities indicated that plant height was least affected by environment. This represent that selection in these genotypes for plant height would be meaningful in further breeding approaches. Similar results of high heritability have been reported by Nataraj et al. 2014 and Shukla et al. (2014). Majidi et al. (2009) and Abadi et al. (2011) observed high estimates for both broad and narrow sense heritability in their studies, while Tengan et al. (2012) reported low narrow sense heritability due high environmental effect.

Ear height

Estimates of broad sense heritability were high for ear height in all the crosses, whereas heritability estimates in narrow sense were also high in most crosses while, in one cross moderate level of heritability (h_{NS}^2) was observed. High levels of heritability shows that ear height was least affected by environment, which

provided enough evidence that ear height was due to additive genetic effects. Crosses with moderate heritability estimates are indicative of smaller environmental influence which suggests that improvement of the said trait could be made easily through simple selection procedures. The present results of high heritability are also supported by those reported by Shukla et al. (2014) and Al-Falahy (2015) for ear height.

Days to 50% maturity

Early and medium-maturing maize hybrids and open pollinated varieties are desirable in the areas where early and cold temperatures could considerably affect the production of popcorn due to early autumn cold stress. Heritability estimates of both broad and narrow sense for days to 50% maturity were high in magnitude indicating a predominant role of additive gene action which means that these parents can be effectively utilized for enhancing early maturity through selection. Such a selection will be effective because in such case phenotype will be true picture of genotype due to the relative small contribution of the environment to the phenotype. Our results of high heritability estimates are also in conformity with those of Sharma et al. (2014) and Kumar et al. (2014) for days to maturity in maize.

Conclussion

The study revealed that Cross-II (PS-Pop-1-1-4 \times BD-Pop-2-1-2) exhibited high magnitudes of both broad sense and narrow sense heritability estimates for days to 50% tasseling, silking, anthesis and maturity. This indicates that the parental combination in Cross-II could be efficiently exploited in maize hybrid development program for early maturity.

Acknowledgements

Authors are cordially thankful to Higher Education Commission, Pakistan for financial support in this study. We also present our gratitude to Director, Cereal Crops Research Institute, Nowshehra and Chairman, Department of Plant Breeding and Genetics, The University of Agriculture, Peshawar, Pakistan for providing all field facilities to conduct this research.

Authors Contribution

Muhammad Noor conducted the research and wrote manuscript; Hidayat ur Rahman supervised the re-





search and provide the field facilities for research at University and Muhammad Iqbal provided the germplasm for research and provide the field facilities for research at CCRI. Durrishahwar helped in data tabulation and manuscript writing and Hidayat Ullah helped in data analysis.

Reference

- Abadi, J.M., S.K. Khorasani, B.S. Sar, S. Movafeg and M. Golbashy. 2011. Estimation of combining ability and gene effects in forage maize (*Zea mays* L.) using line × tester crosses. J. Plant Phys. Breed. 1(1): 57-67.
- Al-Falahy, M.A.H. 2015. Estimation of combining ability, heterosis and some genetic parameters across four environments using full diallel cross method. Int. J. Pure Appl. Sci. Technol. 26(1): 34-44.
- Bekele, A. and T.N. Rao. 2014. Estimates of heritability, genetic advance and correlation study for yield and it's attributes in maize (*Zea mays* L.).J. Plant Sci. 2(1): 1-4.
- Bello, O.B., S.A. Ige, M.A. Azeez, M.S. Afolabi, S.Y. Abdulmaliq and J. Mahamood. 2012. Heritability and genetic advance for grain yield and its component characters in maize (*Zea mays* L.) Int. J. Plant Res. 2(5): 138-145. https://doi. org/10.5923/j.plant.20120205.01
- Dorri, P., S.K. Khorasani, M. Shahrokhi. 2014. Generation mean analysis: a case study of variance components in KSC 500 generations of maize (*Zea mays* L.). Int. Res. J. Appl. Basic Sci. 8(2): 194-200.
- Falconer, D.S. and T.F.C. Mackey. 1997. An introduction to quantitative genetics. Addison Weslay Longman Ltd. Edinburg Gate, Harlow, Essex CM 20 2JE, England, UK.
- Hoseney, R.C., K. Zeleznak, and A. Abdelrahman. 1983. Mechanism of popcorn popping. J. Cereal Sci. 1: 43. https://doi.org/10.1016/S0733-5210(83)80007-1
- Kumar, G.P., V.N. Reddy, S.S. Kumar and P.V. Rao. 2014. Genetic variability, heritability and genetic advance studies in newly developed maize genotypes (*Zea mays* L.). Int. J. Pure
- Laghari, K.A., M.A. Sial, M.A.A. Arain, A.A. Mirbahar, A.J. Pirzada, M.U. Dahot and S.M.

Mangrio. 2010. Heritability studies of yield and yield associated traits in bread wheat. Pak. J. Bot. 42(1): 111-115.

- Majidi, M.M., A. Mirlohi and F. Amini. 2009. Genetic variation, heritability and correlations of agro-morphological traits in tall fescue (*Festucaarundinacea*Schreb.). Euphytica 167: 323-331. https://doi.org/10.1007/s10681-009-9887-6
- Moradi, M. 2014. Genetic analysis to determine the nature and magnitude ofgenetic variances and heritability estimates in maize (*Zea mays* L.). Int. J. Agron. Agric. Res. 5(5): 183-188.
- Nataraj, V., J.P. Shahi and D. Vandana. 2014. Estimates of variability, heritability and genetic advance in certain inbreeds of maize (*Zea mays*, L.). Int. J. Appl. Bio. Pharm. Tech. 5(1): 205-208.
- PBS (Pakistan Bureau of Statics).2015.http://www. pbs.gov.pk/content/table-1-area-and-production-important-crops
- Russell, W.A. and A.R. Hallauer. 1980. Corn. In: W.R. Fehr and H.H. Hadley (eds.) Hybridization of crop plants. pp: 299-312. Am. Soc. Agron. Crop Sci. Madison.
- Sharma, R., S.R. Maloo and A. Joshi. 2014. Genetic variability analysis in diverse maize genotypes (*Zea mays* L.). Elect. J. Plant Breed. 5(3): 545-551.
- Shukla, N., D.K. Mishra, S. Singh, A.S. Chavan and A. Jha. 2014. Genetic studies for growth and yield parameters in germplasm of desi and quality protein maize. Indian Res. J. Genet. Biotech. 6(2): 367-373.
- Sujiprihati, S., G.B. Saleh and E.S. Ali. 2003. Heritability, performance and correlation studies on single cross hybrids of tropical maize. Asian J. Plant Sci. 2(1): 51-57. https://doi.org/10.3923/ ajps.2003.51.57
- Tengan, K.M.L., K. Obeng-Antwi and R. Akromah. 2012. Genetic variances, heritability, and correlation studies on selected phenotypic traits in a backcross breeding program involving normal and Opaque-2 maize. Agric. Biol. J. North Am. 3(7): 287-291. https://doi.org/10.5251/ abjna.2012.3.7.287.291
- Warner, J.N. 1952. A method for estimating heritability. Agron. J. 44: 427-430. https://doi. org/10.2134/agronj1952.00021962004400080 007x