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Assessment of Genetic Variability and Trait Association in Lentil (*Lens culinaris* Medik.) for Yield and Attributing Traits

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ABSTRACT

The present study was conducted at College of Post Graduate Studies in Agricultural Sciences, Meghalaya, India in the *rabi* season (November–April) of 2020–21 to study genetic variability, character association and identify high yielding Al tolerant lentil RILs genotypes suitable for Al toxicity prone acidic soils of Meghalaya. The genotypes were screened through phenotypic evaluation in the field, character association, root morphology studies and determination of root Al content. The pooled variance analysis over two locations revealed highly significant genotype×location interaction for the traits under study except days to maturity, number of primary branches plant^{-1} and number of seeds pod^{-1}, whereas variance due to genotypes was highly significant for all the 10 characters except number of seeds pod^{-1}. Among all the characters, high H_{bs}^2 coupled with high GA percentage were observed in number of primary branches plant^{-1}, plant height and 100 seed weight. Highly positive and highly significant correlation was observed between seed yield plant^{-1} with number of pods plant^{-1} (0.84***), biological yield plant^{-1} (0.79***), number of seeds pod^{-1} (0.47***), number of primary branches plant^{-1} (0.31***) and harvest index (0.31***). From the root morphology analysis, it was observed that high yielding tolerant genotypes constituted of well-established root systems under acidic soil conditions. Based on mean performance of seed yield plant^{-1}, various attributing traits and root morphology studies the best performing genotypes were LRIL-37, LRIL-22, LRIL-96, LRIL-97, LRIL-144, LRIL-92 and LRIL-109. The identified genotypes may be used for further evaluation in multiple environments for final release and also for use in the hybridisation programme.

KEYWORDS: Acidic soils, correlation, genetic variability, lentil, Meghalaya

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1. INTRODUCTION

Lentil (*Lens culinaris* ssp. culinaris), an important cool season legume, is popular both as food and feed attributing to its protein-rich (20.6%–31.4%) seeds and straw (Urbano et al., 2007, Tullu et al., 2011). Genus Lens belongs to the family Fabaceae (Leguminosae) and placed in subfamily Faboideae; tribe Fabeae (Soltis et al., 2011) displays the unique property of biological nitrogen fixation, thus improving soil fertility (Suryapani et al., 2013, Singh et al., 2019). Lentil is a rich source of protein, vitamins, micronutrients, minerals, soluble and insoluble dietary fibres and contain minimum levels of antinutritional factors (Karakoy et al., 2012, Benayad and Aboussaleh, 2021). Lentil is the third most important pulse crop in India after chickpea and arahar. The global production of lentil stands at 6.5 million tonnes in 2020, with Canada being the largest producer contributing a share of 45% while India was the second largest producer of lentil contributing 18% of the world total (Anonymous, 2022). Although, cultivated in 1.32 mha nationally, being highly sensitive to soil acidity, lentil cultivation is mostly restricted to regions with higher soil pH (5.0) (Ryan, 2018). There is immense potential to increase the area under lentil cultivation in Meghalaya attributing to its favourable climatic conditions (Ansari et al., 2015). However, majority of the soils in Meghalaya (2.24 mha) are acidic in nature (Majumdar et al., 2022). Acid soils, characterized by a pH of 5.5 or lower, constitutes approximately 50% of the arable land of the world (Sade et al., 2016). In acidic soils, when pH generally drops below 5, aluminium (Al) the third most abundant metal of earth crust, solubilizes into phytotoxic forms and causes root growth inhibition resulting in reduced vigour and yield in plants (Singh et al., 2016). Thus, Al stress becomes of the prime limitations of crop production in acidic soils (Zheng, 2010). In fact, Al toxicity has been reported in 67% of the world's acidic soils (Lin et al., 2012).

