

PATH ANALYSIS OVER ENVIRONMENT OF MAIN YIELD COMPONENTS GENETIC CONTRIBUTIONS IN GRAPEVINE

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ABSTRACT

Yield components and genetic contribution in final yield have more important in crop plants breeding programs. For this purpose, 20 grapevine genotypes were evaluated in Urmia and Takestan research station (under full irrigation and drought stress). This research was performed in randomized complete block design with three replications and three plants in each plot in 2012. Number of cluster per plant, Number of berry per cluster, berry weight and yield of each plants were recorded. Compound and logarithmic analysis of variance, variance of genetic components and environmental interaction effects were presented by multiplicative three environmental and genotypic elements. Results indicated that number of cluster per plant had the highest genetic contribution in final yield and the most sensitivity and variation in different environments. Direct effect of number of cluster per plant in final yield (0.61) was higher than direct effect of number of berry per cluster (0.48) and berry weight (0.30). V_3 value was higher than V_2 and V_2 was higher than V_1 , therefore sequence of manifestation of yield components were number of cluster per plant, number of berry per cluster and berry weight, respectively. Environmental components of interaction effects were indicated that absolute value of r_1 was higher than r_2 and r_3 . This case indicated that number of cluster per plant was higher sensitivity than other main yield components in different environments.

Keywords: Path analysis, Yield components, genetic contribution, Yield stability.

INTRODUCTION

Grapevine (*Vitis vinifera* L.) is one of the most important horticultural crops in the world and Iran. According to the reports of FAO (2014), grapevine cultivated area is 7,598,570 and 307,721 hectares in the world and Iran, respectively. World production of grape is about 67.5 million tons. Iran with 1.9 million tons production is located in seventh of world ranking. Main yield components have the most importance in many plant breeding research programs. Grapevine breeders' aim is the increase of final yield by selection of main yield components such as number of cluster per plant, number of berry per cluster and berry mean weight. For this reason, they want to know that which one of the main yield components have the most genetic contribution in complicated yield trait. A complicated or complex trait such as yield, can be define as trait that its variations are identified by variations of its components. Using of recombinative heterosis has been suggested for identification of genetic contribution of each yield components in final yield (Sparnaaij and Bos, 1993). This method will has low efficient in fruit trees because the obtaining of the new generations needs several years in sexual hybridization. Huhn (1979) suggested the method of stability analysis based on principal components. In this method, logarithmic variance analysis and path analysis is used in different environmental conditions. On the base of these researchers' idea, yield of plants is a complex trait which its components have developed during growth season. Therefore different environmental factors will have different effects on these trait.

In this article, path analysis and genetic contribution of grapevine main yield components were identified on the base of developmental growth components, model of Tai (1975), Tai (1979), Tai et al. (1994) and Huhn (1979) in different environmental conditions.

MATERIALS AND METHODS

In this study, 20 grapevine genotypes with Russian origin were evaluated in one location of Urmia and two locations of Takestan (under full irrigation and drought stress). This research was performed in randomized complete block design with three replications and three plants in each plot in 2012. Fruit yield (kg/plant), number of cluster per plant, number of berry per cluster and berry mean weight were recorded. Compound analysis of variance was done for yield and yield components. Path analysis over environment was done and genetic contribution of yield components in final yield were identified. In this model, it is assumed that growth chronologically of main yield components are from the number of clusters per plant (X), the number of berry per cluster (Y) to berry weight (Z) and yield (W) that obtain by multiplying of these components ($W = X \times Y \times Z$). Also it is assumed that environmental resources can be divided into three independent components of R_1 , R_2 and R_3 that each group is stimulating the

growth of other traits in growth duration and then path diagram was drawn on the base of this concept.

