

## Correlations and Heritability of Waterlogging Tolerance Traits in Cucumber (*Cucumis sativus* L.)

<sup>1,3</sup>Martin Agyei Yeboah, <sup>2</sup>Chen Xuehao, <sup>2</sup>Cheng Rong Feng, <sup>1</sup>Guohua Liang and <sup>1</sup>Minghong Gu

<sup>1</sup>The Key Laboratory of Plant Functional Genomics of the Ministry of Education,  
Yangzhou University, 12 East Wenhui Road, Yangzhou, Jiangsu 225009, P.R. China

<sup>2</sup>School of Horticulture and Plant Protection, Yangzhou University, Jiangsu 225009, P.R. China

<sup>3</sup>Savanna Agricultural Research Institute (SARI), P.O. Box 52, Tamale, Ghana

**Abstract:** Waterlogging is one of the most important environmental stresses that severely limit crop growth and productivity. Development of tolerant cultivars is one of most cost efficient and environmentally safe method of control. The objectives of this study, was to estimate narrow-sense heritabilities of waterlogging traits and to determine phenotypic and genetic correlations between these traits in F<sub>3</sub> progeny derived from a cross between PW0801 (susceptible) and PW0832 (tolerant) cucumber inbred lines in a green house experiment. Plants were subjected to 10 days waterlogging stress and evaluated for four waterlogging traits, Tolerance score (TOL), Adventitious Root Formation (ARF), Shoot Dry Weight (SDW) and Vine Length (VLH), however control plants were not flooded. The frequency distribution of F<sub>3</sub> families for all the waterlogged traits showed continuous distributions. Some individual plants in the F<sub>3</sub> families had values higher or lower than the parental means suggesting transgressive segregation. Significant genetic correlation coefficient of 0.372, 0.334 and 0.276 were estimated between TOL and SDWw, TOL and ARF and between ARF and VLHw, respectively. Both genetic (0.181) and phenotypic (0.051) correlation coefficients between TOL and VLHw were not significant at p = 0.05. The narrow sense-heritability was 26.0% for TOL, 22.6% for SDWw, 18.0% for VLHw and 12.7% for ARF. From these results, breeding schemes that would allow for higher recombination rates could be effective for the desired tolerance.

**Key words:** Waterlogging, F<sub>3</sub> families, phenotypic and genotypic correlations, narrow-sense heritability

### INTRODUCTION

Waterlogging is one of the most important environmental stresses that severely limit crop growth and productivity. It has been a major risk for cucumber production in China especially along the Yangtze River basin where low lying areas are often prone to flooding during periods of high rainfall (Jiang *et al.*, 2000). Availability of cultivars tolerant to waterlogging could be one of the promising control strategies. However, breeding of crops with higher yields and flood tolerance has been an important objectives for decades, but the experience gained so far has been that it is extremely complex to breed for flood tolerant phenotypes because flooding appears to be controlled by several different abiotic and biotic factors (Sangeeta and Anil, 2006).

Heritability estimates was first used by breeders to predict the effectiveness of artificial selection for particular traits in a given population under specified

conditions (Lush, 1937). Since then predictions of response to selection for the expression of traits has been achieved in early generations (Stoltenberg, 1997). Secondly, heritability also informs us about the proportion of genetic variance present in the total phenotypic variance, which is also an indicator of the confidence towards selection in breeding program. However, estimates of the proportion of the total phenotypic variance that is attributable to the total genetic variance and the environmental genetic variance is important for the improvement of quantitative traits. If a large portion of the variance is genetic, then gains could be made by the selection of high valued individuals in the population. On the other hand, if the genetic variance is low, implying high environmental variance, success could only be obtained by optimizing the environmental conditions under which the population will be cultivated. Models have been developed to enable the predictions of F<sub>3</sub> genotypic mean and variance of a cross between two

inbred lines (Mather and Jinks, 1971). With these predictions, the ability of the cross to produce superior inbred lines can be estimated (Jinks and Pooni, 1976). Oijen (1989) proposed two methods to estimate the additive genotypic variance from an  $F_3$  cross between two inbred lines. One method he proposed is to estimate the genotypic between line variance and the genotypic within line variance which estimate both additive and dominance variances. The second method he proposed is to estimate only the between line variance to estimate the additive variance. In this case the estimator of the genotypic variance is twice as the between  $F_3$  line genotypic variance. The advantage of the latter is that there is no need to estimate the residual variance and is more accurate when dominance is absent.