Legumes such as lentil contribute significantly to the human diet, in addition to being an important and cheap source of protein for the poor (Semba et al., 2021). Thus, there arises an increased need to identify new niches for lentil production for increasing food security while parallelly screening and finding new sources for Al stress tolerance in lentil suitable to be grown in Al-rich acidic soils of Meghalaya in order to bring more area under the production of lentil. For designing an effective selection breeding programme, the knowledge of variability estimates is essential to the plant breeders (Meena et al., 2017, Sharma et al., 2022). The utilization of any species in a breeding programme depends upon its genetic diversity and adaptability in different environments (Rai and Jat, 2022). Yield being a complex trait, depends on several yield attributing traits. Knowledge about genetic parameters and correlation between different yield attributing characters is essential while formulating an efficient breeding program (Singh and Srivastava, 2013, Kumar and Solanki, 2014, Jeberson et al., 2015). Studies on root morphology is important as the root system plays a crucial role in nutrient and water uptake and by increasing root surface area and volume gets exposed to a larger amount of soil available nutrients (Tang et al., 2003, Hodge, 2004, Hodge et al., 2009, Aski et al., 2022). Therefore, the current study is designed for screening of a population of lentil RILs developed from parents contrasting for Al tolerance with the objective to screen genetic variability, identify the high yielding aluminium tolerant RILs suitable to be grown in acidic soils and ascertain the agronomical traits useful for selecting desirable lines based on association studies. (Note: Please Check Spacing)

2. MATERIALS AND METHODS

The experiment was conducted using 150 F_6 RILs of lentil, parents viz. BM-4 (Al sensitive) and L-4602 (Al tolerant) and two checks viz. DPL-62 and PDL-1 (Table 1). The field evaluation was executed during the *rabi* (November–April) season of 2020–21 at two locations; in the lowland rice-fallow experimental field of College of Post Graduate Studies in Agricultural Sciences, Meghalaya, India (longitude of 91°54'40", latitude of 25°40'55" and 959 m above msl) and Agro-forestry experimental plot of ICAR for NEHR (25°40'47", latitude of 91°54'39" longitude and 961 m above msl) .The soil properties of the respective experimental sites are presented in Supplementary Table 1. The genotypes were grown in Randomized Block Design (RBD) with three replications following the recommended package of practices in both the locations. Data was recorded on days to 50% flowering (D50F), days to maturity (DM), plant height (PH) (cm), number of primary branches plant^{-1} (NPB), number of pods plant^{-1} (PPP), number of seeds pod^{-1} (SPP), seed yield plant^{-1} (SYP) (g), 100 seed weight (100SW) (g), biological yield plant^{-1} (BYP) (g) and harvest index (HI) (%).

For studying root morphology, the plants were uprooted at podding stage without damaging the roots, washed in running water and observed under Root Scanner (Biovis P200) for recording the root morphology parameters. Oven dried samples of roots were ground into powder form using a grinder and digested using Diacid mixture (3:1 Nitric acid: perchloric acid). Al content in the samples was quantified using Atomic Absorption Spectrophotometer (Model-Elico SL-194).

Pooled data recorded for different agronomic traits were used for estimating ANOVA, PCV, GCV, Genetic Advance, Heritability, and Correlation using MS Excel,

