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Studies on inbreeding depression, transgressive segregation, genetic variability and heritability in F_2 segregating population of tropical carrot (*Daucus carota* L.)

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Abstract
The present investigation was undertaken at University of Horticultural Sciences, Bagalkot during the 2020-21. The objective of the study was to understand the genetic variability, heritability, transgressive segregation index and inbreeding depression of root productivity and other phenotypic traits in the F2 segregating population obtained from a cross between UHSBC-38 x UHSBC-40 and comprising of 75 individuals. The root length and root width showed higher broad sense heritability, and higher genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) which supports positive selection response and ease in crop improvement of these traits. The population showed high inbreeding depression for root weight and shoulder weight based on the F1 and F2 generation comparison. We obtained fewer transgressive segregants and those can be further used for crop improvement. It was observed that, carrot being a highly cross pollinated crop, greater genetic variation can be created in the segregating population despite having high inbreeding depression.

Keywords: F_2 population; Inbreeding depression; Transgressive segregants; carrot; variability and heritability

Introduction
Carrot (*Daucus carota* L.) is a diploid organism with chromosome number of 2n=2x=18 and a major root crop belonging to Apiaceae family. It is a native of Mediterranean region. Carrot is known for its economic part *i.e.,* smooth textured orange coloured tap root throughout the globe because of its rich carotenoid and other antioxidants, vitamins, and minerals. Carrot is consumed by all the age groups because of its no calorie, fibre rich, nutritious roots. It provides dietary sources of β-carotene, lycopene, anthocyanin, lutein, tocopherol, sugars phenolics, isocoumarines, terpenes and sesquiterpenes (Begum., 2018) [1]. Raw carrots have 88% water, 9% carbohydrates, 0.9% protein, 2.8% dietary fibre, 1% ash and 0.2% fat. Carrot's dietary fibre comprises mostly cellulose, with smaller proportions of hemicellulose, lignin and starch. Free sugars in carrot include sucrose, glucose, and fructose. In recent years, consumer's requirement of carrot has steadily increased due to its nutritionally rich, fresh and functionally enriched processed products. The improved genetic background and nutritional profiling such as improved flavours and more diverse pigments are of immense importance for the vegetable industry and consumers. Global carrot gene pool has a rich diversity in terms of adaptability, nutritional quality, resistance to biotic and abiotic stresses. Despite this usefulness, the exploitation of germplasm adaptable to tropical climate is meagre. However, there is a greater demand for varieties and hybrids of carrot for tropical farmers and consumers. These tropical adaptable germplasm accessions are the rich sources of resistance to various abiotic stresses, having long shelf life, rich in reducing sugars, better texture and require less vernalization for flowering etc. (Poleshi *et al*., 2016). Hence, there is a greater need for utilization of tropical carrot in the breeding program to fulfil the global needs of carrot consumption and production. The F_2 segregating population developed in the present investigation were subjected to analysis of genetic variability, heritability, inbreeding depression, and transgressive segregation index and for important root productivity traits.

Material and Methods

Experiments on evaluation of F_2 (UHSBC-38 X UHSBC-40) was carried out at Haveli farm of UHS, Bagalkot during 2019-20 in regular season. Bagalkot is situated in the Northern Region of Karnataka and positioned at 16°12'N, 75°12'45 E with 610m above mean sea level. The phenotypic observations were recorded for Number of petioles (NP), Shoot length in cm (SL), Root width in mm (RWI), Shoulder width in mm (SHWI), Shoot weight in grams (SWE), Root weight in grams (RWE), Root length to shoot length ratio (RL/SL), Root width to shoulder width ratio (RWI/SWI), Root weight to shoot weight ratio (RWE/SWE), Plant height (PH).

Statistical Analyses

Descriptive statistics (Mean, Range, SEm) and frequency distribution: The mean data of F2 population on quantitative traits were subjected to descriptive statistical analyses along with the parents and F1 population *viz*., mean, range, standard error and Frequency distribution of all the traits using a statistical software SPSS (version 16.0).

Genetic variability components

Phenotypic (PCV) and Genotypic (GCV) coefficient of variation were worked out as suggested by Burton and Devane (1953) [2]. Heritability (h^2) in broad sense h^2b.s. was estimated by following the procedure suggested by Weber and Moorthy (1952) [13] and Mamata *et al*. (2017) [7]. Heritability % age was categorized as present in Mamata *et al*. (2017) [7]. Genetic advance (GA) was predicted by using the formula provided by Johnson *et al.* (1955) [6]. Genetic advance over per cent mean (GAM) in terms of percentage was worked out as suggested by Johnson *et al*. (1955) [6].

Inbreeding depression was calculated from below formula,

Inbreeding depression = (Mean F_2-Mean F_1)/Mean F1 * 100.

Transgressive Index was calculated based on formula,

Transgressive Index= F_2 trait value difference/Parental trait value Difference

Results and Discussion

Creation of genetic variability through hybridization is an age old practice in crop improvement. Assessing the genetic variability in the artificially created population would be beneficial to design the breeding strategies for trait improvement. The F_2 mapping population (UHSBC-38 x UHSBC-40) was subjected to descriptive statistical analysis to understand the *per se* performance. Similarly, the population was also subjected to frequency distribution and genetic variability studies. The results of *per se* performance (Table1), genetic variability (Table 2) and the frequency distribution (Figures 1a, 1b, 2& 3) of the segregating population are presented in the respective tables and figures.