Various studies have shown considerable genetic variability for waterlogging tolerance in several crops such as rice (Toojinda *et al.*, 2003), teosinte (Mano *et al.*, 2005), wheat (Boru *et al.*, 2001) and soybean (Toai *et al.*, 2001) the genetic variability of waterlogging tolerance in cucumber is still rarely studied. The amount of genetic variance between and within segregating populations and the generation in which selection is practiced is important for optimizing selection in breeding. Also, for the successful selection and evaluation of large number of cucumber lines for waterlogging tolerance in breeding to be established, phenotypical and morphological traits showing direct correlations with high waterlogging tolerance are desired for effective and reliable screening. Also, since breeders are interested in improving several attributes of a phenotype simultaneously, previous knowledge about genetic correlations among different traits could enhance indirect selection of one trait based on the selection of the other (Johnson *et al.*, 1955). Although both the environmental and genetic correlations are important to breeders because they collectively determine selection efficiency, little could be done about the environmental correlation, except noting their direction to minimize or exploit them as the situation demands (Kearsey and Pooni, 1996).

The objectives of this study, was to estimate phenotypic and genotypic correlations and narrow-sense heritability of traits associated with waterlogging tolerance in cucumber in the  $F_3$  families in a green house experiment. The main goal of this study, was to provide some understanding of the genetics of waterlogging tolerance of cucumber for the efficient selection at the early growth stages of development.

## **MATERIALS AND METHODS**

**Plant materials:** Two cucumber inbred lines, PW0832 ( $P_1$ ) as female parent and PW0801 ( $P_2$ ) as male parent were used in this study. PW0832 is tolerant to waterlogging

while PW0801 is susceptible. The two lines were obtained from the School of Horticulture, Yangzhou University, China based on wide variation in their abilities to tolerate flooding (Li, 2007). The two parents were crossed to produce  $F_1$  ( $P_1 \times P_2$ ) in the green house between April and July of 2005. A single  $F_1$  plant from this initial mating was self-pollinated to generate 144  $F_2$  individuals, which were subsequently selfed to produce 114  $F_3$  families. Seeds of  $P_1$ ,  $P_2$ ,  $F_1$  and the  $F_3$  families were soaked overnight in water and wrapped in damp cheese cloth for 48 h until sprouting. Seed flats with 72 cells were filled with BM2-commercial germinating soil mixture composed of 70-80% Canadian sphagnum peat moss, 10-15% perlite and 10-15% vermiculite (Berger Tourbieres Peat Moss). One seed per cell was sowed on the 13th September, 2006; the media were moistened and covered with white polythene sheets until germination. At two weeks after sowing, (2 leafed stage seedlings)  $P_1$ ,  $P_2$ ,  $F_1$  and  $F_3$  seedlings were transplanted into polythene pots (15×10×12 cm) filled with sterilized sifted humus soil mixed with 1% organic manure.

### **Waterlogging treatment and determination of tolerance:**

Plants were subjected to waterlogging at 4 weeks old in cement tanks filled with water in a plastic green house. Potted plants were inundated until water level reached 3 cm above soil surface in the pots and left for 10 days before drainage. The control treatment was accomplished by watering plants as required to maintain vigorous growth.

One week after removing waterlogged treatment, individual plants were visually scored for Tolerance (TOL) using an index of 0-5 where 0 = dead plants, 1 = 100-75% of wilt from base to the apex, 2 = 74-50% wilting of leaves from base to midvine, 3 = leaves between base and midvine undulating and recurved, 4 = recurved leaf margins, 5 = green plant with no sign of stress, modified from Navazio and Staub (1994). The higher scale stood for tolerance while the lower scale stood for susceptibility. Adventitious Root Formation (ARF) was also scored visually with 0-3 scale where 0 = none, 1 = low, 2 = medium and 3 = high (Fig. 1), modified from Mano *et al.* (2005). Finally, Vine Length (VLH) and Shoot Dry Weights (SDW) were measured in all the surviving plants 2 weeks after waterlogging stress was removed. Shoots were oven-dried at 65°C for 3 days to estimate Shoot Dry Weights (SDW).