Table 1: List of lentil genotypes used in the present study

Sl. No.	Name of genotype	Source	Sl. No.	Name of genotype	Source	Sl. No.	Name of genotype	Source
1.	BARI MASOOR 4 (BM-4)	Bangladesh Agricultural Research Institute (BARI)	53.	L RIL-49	IARI	105.	L RIL-101	IARI
2.	L-4602	Indian Agricultural Research Institute (L-830×Precoz)	54.	L RIL-50	IARI	106.	L RIL-102	IARI
3.	DPL-62	Indian Agricultural Research Institute (IARI)	55.	L RIL-51	IARI	107.	L RIL-103	IARI
4.	PDL-1	IARI	56.	L RIL-52	IARI	108.	L RIL-104	IARI
5.	L RIL-1	IARI	57.	L RIL-53	IARI	109.	L RIL-105	IARI
6.	L RIL-2	IARI	58.	L RIL-54	IARI	110.	L RIL-106	IARI
7.	L RIL-3	IARI	59.	L RIL-55	IARI	111.	L RIL-107	IARI
8.	L RIL-4	IARI	60.	L RIL-56	IARI	112.	L RIL-108	IARI
9.	L RIL-5	IARI	61.	L RIL-57	IARI	113.	L RIL-109	IARI
10.	L RIL-6	IARI	62.	L RIL-58	IARI	114.	L RIL-110	IARI
11.	L RIL-7	IARI	63.	L RIL-59	IARI	115.	L RIL-111	IARI
12.	L RIL-8	IARI	64.	L RIL-60	IARI	116.	L RIL-112	IARI
13.	L RIL-9	IARI	65.	L RIL-61	IARI	117.	L RIL-113	IARI
14.	L RIL-10	IARI	66.	L RIL-62	IARI	118.	L RIL-114	IARI
15.	L RIL-11	IARI	67.	L RIL-63	IARI	119.	L RIL-115	IARI
16.	L RIL-12	IARI	68.	L RIL-64	IARI	120.	L RIL-116	IARI
17.	L RIL-13	IARI	69.	L RIL-65	IARI	121.	L RIL-117	IARI
18.	L RIL-14	IARI	70.	L RIL-66	IARI	122.	L RIL-118	IARI
19.	L RIL-15	IARI	71.	L RIL-67	IARI	123.	L RIL-119	IARI
20.	L RIL-16	IARI	72.	L RIL-68	IARI	124.	L RIL-120	IARI
21.	L RIL-17	IARI	73.	L RIL-69	IARI	125.	L RIL-121	IARI
22.	L RIL-18	IARI	74.	L RIL-70	IARI	126.	L RIL-122	IARI
23.	L RIL-19	IARI	75.	L RIL-71	IARI	127.	L RIL-123	IARI
24.	L RIL-20	IARI	76.	L RIL-72	IARI	128.	L RIL-124	IARI
25.	L RIL-21	IARI	77.	L RIL-73	IARI	129.	L RIL-125	IARI
26.	L RIL-22	IARI	78.	L- RIL-74	IARI	130.	L RIL-126	IARI
27.	L RIL-23	IARI	79.	L- RIL-75	IARI	131.	L RIL-127	IARI
28.	L RIL-24	IARI	80.	L- RIL-76	IARI	132.	L RIL-128	IARI
29.	L RIL-25	IARI	81.	L- RIL-77	IARI	133.	L RIL-129	IARI
30.	L RIL-26	IARI	82.	L RIL-78	IARI	134.	L RIL-130	IARI
31.	L RIL-27	IARI	83.	L RIL-79	IARI	135.	L RIL-131	IARI
32.	L RIL-28	IARI	84.	L RIL-80	IARI	136.	L RIL-132	IARI
33.	L RIL-29	IARI	85.	L RIL-81	IARI	137.	L RIL-133	IARI
34.	L RIL-30	IARI	86.	L RIL-82	IARI	138.	L RIL-134	IARI
35.	L RIL-31	IARI	87.	L RIL-83	IARI	139.	L RIL-135	IARI

Table 1: Continue...

Sl. No.	Name of genotype	Source	Sl. No.	Name of genotype	Source	Sl. No.	Name of genotype	Source
36.	L RIL-32	IARI	88.	L RIL-84	IARI	140.	L RIL-136	IARI
37.	L RIL-33	IARI	89.	L RIL-85	IARI	141.	L RIL-137	IARI
38.	L RIL-34	IARI	90.	L RIL-86	IARI	142.	L RIL-138	IARI
39.	L RIL-35	IARI	91.	L RIL-87	IARI	143.	L RIL-139	IARI
40.	L RIL-36	IARI	92.	L RIL-88	IARI	144.	L RIL-140	IARI
41.	L RIL-37	IARI	93.	L RIL-89	IARI	145.	L RIL-141	IARI
42.	L RIL-38	IARI	94.	L RIL-90	IARI	146.	L RIL-142	IARI
43.	L RIL-39	IARI	95.	L RIL-91	IARI	147.	L RIL-143	IARI
44.	L RIL-40	IARI	96.	L RIL-92	IARI	148.	L RIL-144	IARI
45.	L RIL-41	IARI	97.	L RIL-93	IARI	149.	L RIL-145	IARI
46.	L RIL-42	IARI	98.	L RIL- 94	IARI	150.	L RIL-146	IARI
47.	L RIL-43	IARI	99.	L RIL- 95	IARI	151.	L RIL-147	IARI
48.	L RIL-44	IARI	100.	L RIL- 96	IARI	152.	L RIL-148	IARI
49.	L RIL-45	IARI	101.	L RIL- 97	IARI	153.	L RIL-149	IARI
50.	L RIL-46	IARI	102.	L RIL- 98	IARI	154.	L RIL-150	IARI
51.	L RIL-47	IARI	103.	L RIL- 99	IARI			
52.	L RIL-48	IARI	104.	L RIL- 100	IARI			

following Singh and Chaudhary (1985) and GENES Software.