In UHSBC-38 x UHSBC-40 F_2 population, no of petioles, shoot length, shoot weight, root length, root weight, plant height, root width, root weight to shoot weight ratio, root length to shoot length, xylem length to phloem length ratio and plant height traits exhibited normal distribution and shape of the curve was bell shaped. This indicates that the trait is probably governed by polygenes. Xylem length and phloem length showed skewed distribution could be due to oligogenic nature of inheritance of traits.

Root length ranged from 6cm to 29cm. The mean of the population for root length is 16.48cm ± 0.611. The shape of the curve is bell shaped and trait under study is normally distributed. GCV (28.99%), PCV (31.07%), GAM (55.71%) and heritability (87.03%) were high for root length trait. The root width ranged from 0.5mm to 59.2mm and the mean value of the population for root width was 9.20mm ± 0.80. There was higher GCV (32.00%), PCV (34.47%), GAM (61.87%) and heritability (86.16%) for root width trait. Shoulder width ranged from 0.67mm to 4.96mm. The mean of the population for shoulder width is 2.08mm ± 0.08. There was high GCV (63.86%) and PCV (74.67%) correlated with high heritability (73.14%) and high GAM (112.49%). The root weight ranged from 1g to 102g. The mean of the population for root weight is 25.10g ± 2.33. There was high GCV and PCV (56.98% and 79.99% respectively) for shoot weight represented in Table 1 and 2. The Highest GCV, PCV, heritability and GAM was recorded for root width to shoot width ratio trait in parental genotypes. The shoot length had lowest GCV, PCV, heritability and GAM among parental genotypes which show similar results in accordance with Meghashree *et al.* (2018). Almost all the traits were having High GCV and high PCV which may be due to additive gene action. Such traits can be improved with the help of simple selection method. The traits having moderate GCV and PCV that shows prevalence of moderate genetic diversity and such traits can be improved by selection in advanced generation. Traits having low GCV and low PCV shows narrow genetic base which can be improved by increasing the genetic base by hybridization or mutation breeding or pedigree method etc, higher heritability coupled with high GAM indicates that the traits were governed by additive gene action and such traits can be easily fixed by selection.

Root weight was having High GAM coupled with low heritability (83.61% and 50.74% respectively). Shoot weight was having moderate heritability (34.28%) and high GAM (79.19%). In contrast, the heritability for root weight was extremely low or near to zero in the experiments of Jagosz *et al* (2012) [5] involving partial diallele analysis of temperate carrot. Presence of high heritability and low GAM indicated that the trait is governed by both additive and non-additive gene action. Such traits can be improved by recurrent selection. Low heritability and low GAM indicates that the trait is governed by non-additive gene action and selection such trait will not be reward good results in plant breeding. Fortunately, we couldn't get such traits in our study. Higher genetic variability is expected when the diverse parents are used for hybridization for generating F_2 population. In the study, many of the traits showed wider range of variability. Higher GCV and PCV coupled with higher heritability supports the presence of higher heritable genetic variability in our F_2 population.

Transgressive segregation index represents the proportion of the difference between the parents and the corresponding range for a phenotype in the F2 population. Identifying the transgressive segregants are extremely useful in segregating populations as these are the individuals that exceed both the parents for the trait value and could be further carried up to F_6-F_7 generation with due care. Unlike heterosis, these superior individuals of the segregating populations are heritable are due to the fixed additive gene effects. In the present F_2 population we observed couple of superior individuals that exceeded the parents for almost all the traits. Highest transgressive index was shown for root width to shoulder width ratio (38.80) followed by xylem length (33.49). Whereas, the lowest transgressive index for shoulder width ratio (2.67) followed by root width (4.50) (Table 3).

Higher transgressive index for trait may be because of recombination and epistatic effects. For important productivity traits, higher transgressive index is highly desirable as they are the result of recombination among the favourable alleles of different loci and expected to be governed by additive gene effects and hence, they are fixable and effective for selection during varietal development.

Inbreeding depression is the reduced biological fitness in a population because of inbreeding or breeding of related individuals' especially in cross pollinated crops. Occurrence of inbreeding depression is high in carrot crop due to its out crossing nature of crop and resulting in reduced fitness with homozygous recessive unfavourable alleles due to inbreeding (Simon, 2001). In F_2 Population (UHSBC-38 x UHSBC-40) inbreeding depression was present in root length (-45.38), root width (-72.28), shoulder width (-56.43), shoot weight (-47.97), root weight (-82.32), root weight to shoot weight ratio (-34.07), root length to shoot length (-47.42), plant height (-13.16). The highest inbreeding depression was present in root width (-64.51) and lowest recorded inbreeding depression was present in plant height (-13.16). Stein *et al*. (1995) [12] reported highest inbreeding depression for root yield (81.9%) and lowest for root length (17.7%) in carrot. Also found that inbreeding depression for root weight was ranging from 39.1% to 55.3% and for weight of leaves ranged from 37.3% to 56.8% (Table 4).

