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ESTIMATION OF HERITABILITY AND CORRELATION ANALYSIS FOR SEEDLING TRAITS IN VARIOUS ACCESSIONS OF TOMATO

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Abstract

The research work pertaining to the estimation of genetic variability parameters, heritability and correlations for various seedling traits in 50 tomato genotypes (35 local, 15 exotic) was carried over during October-November, 2004. Nursery beds were prepared under plastic tunnels with RCB design replicated thrice. After thirty five days of sowing, ten seedlings were selected at random and data related to seedling traits viz., root length (cm), shoot length (cm), primary leaf length (cm), fresh root weight (g), dry root weight (g) fresh shoot weight (g), dry shoot weight (g), plant length (cm) and leaf area (cm²) were taken. It was found that considerable genotypic variations existed between the genotypes for almost all seedling characters. High habitability estimated for shoot length and plant length coupled with highest genetic advance suggested a potential for genetic improvement through breeding and selection. Correlation analysis indicated that all the seedling traits (except fresh root weight and dry root weight) had positive correlations with each other and hence indirect selection would be effective for the improvement of present germplasm collection.

INTRODUCTION

Vegetables are a rich source of valuable nutrients especially vitamins and minerals besides medical attributes. The vegetable production may be expended by increasing area under their cultivation, improving production technologies and most importantly by cultivation of high yielding varieties (hybrids). Therefore, the major emphasis needs to be given to research and development in vegetable breeding. Tomato is one of the most important vegetables grown throughout the world. The leading tomato growing countries in the world are USA, China and India (FAO, 2004). In Pakistan, it is 3rd most important vegetable after onion and potato. Tomato production in the country is not increasing at an appropriate rate since the last five years and causing price escalation in the market especially during the summer months.

Although extensive research work has been carried over on the estimation of heritability and correlation among yield related characters in tomato but information on the seedling traits were limited. However following considerations should be given importance. High estimates of broad-sense heritability for all seedling traits is helpful in order to find out the selection indices in a random mating population of sunflower for seedling traits (Ajma, 1989; Naeem, 1989). High expected genetic advance for seedling traits could be used as selection criteria for comparing germplasm at seedling stage (Mehdi and Ahsan, 2000a). In potato, tuber yield depends on shoot height, shoot number and leaflet index (Sandhu and Kang, 1998). At early stage of selection, it is useful to exploit positive association between fruit yield, shoot length and vigour index based on dry matter accumulation in tomato (Subburamu et al., 1998). Under controlled environmental conditions, the inheritance and interrelationship of seedling vigour and fruit yield may not be ignored for heterosis breeding programmes (Vieira et al., 1995). Under simulated soil moisture stress conditions, the association between yield and other seedling traits (leaf area, root length, root dry weight, shoot dry weight and root shoot ratio) can be useful as indirect selection criteria and leaf area was the major factor directly contributing to fruit yield under drought stress (Natarajan, 1992). High correlation that selection for seedling traits may improve the performance of germplasm (Asim, 1989).

The present study is a scientific attempt to understand the genetic behavior and response of different genotypes of tomato at seedling stage based on the conclusions made by above scientists. The information so gained will be useful in formulating selection criteria for adoptability of exotic accessions.

MATERIALS AND METHOD

The growth media containing upper layer of soil, sand and leaf compost (in 1:1:1 ratio) along with 400 g NPK (17:17:17) was used for nursery preparation. The size of nursery bed was kept 90 x 300 x 15 cm and it was divided into three small beds representing three replications. Borders and surrounding of nursery was dusted with Coopex \mathbb{R} (having permethrin as an active ingredient) to avoid the seed loss from creeping insects especially ants.