3. RESULTS AND DISCUSSION

The pooled analysis of variance for the two locations (Table 2) revealed highly significant variance due to genotypes for all the characters except for SPP, indicating presence of sufficient variability in the genotypes selected for this study. Genotype×location interaction was highly significant for the traits SYP, 100 SW, PPP, D50F, PH, BYP and HI suggesting significant interaction of the genotypes with the specific environment of the two locations for these traits. Similar findings have been reported by Dugassa et al. (2014), Tyagi and Khan (2010) and Crippa et al. (2009) in lentil.

3.1. Mean performance

The mean data for the various parameters under study are presented in supplementary Table 3. Days to 50% flowering in the genotypes under study ranged from 49.25 days to

Table 2: Pooled analysis of variance for ten agronomic characters in 154 genotypes of lentil grown in two locations

	Source of variation			
	Replications Block-1	Treatments	Environments	T×E
Degrees of freedom	4	153	1	153
Days to 50% flowering	53.22	221.38**	14260.71**	24.04**
Days to maturity	48.4	126.24**	9527.15**	0.94
Plant height	11.17	92.80**	6602.06**	3.07**
Number of primary branches plant^{-1}	2.45	6.79**	1631.24**	0.12
Number of pods plant^{-1}	1886.54	3332.4**	50297.80**	942.48**
Number of seeds pod^{-1}	0.032	0.067	0.034	0.006
100 seed weight	5.34	1.63**	0.82	0.14**
Seed yield plant^{-1}	0.84	6.67**	404.99**	1.76**
Biological yield plant^{-1}	1.024	14.2**	1277.10**	3.66**
Harvest index	0.003	0.164**	0.004	0.12**

**=(p=0.01) level of significance; *=(p=0.05) level of significance

Table 3: mean performance of seed yield and various attributing traits in the best performing genotypes

	Genotype	D50F	DM	PH	NPB	PPP	SPP	100SW	SYP	BYP	HI
1.	L RIL-37	67	113.5	22.55	5.32	109.99	1.67	3.77	6.8	9.58	0.72
2.	L RIL-22	69	121.75	27.75	5.52	145.44	1.97	2.5	5.95	8.45	0.71
3.	L RIL-68	53.25	110.25	24.05	6.65	104.72	2	3.37	5.89	8.4	0.69
4.	L RIL-96	62.5	111.75	24.33	5.48	72.71	2	4.8	5.71	8.36	0.69
5.	L RIL-97	67.25	124.25	31.29	4.98	114.57	1.97	2.99	5.38	9.91	0.55
6.	L RIL-144	73.5	123.75	26.17	6.15	110.57	1.87	2.96	5.38	9.02	0.59
7.	L RIL-18	66.25	114.25	26.35	5.6	84.88	2	4.07	5.23	11.12	0.47
8.	L RIL-63	61	113.25	26.78	10.02	85.05	1.6	3.61	5.16	9.94	0.51
9.	L RIL-92	70.5	114.25	29.3	6.15	113.22	2	2.42	5.11	8.57	0.56
10.	L RIL-109	59.75	123.25	23.58	4.98	120.05	1.87	2.75	5.08	7.48	0.68

