## A Note on Genotype Variabilities of Mustard under Saline Vertisol

It is estimated that 8000 ha of land are salt affected in Tungabhadra Command Area which is increasing every yar. Screening genotypes for salt tolerance is one of the alternatives suggested for cropping in such soils (Shannon, 1984) and is being intensively persued to tackle the problem of soil salinity, apart from reclaiming them by other means. Most of the salt tolerance data obtained so far have been generally generated by establishing crops in good soil conditions in early growth stages and then imposing salinity. Data thus generated under such conditions become most often unrealistic as most crops are sensitive to salinity at germination. The model proposed by Van Genuchten (1983) is used in the present investigation to screen mustard genotypes on fine textured saline black soil of Tungabhadra Project Area of Karnataka.

Nine mustard genotypes were sown during rabi 1990-91 in black soil with natural salinity gradient which varied from 3.8 to 14.1 dS/m. The genotypes included were local, CS-52, CS-209, CS-395, CS-438, SCN-26, SCN-27, SCN-28 and SCN-29. Soil salinity was estimated genotype wise and blockwise, at 0-15 and 15-30 cm depths, various growth stages like sowing, early germination, flowering and harvest. Time weighted mean salinity was computed for each salinity block and related to their respective yield value using piece-wise linear regression function as suggested by Van Genuchten (1983). The critical soil salinity at which yield begins to decline is henceforth referred as the threshold salinity (EC,) or break point (BP), which was calculated by using the equation

$$EC_{t} = \frac{Y_{o} - Y_{m}}{S_{t}}$$

where  $Y_0 = yield$  at zero salinity in the equation  $Y = Y_0 + S_1 EC_0$ .

Y<sub>m</sub>= yield maximum recorded in the expeirment.

Y<sub>o</sub> is calculated by

$$Y_0 - \overline{Y} - S_1 (\overline{x})$$

Y = Average yield at all levels of salinity.

X = Average salinity of the naturally graded plots.

S, = Yield reduction per unit increase in salinity over the entire range of salinity.

From the calculated EC, value for each genotype, the expected yield (Y exp) levels for all genotypes at fixed salinity intervals were worked out using the relation

All the genotypes included in the investigation received same package of cultivation practices. The genotypes variabilities which are described in terms of yield maxima (Y<sub>m</sub>), threshold salinity (EC<sub>1</sub>), rate of reduction for every unit increase in salinity (slope) and estimated yield are presented in Table. An ideal genotype would be one with higher yield maxima (Y<sub>m</sub>), higher threshold value (EC<sub>1</sub>) and lower slope. But in practice it is difficult to find a genotype combined with all these quantitative characters.

The results revealed that varieties CS-209, CS-52 and SCN-27 in that order were suited for a range of soil salinity. The genotype CS-209, which recorded slightly loweryield maxima than local, ranked first because of higher EC, value, lower slope and betetr performance over a range of salinity levels. The local with highest yield maxima

**Table** Yield maxima  $(Y_m)$ , rate of reduction in yield (S), threshold salinity  $(EC_t)$  and the estimated grain yields of mustard genotypes.

ō		``	٢	2	-	Estim	ated yield	d at fixed	Estimated yield at fixed salinity levels (dS/m)	'Sp) sleve	(E,
S. S.	ad king a	5 m/ 5 m/ row	(dS/m)	ados (g)	٥	4	ထ	σ	6	17	2
			- 1		,		,	,	2	:	-
<del>-</del> :	Control	153.5	1.33	- 0.098	143.52	113.43	83:55	38.12	I	İ	l
ત્યં	CS-52	89.5	4.60	- 0.085	I	1	78.84	56.02	25.59	1	I
က်	CS-209	88.7	9.80	- 0.033	1.	1	1	I	79.33	67.62	55.91
₹	CS-395	9.50	0.12	- 0.067	8.31	7.03	5.75	3.84	ı	1	ı
က်	CS-438	15.5	4.45	- 0.097	1	I	13.16	10.10	2.64	ı	
6.	SCN-26	71.8	4.71	- 0.165	l		56.57	20.97	l	1	I
7.	SCN-27	59.4	6.91	- 0.084	l	l	1	48.97	29.01	9.05	I
œί	SCN-28	34.5	1.28	- 0.074	32.66	27.55	22.44	14.79	4.57	ł	1
တ်	SCN-29	66.5	4.45	- 0.136	1	1	52.46	25.34		l	i

(153.5 g) became less promising when salinity was higher than 4 dS/m. The poor performance of this genotype was attributed to higher rate of reduction (slope) at higher salinities. However, for the soil salinity level ranging from 0 to 8 dS/m, the genotypes local, CS-209 and CS-52 in that order performed well as they recorded higher yields. The genotype CS-395 ranked last amongst all genotypes under trial with very low yield maxima (9.50) and threshold value (0.12 dS/m) despite recording lower slope and was unfit for cultivation. Similarly, CS-438 and SCN-28 also fell into this category. The genotype CS-209 recorded 35.6 per cent higher yield maxima (88.79 g/5m row length) over the average yield maxima (65.43 g/5m row length) of all nine genotypes and was found to be suitable for adverse saline conditions. Therefore, it can be inferred that the genotype CS-209 followed by CS-52 and SCN-27 are suitable for marginally saline to saline soils.

In conclusion, the genotype CS-209 performed well over a wide range of soil salinities followed by CS-52, whereas local was best suited for normal to marginally saline conditions. Thus, there is existence of genetic variation amongst various genotypes in respect of salt tolerance. Genotype local which recorded higher grain yield also suffered at higher salinity, while CS-209 and SCN-27 performed better with lower (slope) rate of reduction in yield at higher salinities. This gave ample evidence of the existance of

genes that were responsible for higher salt tolerance in the latter genotypes compared to local. The incorporation of genes especially of CS-209 into local holds the key for the better performance of the latter (local) under saline conditions or vice-versa. Further, research efforts on genetic improvement through crossing of genotypes having desirable but constrasting character appears to be a priority area for development of genotypes suited to adverse saline conditions.

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