In order to discover the relationship between these three independent environmental groups in path analysis, it is assumed that ρ_{xy} , ρ_{xz} , ρ_{yz} , ρ_{xw} , ρ_{yw} and ρ_{zw} are correlation coefficients between yield and its main components. Also a_1 to a_6 are path coefficients. Therefore, the following relationships will be:

$$\begin{aligned} \rho_{xy} &= a_1 \\ \rho_{xz} &= a_2 + a_1 a_3 \\ \rho_{yz} &= a_3 + a_1 a_2 \\ \rho_{xw} &= a_4 + a_1 a_5 + a_2 a_6 + a_1 a_3 a_6 \\ \rho_{yw} &= a_5 + a_1 a_4 + a_3 a_6 + a_1 a_2 a_6 \\ \rho_{zw} &= a_6 + a_2 a_4 + a_3 a_5 + a_1 a_3 a_4 + a_1 a_2 a_5 \end{aligned}$$

Six path coefficients can be obtained by solving the following simultaneous equations.

$$\begin{aligned} A &= \Delta^{-1} \rho \\ A' &= (a_1 \ a_2 \ a_3 \ a_4 \ a_5 \ a_6) \\ \rho' &= (\rho_{xy} \ \rho_{xz} \ \rho_{yz} \ \rho_{xw} \ \rho_{yw} \ \rho_{zw}) \end{aligned}$$

$$\Delta = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & \rho_{xy} & 0 & 0 & 0 \\ 0 & \rho_{xy} & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & \rho_{xy} & \rho_{xz} \\ 0 & 0 & 0 & \rho_{xy} & 1 & \rho_{yz} \\ 0 & 0 & 0 & \rho_{xz} & \rho_{yz} & 1 \end{bmatrix}$$

U_1 , U_2 and U_3 are the path coefficients from R_1 to X , R_2 to Y and R_3 to Z , respectively as follow:

$$\begin{aligned} U_1 &= \pm 1 \\ U_2 &= \pm (1 - a_1^2)^{0.5} \\ U_3 &= \pm (1 - a_2 \rho_{xy} - a_3 \rho_{yz})^{0.5} \end{aligned}$$

These coefficients can be positive or negative according to the used scale. Here, positive coefficients were used. If W , r_1 , r_2 and r_3 represent yield and three different environments, respectively, then the following equation will be established.

$$W = V_1 r_1 + V_2 r_2 + V_3 r_3 + e'$$

In this equation, V_1' , V_2' and V_3' are path coefficients from R_1 , R_2 and R_3 to yield (W), respectively, and e' is residual. V_1' , V_2' and V_3' can be obtained by the following formulas:

$$\begin{aligned}V_1' &= U_1 (a_4 + a_1a_5 + a_2a_6 + a_1a_3a_6) = U_1 \rho_{xw} \\V_2' &= U_2 (a_3a_6 + a_5) \\V_3' &= U_3a_6\end{aligned}$$

Yield of i^{th} genotype can be obtained by the following formula in j^{th} environment:

$$W = \mu_{wi} + V_{1i}r_{1j} + V_{2i}r_{2j} + V_{3i}r_{3j} + e'$$

In this formula, $V_{gi} = V'_{gi}\sigma_{wi}$ is for $g=1, 2, 3 \dots$ and σ_{wi}^2 is the yield variance of i^{th} genotype. Also this formula is a mathematical model for the observed yield (W_{ij}). This model includes genotypic mean effect (μ_{wi}), three multiplicative components of interaction effects of genotype and environment (including three genotypic components V_{1i} , V_{2i} , V_{3i} and three environmental components r_{1j} , r_{2j} and r_{3j}) and error component (e_{ij}). Each of the three genotypic components identifies the contribution of the three components X, Y and Z in the interaction of genotype and environment. Also, each of the three environmental components indicates contribution of these components in the environment.

In logarithmic model, if $\text{Log}(Y) = \text{Log}(x_1) + \text{Log}(x_2) + \text{Log}(x_3)$, then covariance of yield and its main components will be $C_i = \text{cov}[\text{Log}(w), \text{Log}(x,y,z)]$ and $\sigma^2(Y) = \Sigma c_i$.