75.75 days. Days to maturity in the genotypes under study ranged from 108.75 days to 126.75 days. Some of the early maturing genotypes were LRIL-100 (108.75 days) followed by LRIL-120 (108.75 days), LRIL-138 (108.75 days), LRIL-140 (108.75 days), LRIL-36 (109 days), LRIL-119 (109.25 days) etc., which were at par with the lowest value and with the two parents viz. L-4602 (109.5) and BM-4 (111.17). Plant height in the studied genotypes ranged from 14.45 cm to 38.08 cm with an average plant height of 26.39 cm. The shortest plants were observed in LRIL-44 (14.45 cm) followed by LRIL-8 (18.45 cm), LRIL-90 (18.7 cm), LRIL-52 (18.83 cm) and LRIL-55 (19.43 cm). The number of primary branches ranged from 2.22–10.02, with the average primary branches of 5.14. There was significant variability for number of pods plant^{-1} among the genotypes which ranged from 29.02–145.45 with an average of 72.66 plant^{-1}. 100 seed weight ranged from 2.17–4.96 g with an average 100 seed weight of 3.00 g. Seed yield plant^{-1} among the genotypes ranged from 1.27–6.8 g plant^{-1} with an average of 3.46 g plant^{-1}. Biological yield plant^{-1} ranged from 3.23–11.12 g plant^{-1} with an overall mean of 6.47 g plant^{-1}, while harvest index ranged from 0.31-0.74, with an average value of 0.53. Based on mean performance of seed yield plant^{-1} and various attributing traits in the best performing genotypes LRIL-37, LRIL-22, LRIL-68, LRIL-96, LRIL-97, LRIL-144, LRIL-18, LRIL-63, LRIL-92and LRIL-109 (Table 3).

3.2. Estimates of genetic parameters of variability

Genotypic coefficient of variation estimate (Table 4) was highest (>20%) for PPP (27.46 %), followed by SYP (26.15 %), BYP (20.52%) and NPB (20.51%), while moderate GCV (10-20%) was observed for 100 SW (16.59%), HI (15.60 %), and PH (14.65%).PCV was high for the traits namely, HI (41.17%), PPP (39.89%), SYP (36.20), BYP (28.66%), and NPB (22.72%) indicating the pronounced influence of environmental effects and interactions in the expression of these characters.

Table 4: Estimates of means, range, genotypic coefficient of variation (GCV%), phenotypic coefficient of variation (PCV%), heritability (H2bs %) and genetic advance as percentage of mean for 154 genotypes of lentil grown in two locations

Sl. No.	Characters	Mean	Range	GCV (%)	PCV (%)	Heritability (H^2bs) (%)	Genetic advance as percent of mean (GA%)
1.	Days to 50% flowering	62.54	49.25-75.75	9.17	10.56	75.29	16.39
2.	Days to maturity	115.74	108.75-126.75	3.94	4.16	90.18	7.72
3.	Plant height	26.39	14.45-38.08	14.65	15.72	86.82	28.12
4.	No. of primary branches plant^{-1}	5.14	2.22-10.02	20.51	22.72	81.52	38.15
5.	No. of pods plant^{-1}	72.66	29.02-145.44	27.46	39.86	47.46	38.98
6.	No. of seeds pod^{-1}	1.87	1.6-2.00	5.39	6.94	60.39	8.63
7.	100 seed weight	3.00	2.17-4.96	16.59	20.24	67.20	28.03
8.	Seed yield plant^{-1}	3.46	1.27-6.80	26.15	36.20	52.20	38.93
9.	Biological yield plant^{-1}	6.46	2.10-11.12	20.52	28.66	51.21	30.24
10.	Harvest index	0.54	0.31-0.74	15.60	41.17	14.36	12.18

Heritability determines the extent of phenotypic variation attributed to the genotype or genetic causes. In the current experiment, the highest estimate of heritability (>60%) was recorded for DM (90.18%), followed by PH (86.82%), NPB (81.52%), D50F (75.29%), 100 SW (67.20%) and SPP (60.39%). Moderate (30-60%) estimates of heritability were observed for SYP (52.20%), BYP (51.22%) and PPP (47.46%). Highest genetic advance as percentage of mean (>20%) was recorded for PPP (38.98%) followed by SYP (38.93%), NPB (38.15%), BYP (30.24%), PH (28.12%) and 100 SW (28.03) while GA% was moderate for D50F and HI. Low genetic advance was observed for DM and SPP.

High heritability with high genetic advance indicates the presence of additive gene effects (Panse and Sukhatme, 1957). High heritability coupled with high genetic advance were observed in NPB, PH and 100 SW for which additive genes were probably more influential, while non-additive genes were probably responsible in the inheritance of the other characters. Chakrabarty and Haque (2000) reported high heritability and high genetic advance for grain yield plant^{-1}, 100-grain weight and number of pods plant^{-1} while high heritability values coupled with high genetic advance as percent mean were observed for number of pods plant^{-1} and biomass yield by Dugassa et al. (2014). Moderate to high estimates of heritability, GCV, PCV and genetic gain were reported for seed yield plant^{-1}, number of primary branches plant^{-1}and number of secondary branches plant^{-1} (Singh and Srivastava, 2013).