**Experimental design and statistical analysis:** The experiment was performed at the Research Farm of Department of Horticulture of Yangzhou University, Yangzhou, China from 16th September to 10th November, in 2006. The experiment was conducted in a Randomized Complete Block (RCB) design with 6 replications

consisting of factorial combinations of treatments (control, waterlogged) and generations ( $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ). In each block, the experimental units consisted of two plots each (one for each treatment) of 5 individual plants of each non-segregating generation ( $P_1$ ,  $P_2$  and  $F_1$ ) and 114  $F_2$  plants (one plant represents each of the 114  $F_2$  families), such that there were 8 plots with 258 plants in each of the 6 blocks.

Statistical analyses were performed using SAS systems for Microsoft Windows, version 9.1 (SAS Institute, 2002). Since the number of plants for the generations were different, PROC MIXED covtest procedure of SAS was employed to test least square means (lsmeans) comparisons among generations with generation as fixed effect while block and block x generation were random effects. Graphs for the frequency distributions of traits were constructed by means of SigmaPlot for window version 10 (Systat Software, 2006).

Analysis variance of  $F_2$  families was done (Table 1) to test the differences between  $F_2$  families. After detecting significance between families, the variance of the  $F_2$  family mean ( $\delta_a^2$ ) and the average variance within  $F_2$  families ( $\delta_w^2$ ) were derived from the ANOVA Table 2 as follows:  $\delta_a^2 = (MS_B - MS_W)/r$  and  $\delta_w^2 = MS_W$ , where  $MS_B$  = between families mean square and  $MS_W$  = within families mean square and  $r$  = family size (six in this study). The estimates of  $V_A^*$  and  $V_E$  and narrow sense heritability ( $h^2$ ) as  $V_A^* =$

$\delta_a^2$ ,  $V_E = \delta_w^2 - 1/2 V_A^*$  and  $h^2 = V_A^* / (V_A^* + V_E)$ , respectively. Where  $V_A^*$  = additive genetic variance,  $V_E$  = environmental variance (Hallauer and Miranda, 1981; Kearsey and Pooni, 1996; Van Ooijen, 1989).

Phenotypic and genotypic correlation coefficients and their standard errors were estimated by the multivariate Restricted Maximum Likelihood (REML) method with SAS Proc Mixed procedure as described by Holland (2006). Replication was considered fixed effect while family was random effect. The multivariate REML was performed to estimate the variance and covariance components matrix by using the Proc Mixed "asycov" option of SAS to obtain the asymptotic variance and covariance matrix of the estimates. After these estimates, the Proc IML, also of SAS, was employed to read the variance and covariance to estimate the correlations and their standard errors.

Table 1: Expected values of Mean Square (EMS) in the Analyses of Variance (ANOVA) of 114  $F_2$  families for waterlogging tolerance traits of cucumber grown in pot experiment at Yangzhou, China

Source	df	MS <sub>e</sub>	EMS <sup>1</sup>
Replications	r-1	$M_B$	-
Between $F_2$ families	n-1	$MS_B$	$\delta_a^2 + k \delta_w^2$
Within $F_2$ families	nr(r-1)	$MS_W$	$\delta_w^2$

r = Number of replication (6 in this study); n = Number of families (114), k = Family size, <sup>1</sup>MS<sub>e</sub> = Mean Square for replication; MS<sub>B</sub> = Between families Mean Square; MS<sub>W</sub> = Between families Mean Square,  $\delta_a^2$  = Residual variance component;  $\delta_w^2$  = Between  $F_2$  variance component



Fig. 1: Variations among flooded  $F_2$  progeny in Adventitious Root Formation (ARF) after 10 days flooding. Numbers 0, 1, 2 and 3 are the score ratings

Table 2: Generation least square means (lsmeans) and standard errors of water logging tolerance traits for cucumber (*Cucumis sativus* L.) tolerant parents PW0832 ( $P_1$ ) and susceptible parent PW0801 ( $P_2$ ) and offspring generations ( $F_1$  and  $F_2$ ) in greenhouse at Yangzhou, China

Generation	TOL	ARF	$n_{w_1}$	SDWw (g)	SDWc (g)	VLHw (cm)	VLHc (cm)	$n_{w_2}$	$n_c$
$P_1$	3.47±0.29a	2.13±0.07a	30	2.42±0.14a	5.90±0.28a	55.46±2.1b	101.32±3.2a	22	30
$P_2$	2.52±0.36b	0.91±0.07c	30	1.97±0.13b	4.57±0.15b	70.36±1.2a	103.94±3.1a	18	30
$F_1$	2.64±0.34b	1.08±0.07bc	30	2.07±0.14b	4.54±0.31b	52.08±2.1b	95.99±3.1b	25	30
$F_2$	2.71±0.38b	1.24±0.08b	684	2.17±0.16b	4.44±0.38b	49.89±2.3b	98.28±3.9ba	462	684