After nursery bed preparation, 15 seeds from each genotype (total = 50 genotypes) for each replication were treated with Confidor® (fungicide) and sown at 5 cm apart and 2 cm deep. The seedlings were uprooted after 35 days of sowing with hand after application of irrigation to soften the seedbed. The seedlings were gently shaken to shed off the sand and were washed in a tub of water, taking care that not to damage the seedlings roots. Ten seedlings per line were taken randomly from each replication and brought to laboratory in Kraft paper bags for data recording. Data was recorded for seedling traits viz., root length (cm), shoot length (cm), primary leaf length (cm), fresh root weight (g), dry root weight (g) fresh shoot weight (g), dry shoot weight (g), plant length (cm) and leaf area (cm²).

The data recorded related to seedling traits were subjected to analysis of variance techniques (Steel and Torrie, 1984). Heritability in broadsense was estimated according to the technique of Burton and De Vane (1953). Genetic advance was calculated at 20% selection intensity (i=1.4) using formula given by Poehlman & Sleeper (1995). All possible correlations (genotypic and phenotypic) were computed following the statistical technique prescribed by Kowon & Torrie (1964). Genotypic correlation coefficients were tasted against the double value of standard error of genotypic correlation following the method of Lotherop et al. (1985). Statistical significance of phenotypic correlation was determined by t-test as described by Steel and Torrie (1984).

RESULTS AND DISCUSSION

The analysis for variance revealed that considerable variation existed in 50 genotypes for all seedling traits studied (Table 1). Heritability is used for predicting the progress from selection. Broadsence heritability indicates the ratio of total genetic variance to the total phenotypic variance where as in narrowsense, heritability is the ratio of additive genetic variance to the phenotypic variance. Higher estimates of genetic advance indicate that the character is governed by additive genes and genetic variance is fixable and selection would be useful for the improvement of traits (Singh and Narayanan, 2000).

It is obvious from the Table 1 that all the traits exhibited higher values for broad sense heritability (Heritability more than 0.5 or 50%). As the broad sense heritability is higher (ranging from 0.762 to 0.970), it indicated that the characters were less influenced by the environmental factors.

Genetic advance is the expected genetic gain in one cycle of selection (Poehlman and Sleeper, 1995). The highest value for genetic advance was observed for plant length (3.616 cm) followed by shoot length (3.396 cm) while it was minimum for dry root weight (0.011 g). The higher value of genetic advance for plant and shoot length indicated that these characters are governed by additive genes and selection may be effective for these traits (Singh and Narayanan, 2000). High heritability estimated for shoot length and plant length coupled with highest genetic advance for shoot length and plant length revealed the presence of additive gene effects (Singh and Narayanan, 2000). Assuming the predominance of additive gene effects, the characters are fixable and selection should be practiced on the basis of shoot length and plant length in the present germplasm collection. Similar findings have been reported by Naeem (1989), Loresto and Chang (1994). Results are opposite to the findings of Mehdi and Ahsan (2000a) who reported moderate broad sense heritability for fresh shoot length, fresh shoot weight, dry root weight and root length.

In the present study, the genotypic and phenotypic correlations were also estimated for various seedling traits of 50 accessions of tomato, belonging to three species. From these correlations at the seedling stage, it is logical to predict that the yield of rapidly growing plants, with greater root and shoot growth, would be more than those of slowly growing plants. Therefore, these correlation coefficient estimates may be used for indirect selection at seedling stages for yield and yield contributing traits. The estimates of phenotypic and genotypic correlation coefficient among seedling traits of 50 genotypes of tomato are given in the Table 2.

Genotypic and phenotypic correlations for all the characters were positively and highly significant indicating the scope for need of indirect selection (if desirable and feasible) except between fresh root weight and dry root weight. Sandhu and Kang (1998), Subburamu et al. (1998) also reported that yield was significantly and positively correlated to shoot length. Similarly, Natarajan (1992) revealed that yield was positively and significantly correlated with leaf area, root length, dry root weight in tomato. Vieira et al. (1995) and Asim (1989) also reported similar findings.