RESULTS

Results of compound analysis of variance of yield and its main components in three different environments had been presented in Table 1. Also, genetically components and heritability of yield and its main components had been indicated in Table 2. Effects of genotype, environment and their interactions were significance in all traits (P. value < 0.01). In genetically analysis of yield and its components (table 2), heritability of yield was very low because of its complicating and high effects of environment. Covariance of yield and its main components and values of C_i had been estimated in table 3 on the base of logarithmic model for each genotype.

Table 1- Variance analysis of yield and its component in different environments

Source of variation	Degree of freedom	Number of cluster per plant	Number of Berry per cluster	Berry weight (gr)	Yield (kg/p)
Environment	2	3491.3**	29240.1**	10.21**	1301.89**
Replication/ Environment	6	92.2	367.2	0.02	36.01
Genotype	19	2178.7**	13382.8**	9.7**	257.64**
Genotype × Environment	38	265.7**	3008.1**	1.4**	96.66**
Error	114	130.9	748.5	0.07	17.46

** : significance in $\alpha= 0.01$

Table 2- Genetically parameters estimation of yield and its component.

parameters	Number of cluster per plant	Number of Berry per cluster	Berry weight (gr)	Yield (kg/p)
Coefficient of Variation (%)	9.5	15.8	8.4	11.2
Phenotypic variance	343.46	1901.24	0.99	35.35
Genotypic variance	212.56	1152.74	0.92	17.89
Environmental variance	130.90	748.50	0.07	17.46
Genotype × Environment Var.	44.93	753.20	0.44	26.40
Broad-sense heritability (%)	54.7	43.4	64.3	29

Table 3- Genotypic components (V_1 , V_2 and V_3) and covariance of yield with its components in different environments.

Genotypes	Coefficient of Variation (%)	Mean	C_1	C_2	C_3	Yield variance	V_1	V_2	V_3
Uliskibiser	14.42	9.4	0.26	0.83	0.10	1.19	-1.68	3.75	3.46
Aligoneh	33.64	3.7	0.39	0.16	0.38	.81	-0.53	1.19	1.10
Ramfi TCXA	20.19	5.7	0.44	0.39	-0.03	.72	-0.81	1.82	1.68
46X	9.04	14.1	0.53	0.38	0.12	1.04	-3.14	7.01	6.47
Gezgiski Ramfi	5.70	12.7	0.12	-0.04	0.23	.31	-1.91	4.26	3.93
Superan Bulgar	11.67	9.6	0.37	0.35	0.30	.99	-2.50	5.60	5.17
Uzbakestan Moscat	10.46	10.1	0.35	0.34	0.05	.71	-1.19	2.66	2.46
Bobili Magaracha	48.77	2.8	0.21	0.50	0.47	1.18	-0.31	0.69	0.64
Bli Ramfi	12.29	8.1	0.32	-0.05	0.29	.56	-1.38	3.08	2.84
Skieve	10.73	16.0	0.93	0.66	0.56	2.15	-2.53	5.65	5.21
Tambuzh Shaki Ramfi	21.95	5.0	0.25	0.29	0.14	.68	-0.88	1.96	1.81
Ramfi ezdangara	20.65	6.5	0.68	0.38	0.41	1.46	-1.80	4.02	3.71
Muscat	6.51	16.0	0.01	0.65	0.20	.87	-2.48	5.54	5.11

Apozoski Ramfi	8.01	22.4	0.79	0.57	0.75	2.11	-4.46	9.97	9.20
Muscat Ruskovi	16.83	6.5	0.30	-0.05	0.49	.74	-0.65	1.45	1.34
Kishmish Ramfi Azos	18.64	8.4	1.02	0.44	0.14	1.60	-1.03	2.30	2.12
Ukranski Ramfi	8.96	9.1	0.07	0.42	0.21	.55	-2.44	5.46	5.04
Negrod yalon	8.98	10.8	0.51	0.08	-0.04	.56	-2.23	4.98	4.60
X45	17.55	4.5	0.19	0.04	0.09	.32	-1.11	2.48	2.29
Anapiski Ramfli	7.72	19.9	0.85	0.63	0.59	2.06	-4.79	10.71	9.88
Mean			0.42	0.35	0.27				

