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## Original Article

# Genetic Contribution of Grapevine (*Vitis Vinifera* L.) Main Yield Components in Final Yield

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## ABSTRACT

**Objective:** Yield components and genetic contribution have the most important in final yield and breeding programs of crop plants. For this purpose, 20 varieties of grapevines with Russia origin were evaluated in Urmia and Takestan research station (under full irrigation and drought stress). **Methods:** Twenty grapevine genotypes were evaluated in Urmia and Takestan research station (under full irrigation and drought stress) in randomized complete blocks design with three replications and three plants in each plot. 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 interactions were presented by multiplicative three environmental and genotypic elements. **Results:** Results indicated that number of cluster per plant had the highest genetic contribution in final yield and also had the most sensitivity and variation in different environments. Direct effect of number of cluster per plant in final yield was higher than other studied traits.  $V_3$  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 interactions were indicated that absolute value of  $r_1$  was higher than  $r_2$  and  $r_3$ . **Conclusion:** These results indicated that number of cluster per plant has higher sensitivity than the other main yield components in different environments.

## 1. INTRODUCTION

Grapevine (*Vitis vinifera* L.) is one of the most important horticultural crops in the world and Iran. According to the reports of FAO (2009), grapevine cultivated area was 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 (FAO, 2009). Main yield components have the most importance in many plant breeding research programs. Grapevine breeders' aim is to increase the 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 which one of the main yield components has the most genetic contribution in complicated yield trait. A complicated or complex trait such as yield, can be define as trait which its variations are identified by variations of its components (Farshadfar, 1999). 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 less efficient in fruit trees because access to new generations requires several

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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 are used in different environmental conditions. According to these researchers, yield of plants is a complex trait which its components have developed during plant growth period. Therefore different environmental factors will have different effects on these traits.

In this article, path analysis and genetic contribution of grapevine main yield components were identified on the basis of developmental growth components in different environmental conditions.

## 2. 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 blocks 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 in different environment was done and genetic contribution of yield components in final yield were identified. In this model, firstly, it is assumed that growth chronologically of main yield components are in this way that the number of clusters per plant (X), the number of berry per cluster (Y) the berry weight (Z) and yield (W) that obtain by multiplying of these components ( $W = X \times Y \times Z$ ). Secondly it is assumed that environmental resources can be divided into three independent components such as R1, R2 and R3 that each group is stimulating the growth of other traits in growth period and then path diagram was drawn on the basis of this concept.

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

$$\rho_{xy} = a_1$$

$$\rho_{xz} = a_2 + a_1 a_3$$

$$\rho_{yz} = a_3 + a_1 a_2$$

$$\rho_{xw} = a_4 + a_1 a_5 + a_2 a_6 + a_1 a_3 a_6$$

$$\rho_{yw} = a_5 + a_1 a_4 + a_3 a_6 + a_1 a_2 a_6$$

$$\rho_{yz} = a_6 + a_2 a_4 + a_3 a_5 + a_1 a_3 a_4 + a_1 a_2 a_5$$

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

$$A = \Delta^{-1} \rho$$

$$A' = (a_1 \ a_2 \ a_3 \ a_4 \ a_5 \ a_6)$$

$$\rho' = (\rho_{xy} \ \rho_{xz} \ \rho_{yz} \ \rho_{xw} \ \rho_{yw} \ \rho_{zw})$$

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

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

$$U_1 = \pm 1$$

$$U_2 = \pm (1 - a_1^2)^{0.5}$$

$$U_3 = \pm (1 - a_2 \rho_{xy} - a_3 \rho_{yz})^{0.5}$$

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:

$$V_1' = U_1 (a_4 + a_1 a_5 + a_2 a_6 + a_1 a_3 a_6) = U_1 \rho_{xw}$$

$$V_2' = U_2 (a_3 a_6 + a_5)$$

$$V_3' = U_3 a_6$$

Yield of  $i^{\text{th}}$  genotype can be obtained by the following formula in  $j^{\text{th}}$  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  $\sigma_{wi}^2$  is the yield variance of  $i^{\text{th}}$  genotype. Also this formula is a mathematical model for the observed yield ( $W_{ij}$ ). This model includes genotypic mean effect ( $\mu_{wi}$ ), three multiplicative components of interactions 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  $\sigma^2(Y) = \sum C_i$  (Tai, 1975, Tai, 1979, Tai et al., 1994 and Huhn, 1979).