3.3. *Correlation among yield and attributing traits*

Higher magnitude of genotypic correlation facilitates in selection of genetically controlled characters that are associated and provides a better chance for improving seed yield than that expected on the basis of phenotypic association alone (Robinson et al., 1955). A highly positive and highly significant correlation (Figure 1) was observed between SYP and PPP (0.84***), followed by BYP (0.79***), SPP (0.47***) and NPB (0.31***), HI (0.31***) and a positively significant correlation with 100 SW (0.20*) (Figure 1), from which it can be suggested that SYP can be successfully improved by selecting for more number of PPP, more NPB, higher BYP and higher 100 SW. Chauhan and Singh (2001) reported positively significant and strong association between seed yield and total biological yield plant^{-1} while Singh et al. (2009) observed that pods plant^{-1}, seeds pod^{-1}, biological yield and harvest index had significantly positive correlation with seed yield.

3.3.1. *Correlation analysis for 10 agronomic characters in 154 lentil genotypes grown in two locations*

Among the yield attributing characters, positive and significant correlation was observed between PPP and BYP (0.68***), number of SPP, HI and NPB. D50F had positive and highly significant correlation with DM (0.43***) and PH (0.27***) which suggests that earliness or late maturity was

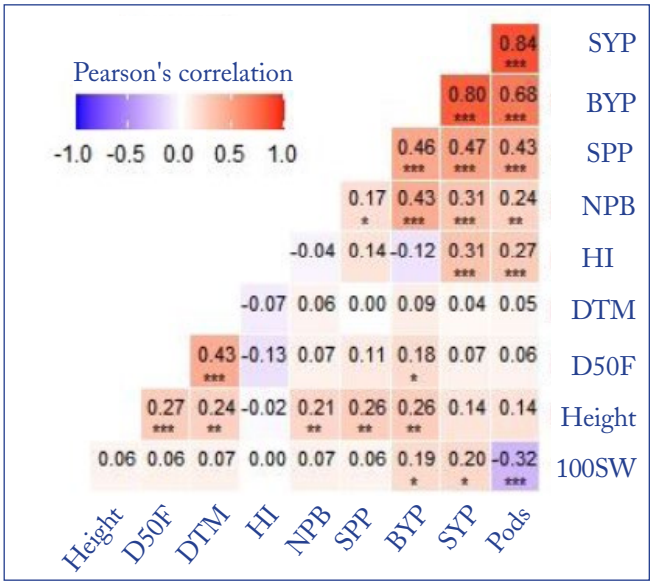

Figure 1: Correlation analysis for 10 agronomic characters in 154 lentil genotypes grown in two locations

dependent on the flowering duration while, short plants matured early and taller plants had late maturity. Most of the traits having significant correlation with BYP revealed that increased expression of these traits will lead to increase in BYP and vice-versa. The results are in agreement with Tullu et al. (2001) and Kumar (2020).

A highly significant but negative correlation observed between 100 SW and PPP (-0.32***) may be due to differential partitioning of photosynthates which results in seeds with higher seed weight but lesser number of pods and vice-versa as bold seeded genotypes had relatively lesser number of pods when compared to small seeded genotypes as evident in this study.

3.4. *Root morphology studies*

The root system and its architecture are an important aspect while screening the genotypes for Al toxicity tolerance since a well-established root system in the tolerant genotypes proliferates better roots in the acidic medium thus absorbing more water and nutrients from the soil which in turn leads to better growth and development of above ground plant parts and ultimately results in higher yields.