<sup>1</sup>TOL (Tolerance rating) = 0 (dead plant)-5 (green plant with no sign of stress). ARF (Adventitious Root Formation) = 1 (none)-3 (high), SDWw (waterlogged Shoot Dry Weight), SDWc (control Shoot Dry Weight) VLHw (waterlogged Vine Length), VLHc (control Vine Length). Means within trait followed by the same letter are not significantly different at  $p \leq 0.01$ .  $n_{w_1}$  = Sample size for TOL and ARF waterlogged traits,  $n_{w_2}$  = Sample size for VLHw and SDWw,  $n_c$  = Sample size for control (unflooded)

**RESULTS**

**Means among F<sub>3</sub> lines:** The frequency distribution of F<sub>3</sub> families for all the traits is presented in Fig. 2, which showed that the distributions of all the waterlogged traits were continuous confirming that they are quantitatively inherited. It also showed the extent of segregation in the F<sub>3</sub> families under waterlogged stress. The F<sub>1</sub> mean values were intermediate between the two parents for Tolerance score (TOL), Adventitious Root Formation (ARF) and Shoot Dry Weight (SDWw) but lower than the two parents in Vine Length (VLHw). However, some individuals had values higher or lower than the parental means; this suggests transgressive segregation in the cross used in this study (Fig. 2).

The generation least square means in Table 2 indicates that the two parents exhibited different responses in all the waterlogging traits with significant differences between them in all the traits. Significant difference also occurred between P<sub>1</sub> and F<sub>3</sub> in TOL, ARF and SDWw. However, difference between P<sub>1</sub> and F<sub>3</sub> in VLHw was not significant.

**Phenotypic and genotypic correlation among waterlogging traits:**

Phenotypic and genotypic correlations coefficients and their standard errors among waterlogging traits are presented in Table 3. Generally, the phenotypic and genetic correlation coefficients among waterlogged traits were low and positive ranging from 0.051-0.381 and 0.181-0.457 for phenotypic and genetic correlations, respectively. SDWw and VLHw had significantly positive phenotypic (0.381, p<0.01) and genetic (0.457, p<0.01) correlation coefficients. Also highly significant (p<0.01) genetic correlation coefficient of 0.372, 0.334 and 0.276 were estimated between TOL and SDWw, TOL and ARF and between ARF and VLHw, respectively. Both genetic (0.181) and phenotypic (0.051) correlation coefficients between TOL and VLHw were not significant at p = 0.05. Generally, the genetic correlation coefficients values were higher than their corresponding phenotypic values.

**Estimates of variances and narrow-sense heritability:**

Variance component estimates of waterlogged treatment varied greatly across traits (Table 4). The magnitudes of