Covariance of yield with number of cluster per plant (C_1) was higher than covariance of yield with other yield components in many genotypes. Also, these values were positive in all genotypes. Mean of covariance of yield with number of cluster per plant (0.42) was higher than means of covariance of yield with other yield components. Positivity and high value of C_1 represented the fact that genetic contribution of number of clusters per plant was higher than other components in the increase or decrease of final yield. Also, variations of yield in different environments and interaction between yield and environment were most affected by this trait in many grapevine genotypes. Negative values of C_i in number of berry per cluster and mean weight of berry in some genotypes indicated the lower contribution and effect of these traits in final yield.

In path analysis of yield and its components in different environments (Fig. 1), direct effect of number of cluster per plant (0.61) was higher than direct effects of number of berry per cluster (0.48) and berry mean weight (0.3) in final yield. On the other hand, indirect effect of number of cluster per plant by number of berry per cluster (0.17) and berry mean weight (0.28) path way were lower than their direct effects in final yield. These results were confirmed the findings of logarithmic analysis and high contribution of number of cluster per plant in final yield.

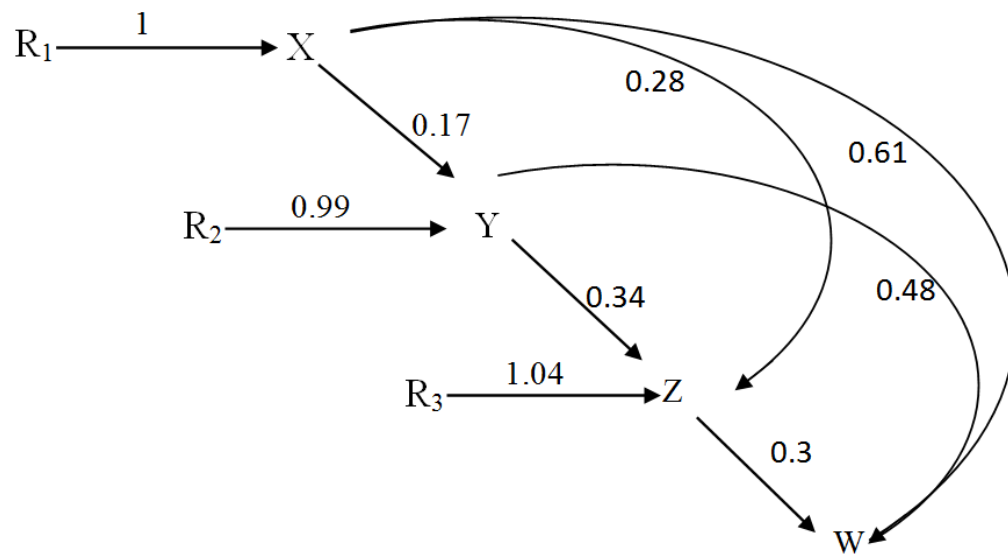


Fig. 1- Path analysis of grapevine yield and its components in different environments.

Mean of yield and genotypic components (V_1 , V_2 and V_3 in table 3) indicated that V_3 values were higher than V_2 values and V_2 values were higher than V_1 values. On the other word, emergence of grapevine yield components were the number of clusters per plant, number of berry per cluster and berry weight, respectively. Also genotypic components values of Anapiski Ramfli and Apozoski Ramfi were higher than genotypic components values of other genotypes. These genotypes will have higher yield than other genotypes in ideal environments. This case was indicated by higher percentage of coefficients of variation of these genotypes. Genotypes Aligoneh and Bobili Magaracha will have more stable yield than other genotypes because of the lower genotypic components values and percentage of coefficients of variation in different environments.