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Table 1:	Components of variance, heritability and genetic advance estimates for seedling
	traits

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	Replication	Genotype	Error Mean Square	h ²	G.A.
Traits	Mean Square	Mean Square	(d.f. = 98)	(B.S.)	
	(d.f. = 2)	(d.f. = 49)			
Root length (cm)	0.0227 n.s	2.5007**	0.4251	0.8300	1.0609
Shoot length (cm)	13.0506 n.s	26.2970**	4.7514	0.8193	3.3960
Primary leaf length (cm)	0.1301 n.s	0.4910**	0.0626	0.8723	0.4936
Primary leaf width (cm)	0.0029 n.s	0.1571**	0.0136	0.9137	0.2928
Fresh root weight (g)	0.0003 n.s	0.0062**	0.0002	0.9607	0.0617
Dry root weight (g)	0.00005*	0.0002**	0.0000	0.9545	0.0116
Fresh shoot weight (g)	0.0228 n.s	1.2603**	0.434	0.9655	0.8761
Dry shoot weight (g)	0.0001 n.s	0.0252**	0.0004	0.9856	0.1266
Plant length (cm)	7.5181 n.s	34.3814**	8.1500	0.7629	3.6160
Leaf area (cm ²)	0.2373*	1.8476**	0.0600	0.9675	1.0630

* = Significant at 0.05 probability level

** = Significant at 0.01 probability level

n.s = non-significant

Table 2:	Genc	Genotypic (rg) and ph	nd phenotyic cor	enotyic correlation coefficients (rp) for all seedling traits	ients (rp) for a	Il seedling traits				
Traits	(r)	Shoot	Primary leaf	Primary leaf	Fresh root	Dry root	Fresh shoot	Dry shoot	Plant	Leaf
		length	length		weight	weight (g)	weight	weight	length	area
		(cm)	(cm)	(cm)	(g)		(g)	(g)	(cm)	(cm^2)
Root length	r(g)	0.370*	0.198n.s	0.205n.s	0.119n.s	0.224*	0.326^{*}	$0.23\mathrm{ln.s}$	0.653*	0.241n.s
(cm)	r(p)	0.355**	0.206^{*}	0.204^{*}	0.105n.s	0.198*	0.293**	0.216^{*}	0.578^{**}	0.216*
Shoot length	r(g)	1	0.602^{*}	0.485*	0.448^{*}	0.458*	0.768*	0.705*	0.976*	0.574^{*}
(cm)	r(p)	1	0.541^{**}	0.442**	0.408^{**}	0.417^{**}	0.683^{**}	0.648^{**}	0.900^{**}	0.537**
Primary leaf	r(g)		1	0.752*	0.542*	0.425*	0.629*	0.492*	0.615*	0.898*
length (cm)	r(p)		1	0.713^{**}	0.502**	0.383^{**}	0.575**	0.453**	0.529^{**}	0.841^{**}
Primary leaf	r(g)			1	0.178*	0.472*	0.576*	0.511*	0.498*	0.865*
width (cm)	r(p)			1	0.172n.s	0.439**	0.535**	0.491^{**}	0.441^{**}	0.825**
Fresh root	r(g)				1	-0.215n.s	0.428*	0.333*	0.450*	0.430^{*}
weight (g)	r(p)				1	-0.207*	0.418^{**}	0.326^{**}	0.384^{**}	0.419**
Dry root	r(g)					1	0.634^{*}	0.499*	0.495*	0.469*
weight (g)	r(p)					1	0.607**	0.488^{**}	0.418^{**}	0.451**
Fresh shoot	r(g)						1	0.745*	0.762^{*}	0.613*
weight (g)	r(p)						1	0.726^{**}	0.675**	0.592^{**}
Dry shoot	r(g)							1	0.710*	0.541^{*}
weight (g)	r(p)							1	0.624^{**}	0.530^{**}
Plant length	r(g)								1	0.591*
(cm)	R(p)								1	0.528**
* = Significant										

* = Significant
** = Highly significant
n.s. =Non-significant
r (g) = Genotypic correlation
r (p) = Phenotypic correlation

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