The analysis of variance for root morphology traits of 154 lentil genotypes grown in natural acidic field (Table 5) suggested that highly significant differences existed due to genotypes for all the five root morphology traits under study indicating the presence of sufficient variability in the 154 genotypes evaluated in this study. The mean trait value (Supplementary table 4) for root tips ranged from 21.5 to 174, average root diameter in the genotypes under study ranged from 0.88 cm^2 to 2.98 cm^2 while the total root length ranged from 270.52–3324 cm. Total root surface area in the genotypes under study ranged from 386.01–2924.61

Table 5: Analysis of variance (ANOVA) for five root traits in 154 genotypes of lentil evaluated in acidic fields

	Source of Variation		
	Genotypes	Replications	Error
DF	153	2	306
Root tips (RT)	2594.09**	984.98	102.35
Average root diameter (ARD)	0.35**	0.08	0.11
Total root area (TRA)	873483.33**	3381.64	32253.6
Total root length (TRL)	459840.26**	483593.7	18372.72
Total root volume (TRV)	36071460.28**	131287.6	1010062

cm^2 and the estimate of total root volume of the genotypes studied in the present experiment ranged from 638.39–25646.08 cm^3. It was observed that most of the genotypes like LRIL-37, LRIL-22, LRIL-96, LRIL-97, LRIL-144, LRIL-92, LRIL-109 etc (Table 6) exhibiting higher yields under acidic field conditions constituted of well-established root systems with proliferating root traits while most of the low yielders like LRIL-2, LRIL-40, LRIL-65, LRIL-24, LRIL-141 etc. had relatively lesser root growth and poor root systems (Figure 2). Tang et al. (2003) reported that the tolerant genotype produced more than five times the root length in the acidic subsurface soil compared to sensitive variety and suggests that the difference in root proliferation in the subsurface soil and hence in utilizing nutrient and water reserves in the subsurface soil layer has resulted in the genotypic variation in growth and yield of wheat grown with subsurface soil acidity. Bushamuka and Zobel (1998) observed that the tap roots, basal roots and lateral roots of maize and soybean genotypes grown in a stratified acid Al-toxic soil medium were comparable to the control in the tolerant genotypes while the sensitive genotypes exhibited

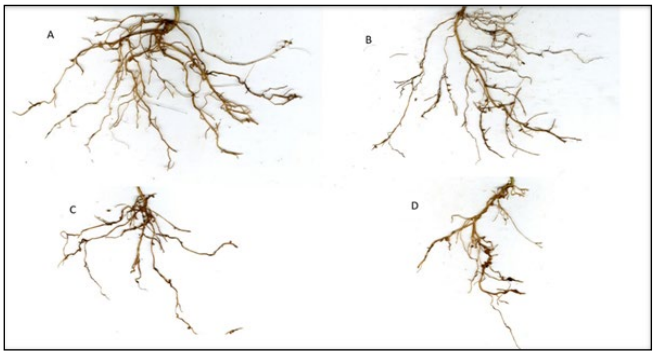

Figure 2: Root morphology of lentil genotypes collected from field evaluation observed under root scanner, tolerant genotypes (A) LRIL-92 and (B) LRIL-144 vs sensitive genotypes (C) LRIL-2 and (D) LRIL-40

Table 6: Mean estimates of various root morphology traits of high yielding RILs

Genotypes	Root tips (RT)	Average root diameter (ARD)	Total root area (TRA)	Total root length (TRL)	Total root volume (TRV)
L RIL-37	87.5	1.94	1400.68	1124.57	4227.37
L RIL-22	108	1.6	2500.61	1368.29	5073.19
L RIL-96	89.5	2.16	1558.46	1029.51	5539.11
L RIL-97	47.5	1.32	1255.9	962.2	3032.24
L RIL-144	98.5	2.3	1656.47	1175.7	5777.11
L RIL-92	68.5	1.78	1257.81	1224.62	3120.11
L RIL-109	119.5	1.48	1690.73	1501.2	6094.14

no root growth in the Al toxic bottom layer.

3.5. Estimation of Al content

The aluminium content of the genotypes evaluated under acidic field conditions ranged from 0.606 mg g^{-1} to 1.382 mg g^{-1} (Figure 3).