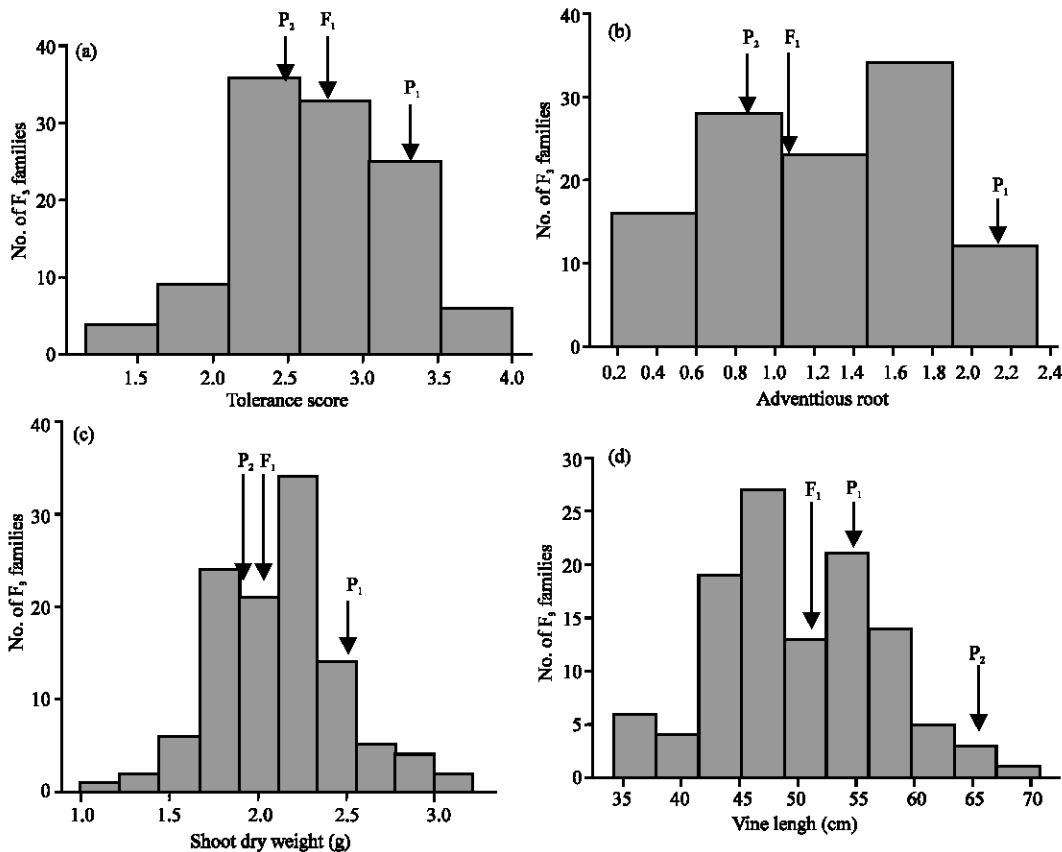


Fig. 2: The distribution patterns of two cucumber (*Cucumis sativus* L.) parents and progenies from the cross PW0832×PW0801 for waterlogging tolerance in 114 F<sub>3</sub> families in a green house experiment in 2006

Table 3: Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients with standard errors between waterlogging traits in 114 F<sub>3</sub> Cucumber (*Cucumis sativus* L.) families derived from a cross between tolerant parent PW0832 (P<sub>1</sub>) and susceptible parent PW0801 (P<sub>2</sub>) in greenhouse at Yangzhou, China, 2006

Trait <sup>1</sup>	TOL	ARF	SDWw (g)	VLHw (cm)
TOL	-	0.131±0.037ns	0.182±0.046ns	0.051±0.046ns
ARF	0.334**±0.129	-	0.082±0.038ns	0.076±0.002ns
SDWw	0.372**±0.123	0.184±0.119ns	-	0.381**±0.023
VLHw	0.181±0.129ns	0.276**±0.119	0.457**±0.094	-

<sup>1</sup>TOL (Tolerance rating) = 0 (dead plant)-5 (green plant with no sign of stress). ARF (Adventitious Root Formation) = 0 (none, susceptible)-3 (high, tolerant), SDWw (waterlogged shoot dry weight), VLHw (waterlogged vine length), \*\* = Significance at p<0.01, ns = not significant at p = 0.05

Table 4: Additive genetic (V<sub>A</sub><sup>\*</sup>), environmental (V<sub>E</sub>) variance components and narrow-sense heritabilities (h<sup>2</sup>) for waterlogging traits of F<sub>3</sub> families of cucumber (*Cucumis sativus* L.) cross between tolerant parent PW0832 (P<sub>1</sub>) and susceptible parent PW0801 (P<sub>2</sub>) in greenhouse at Yangzhou, China, 2006

Genetic parameter	Traits <sup>1</sup>					
	TOL	ARF	SDWw (g)	SDWc (g)	VLHw (cm)	VLHc (cm)
V <sub>E</sub>	0.687	0.829	0.294	0.896	132.71	338.78
V <sub>A</sub> <sup>*</sup>	0.239	0.121	0.086	0.313	29.01	108.68
h <sup>2</sup> (%)	26.0	12.7	22.6	25.8	18.0	24.3

<sup>1</sup>TOL (Tolerance rating) = 0 (dead plant)-5 (green plant with no sign of stress). ARF (Adventitious Root Formation) = 1 (none)-3 (high), SDWw (waterlogged Shoot Dry Weight), SDWc (control Shoot Dry Weight) VLHw (waterlogged Vine Length), VLHc (control Vine Length)

the environmental variance component (V<sub>E</sub>) were generally higher across traits. The estimates of the additive genetic Variance (V<sub>A</sub><sup>\*</sup>) for the waterlogged treatment were positive. Narrow sense-heritabilities were generally low (28-12%) for all traits in the F<sub>3</sub> family. The narrow sense heritabilities were 26.0% for TOL, 22.6% for SDWw, 18.0% for VLHw and the least value of 12.7% for ARF. Among the control traits, values of 25.8 and 24.6% were estimated for SDWc and VLHc, respectively.