Estimating of three environmental components of interaction effects r_1 , r_2 and r_3 had been shown in table 4. Environmental components of interaction effects were indicated that absolute value of r_1 was higher than r_2 and r_3 . This indicated that number of cluster per plant had the highest sensitivity in different environments. Drastic changes in the environment will have a very different impact on this trait. Effects of environmental variations in berry weight was lower and therefore this trait had less sensitivity to the environmental changes.

Table 4- Environmental components estimation (r_1 , r_2 and r_3) of variety and Environment Interaction.

Environmental component	Takestan	Takestan (drought stress)	Urmia
r_1	1.8	0.2	0.4
r_2	0.6	0.0	0.3
r_3	0.4	0.1	0.4

DISCUSSION

Tai (1979) surveyed adaptability of potato yield components in different environments by path analysis and concluded that r_3 was higher and more variable than r_1 and r_2 in different environments. Also Tai et al. (1994) investigated sensitivity temperature index of potato yield components and concluded that environmental component r_4 was higher than others. Farshadfar (1999) reported that the genetic contribution of seed number per spike in genotype and environment interaction was more than genetic contribution of spike per plant and grain weight in wheat chromosome addition lines. Also he indicated that sensitivity of seed per spike to environmental variation was lower than other two components. Therefore the seed per spike had the most important role in phenotypic stability of wheat in different environments. Also he identified chromosomal genes location of genotype and environment interaction by this method. These results were similar to the finding of the present study, because the first multiplicative component of yield had higher genetic contribution in final yield.

Phenotypic stability of bread wheat was investigated by using path analysis method in drought stress and non-drought conditions by Farshadfar et al. (2012). They concluded that genetically contribution of thousand seed weight in yield stability of genotypes was more than other yield components. Results of this research was not similar to finding of presence research because of the higher genetic contribution of second multiplicative component of final yield. Therefore it can be concluded that the genetically contribution of yield components will be different in plant species. Also this result was confirmed by Farshadfar et al. (2013). In their research, number of seed per pod of pea (the second multiplicative component) had the highest genetically contribution in final yield and its non-stability in different environmental conditions.

Path analysis of grapevine yield and its main components was conducted only by (Fanizza et al., 2005). In this study, complete and partial correlation method was used for yield path analysis in an environment. They concluded that number of cluster per plant, number of berry per cluster and berry weight had significance positive correlation with yield, but number of cluster per plant

had significance negative correlation with number of berry per cluster and berry weight. This method is not able to determination of the genetically contribution of main yield components in yield variance. Also this method is not show sensitivity of main yield components in different environmental conditions. While in the present study, data of three different environment were provided genetically contribution determination of main yield components in yield variance.

Other applications of logarithmic and path analysis methods in different environments is the yield stability analysis of each cultivar in different environmental conditions and determination of cultivars with sustainable yield for each environment. It also has a high capability in selecting parents for heterosis breeding. This method is not require to the factors rotation (in factor analysis method), because position of each yield components are considered assuming the path relationship among yield and its components.

CONCLUSION

This research indicated that number of cluster per plant had the highest genetic contribution, variations and sensitivity in final yield in different environment conditions. Therefore number of cluster per plant will has more importance than other yield components in selection of the high yield grapevine genotypes for ideal environments. Also number of berry per cluster and berry weight will have more importance in selection of grapevine genotypes with higher stabile yield for different environmental conditions. Findings of this research showed that the high variance in yield had correlation with high variance of main yield components. If the plant under study shows great flexibility in the yield structure, it may increase one component with reduction in other component that this indicates the negative covariance among yield components. Therefore the component that has very variation (high variance) but it compensate by other components (negative covariance), it has little effect on the yield variance. This case is seen in the low C_i value of that component. One of advantages of logarithmic method is the independent of variance and covariance with measurement units. Therefore variance of different trait with different measurement unit will be comparable.

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