## 3. RESULT AND DISCUSSION

Results of compound variance analysis of yield and its main components in three different environments had been presented in Table 1. Also, genetic components and heritability of yield and its main components had been indicated in Table 2. Effects of genotype, environment and their interactions were significant 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 complicated nature and high effects of environment on this factor. In other words, the number

of genes controlling this trait is higher and the contribution of each gene to control it will be lower. Therefore it has a high environmental impact. Covariance of yield and its main components and values of  $C_i$  had

been estimated in table 3 on the basis 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 (g)	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 at  $\alpha=0.01$

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

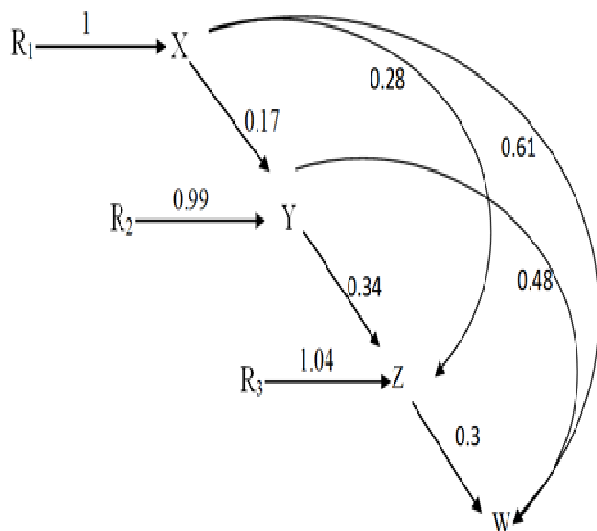
parameters	Number of cluster per plant	Number of berry per cluster	Berry weight (g)	Yield (kg/p)
Coefficient of Variation (%)	9.5	15.8	8.4	11.2
Phenotypic variance	343.46	1901.24	0.99	35.35
Genotypic variance	212.56	1152.74	0.92	17.89
Environmental variance	130.90	748.50	0.07	17.46
Variance of				
Genotype × Environment	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
Uzbekistan 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 ez dangara	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 (Table 3). Positive and high value of  $C_1$  represented the fact that genetic contribution of number of clusters per plant has the higher impact on increase of final yield than the other components. Also, variations of yield in different environments and interaction between yield and environment were most affected by this trait in all grapevine genotypes but Gezgiski Ramfi, Muscat and Ukranski Ramfi (Table 3). Negative values of  $C_i$  in number of berry per cluster and mean weight of berry in some genotypes indicated the lower genetics contribution 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  $V_3$ ) indicated that  $V_3$  and  $V_2$  values were higher than  $V_1$  values (Table 3). Also, difference between  $V_3$  and  $V_2$  values was very low. On the other word, number of clusters per plant was earlier than other yield components in grapevine. 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 also proved by lower percentage of variation coefficients of these genotypes (table 2). Genotypes Aligoneh and Bobili Magaracha will have more stable yield than other genotypes because of the lower genotypic components values and percentage of variation coefficients in different environments (table 3) (Farshadfar, 2010). Estimating of three environmental components of interactions  $r_1$ ,  $r_2$  and  $r_3$  had been shown in table 4. Environmental components of interactions were indicated that absolute value of  $r_1$  was higher than  $r_2$  and  $r_3$  in all environments. This indicated that number of cluster per plant had the highest sensitivity in different environments. Drastic environmental changes will have more different impact on this trait. Effects of environmental variations on berry weight was low and therefore this trait had less sensitivity to the environmental changes (table 4).

**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

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 to temperature index in potato yield components and concluded that environmental component  $r_4$  was higher than the others. Farshadfar (1999) reported that, 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 findings of the present study, because the first multiplicative component of yield had the highest genetic contribution in final yield.

Phenotypic stability of bread wheat was investigated by using path analysis method in drought stress and complete irrigation by Farshadfar *et al.* (2012). They concluded that genetic contribution of thousand seed weight in yield stability of genotypes was more than other yield components. Results of this research was not similar to findings of present research because of the

higher genetic contribution of second multiplicative component of final yield. Therefore it can be concluded that the genetic 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 genetic 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 their 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 significant positive correlation with yield, but number of cluster per plant had significant negative correlation with number of berry per cluster and berry weight. This method is not able to determine the genetic contribution of main yield components in yield variance and also will not show sensitivity of main yield components in different environmental conditions. While the present study, provided the data of three different environment about genetic contribution which determine the main yield components in yield variance that is the strong point of this research. 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 (Farshadfar, 2010).

## CONCLUSION

This research indicated that number of cluster per plant had the highest genetic contribution, variations and sensitivity in final yield in different environmental conditions. Therefore number of cluster per plant will have more importance than other yield components in selection of high yield grapevine genotypes in ideal environments. Also number of berry per cluster and berry weight will have more importance in selection of grapevine genotypes with higher stable yield indifferent 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 which is under study shows great flexibility in the yield structure, it may increase one component with decrease in another component which indicates the negative covariance among yield components. Therefore the component that has more variation (high variance) but it can be compensated 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 the advantages of logarithmic method is the independence of variance and covariance with

measurement units. Therefore variance of different traits will be comparable with different measurement units.

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