## DISCUSSION

The genetic architecture of waterlogging tolerance in cucumber is poorly understood and this study has attempted to elucidate the underlying genetic effects of some major trait in F<sub>3</sub> families derived from two inbred parents, PW0832 waterlogging tolerant and PW0801 for waterlogging susceptible in a green house experiment.

Comparison among traits in the frequency distribution indicated that the F<sub>1</sub> generation exhibited comparable waterlogging tolerance in most of the traits with mean values generally intermediate between the parental lines. This explains the level of additivity observed in our genetic variance estimation. Transgressive individuals observed in most of the traits are likely due to substantial genetic variations between the parental lines or could be due to complementary positive or negative alleles from both parents. More importantly, because of the relatively high heritability values for both TOL and SDWw in this study, it should be possible to develop varieties with high levels of tolerance by selecting transgressive segregants in this cross. Selection of transgressive segregants via sib-mating of F<sub>3</sub>s' could be employed to develop waterlogged

tolerant varieties with these parents. On the other hand, recurrent selection with the intermating of the superior segregants could also be an alternative breeding technique to increase the frequencies of these favorable alleles.

The narrow-sense heritabilities based on F<sub>3</sub> families ranged from 12-26%. Although these findings may have been affected by the small sample size of F<sub>3</sub> families derived from the cross in this study, our results still proved that selection of the waterlogged tolerance in the early generations could be possible with TOL and SDWw due to their comparatively larger positive additive effects and narrow sense-heritabilities. Generally the low narrow-sense heritabilities of waterlogging traits found in our studies also corroborates with findings by Collaku and Harrison (2005) in their studies on the heritability of waterlogging tolerance in wheat which they attributed to the effects of waterlogging stress.

Our results on phenotypic and genotypic correlations indicate that developing cucumber varieties with high waterlogging tolerance is possible by employing a selection index that could take into accounts simultaneous variations of two traits, with high correlation coefficients. The significantly positive correlation coefficient between TOL and SDWw suggests the ability to sustain shoot dry weight of tolerant cucumber plants under waterlogging stress. This indicates that the selection for high shoot dry weight with relatively high heritability, under waterlogged conditions will automatically increase tolerance to waterlogging in cucumber. However, significant correlations between TOL and ARF and also between VLHw and SDWw were also high. Therefore, as it would be more accurate to measure SDWw than both TOL and ARF, the selection for

SDWw in a breeding programme could increase both TOL and VLHw by taking advantage of their significant genetic correlations with SDWw. This assertion is supported by the fact that three-quarter of the loci in each inbred line are fixed and therefore, larger proportion of the genetic variance is expected to be additive (Mokhtari *et al.*, 2002). It is therefore, expected that the estimated genetic correlation between these traits could give a reasonable prediction of response to selection for waterlogging tolerance in this study. The low phenotypic correlation estimated between TOL and VLHw and also between other traits suggests that there is little environmental correlation between these traits.

The low narrow-sense heritabilities of the waterlogging traits indicate that little progress would be made with these traits from a mass selection breeding strategy. For these traits, higher gains in waterlogging tolerance can be achieved if family information is used to improve the individual plant performance (Falconer, 1989). Also, since the efficiency of selection depends on the nature of the genetic system and the extent to which the environmental effect influence their expression (Collaku and Harrison, 2005) therefore, it could be possible to improve waterlogging tolerance of these traits in cucumber with low selection intensities. Breeding schemes that would allow for higher recombination rates could also be effective for the desired tolerance. Therefore, recurrent selection for population improvement could be employed; however lower gain per cycle could be obtained as a result of its lower selection intensities (Hallauer and Miranda, 1981).

### CONCLUSION

It should also be emphasized that waterlogging tolerance seems to be generally influenced by the environment (Kozlowski, 1984; Waters *et al.*, 1991). For this reason, it would be necessary to repeat our experiment in field under different environmental conditions. This should be established at multiple sites and in multiple years within a location were possible so that the variation among years within a location can be estimated. Furthermore, this would confirm if the positive correlation observed between some of the traits in this study is attainable in the field.

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