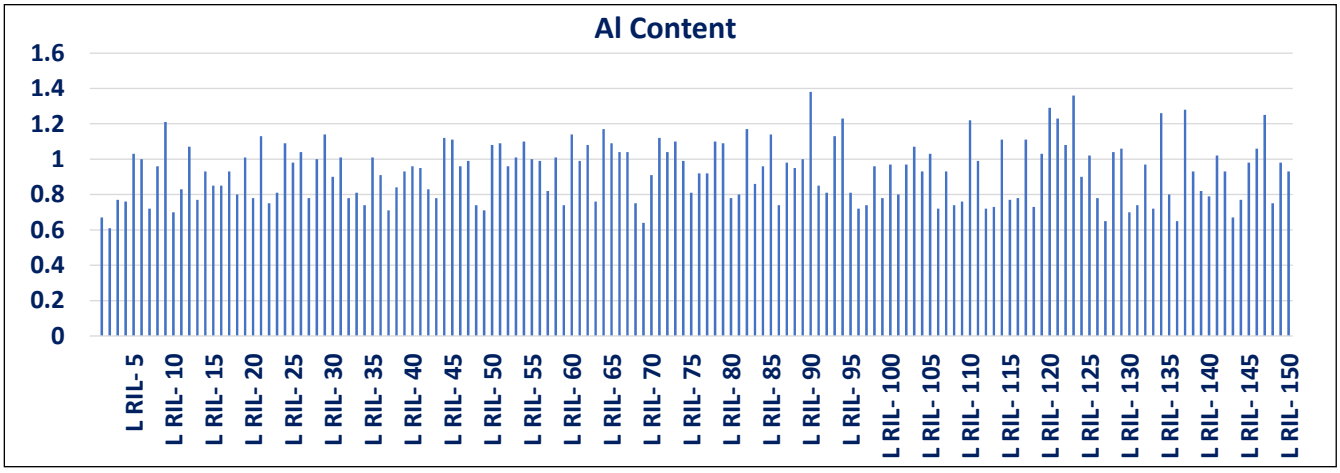

Figure 3: Aluminium content (mg g^{-1}) in lentil RILs evaluated under acidic field conditions of Meghalaya

A negative trend (R^2=49.42 %) was observed from regression analysis between root Al content and yield (Figure 4) obtained under field conditions which suggests that in most of the cases higher yields were obtained in Al stress tolerant genotypes having lower levels of Al content in their roots, while genotypes containing higher levels of Al in their roots exhibited lower yield under acidic field conditions.

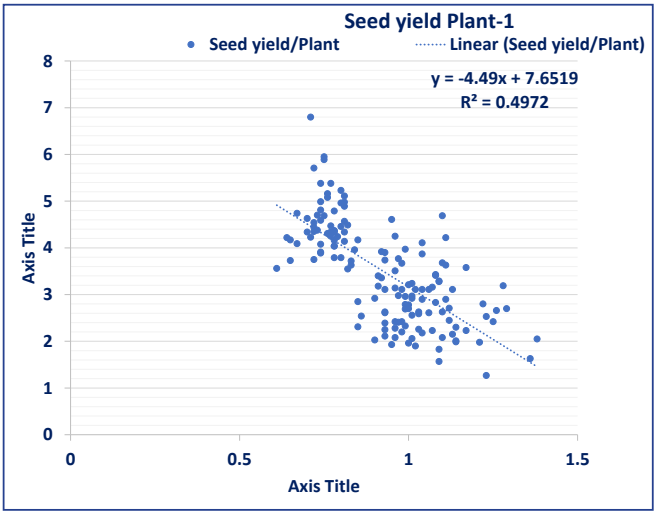

Figure 4: Regression of seed yield plant^{-1} vs root Al content in lentil RILs

The relatively lower Al content in the roots of high yielding tolerant genotypes may be due to plants' ability to release organic acids which form complexes with Al and prevents the toxic effects on plants. Various studies have suggested that Al tolerant plants use organic acids for the sequestration of Al in the cytosol of the root cells followed by remobilization or translocation of Al toward the shoots which is the mechanism behind internal detoxification of Al (Quintal et al., 2017), while the most widely described exclusion mechanism (external detoxification) for toxic Al is the release of organic acids from the root of plants (Kochian et al., 2015).

4. CONCLUSION

The genotypes LRIL-37, LRIL-22, LRIL-96, LRIL-97, LRIL-144, LRIL-92 and LRIL-109 identified as tolerant from field evaluation and root morphology studies would serve as potential genotypes to be released as high yielding Al toxicity tolerant varieties. Number of pods plant^{-1}, biological yield plant^{-1}, number of seeds pod^{-1}, number of primary branches plant^{-1} and harvest index were the most important traits for improving seed yield. Most of the high yielding lines constituted of relatively lower levels of Al content in the roots.

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