Understanding of the genetic mechanisms governing the inheritance and behaviour of traits in segregating population is very much important for designing the crop improvement strategies. Presence of high genetic variability is prerequisite in plant breeding, which will serve as resource material for crop improvement programme. Transgressive segregants having high heritability and lower inbreeding depression will have better fitness value and are valuable in varietal development. In the present study, tropical adapted germplasm lines were exploited to develop F2 population in order to understand the transgressive index and pattern of distribution of root productivity traits in addition to genetic variability and heritability of these traits.

Table 1: *Perse* performance of quantitative traits in F2 mapping population

Traits	UHSBC-38XUHSBC-40			
	Minimum	Maximum	Mean	Std. Error
NP	4.00	23.00	9.65	0.38
SL (cm)	28.00	122.00	56.88	1.54
RL (cm)	6.00	29.00	16.93	0.61
RWI (mm)	0.50	59.52	9.20	0.80
SHWI (mm)	0.67	4.96	2.08	0.08
SWE (Gms)	1.00	342.00	63.48	8.27
RWE (Gms)	1.00	102.00	25.11	2.33
RWE/SWE	0.08	6.00	0.77	0.11
XL	0.16	15.23	2.07	0.43
PL	0.07	7.47	1.15	0.21
XL/PL	0.32	2.46	0.83	0.05
PH	35.00	140.00	73.81	1.89

Note: NP: No of petioles; SL: Shoot length; RWI: Root width; SHWI: Shoulder width; SWE: Shoot weight; RWE: Root weight; RL/SL: Root length to shoot length ratio; RWI/SWI: Root width to shoulder width ratio; RWE/SWE: Root weight to shoot weight ratio; PH: Plant height

Table 2: Genetic variability and heritability components for quantitative traits in F2 mapping populations (UHSBC-38 x UHSBC-40)

UHSBC-38 X UHSBC-40 F_2 Mapping population								
Traits	Vp	Vg	Ve	GCV	PCV	$h^{2b,s}$	GA	GAM
NP	10.84	9.25	1.59	31.51	34.11	85.34	5.79	59.962
SL	175.73	155.07	20.66	21.89	23.31	88.24	24.10	42.366
RL	27.69	24.10	3.59	28.99	31.07	87.03	9.43	55.713
RWI	51.52	44.39	7.13	32.00	34.47	86.16	12.74	61.187
SWI	47.20	34.52	12.68	63.86	74.67	73.14	10.35	112.499
SWE	5067.05	1737.05	3330.00	65.66	112.13	34.28	50.27	79.189
RWE	403.32	204.66	198.67	56.98	79.99	50.74	20.99	83.613
RWE/SWE	0.01	0.01	0.00	27.79636	29.70	87.56	0.16	53.581
RL/SL	0.70	0.36	0.34	78.19	109.03	51.43	0.89	115.509
RWI/SWI	0.04	0.02	0.02	32.10098	45.47	49.84	0.21	46.685
PH	263.33	250.21	13.11	21.43	21.98	95.02	31.76	43.033

Note: NP: No of petioles; SL: Shoot length; RWI: Root width; SHWI: Shoulder width; SWE: Shoot weight; RWE: Root weight; RL/SL: Root length to shoot length ratio; RWI/SWI: Root width to shoulder width ratio; RWE/SWE: Root weight to shoot weight ratio; PH: Plant height

Vp: Phenotypic variance; Vg: Genotypic variance; Ve: environmental variance; GCV: Genotypic coeffienct of variation; PCV: Phenotypic coeffienct of variation; $h^{2b.s}$: heritability in broad sense; GA: Genetic advance; GAM: Genetic advance as *per cent* mean

Table 3: Transgressive segregation index for quantitative traits for 2 F_2 mapping populations (UHSBC-38 x UHSBC-40)

Traits	TSI
NP	9.50
SL	13.06
RL	5.11
SWE	28.42
RWE	6.31
RWE/SWE	23.67
SHWI	2.67
RWI	4.50
XL	33.49
PL	24.68
XL/PL	16.94
RWI/SWI	38.89
PH	6.91

TSI: Transgressive segregation index

Note: NP: No of petioles; SL: Shoot length; RWI: Root width; SHWI: Shoulder width; SWE: Shoot weight; RWE: Root weight; RL/SL: Root length to shoot length ratio; RWI/SWI: Root width to shoulder width ratio; RWE/SWE: Root weight to shoot weight ratio; PH: Plant height

Table 4: Inbreeding depression quantitative traits in 2 F_2 mapping populations

Traits	F_2 Population (UHSBC-38 x UHSBC-40)		
	F_1	F_2	ID (%)
NP	8.00	9.65	20.67
SL	54.00	56.88	5.33
RL	31.00	16.93	-45.38
RWI	33.19	9.20	-72.28
SHWI	47.79	20.82	-56.43
SHWE	122.00	63.48	-47.97
RWE	142.00	25.11	-82.32
RWE/SHWE	1.16	0.77	-34.07
RL/SHL	0.57	0.30	-47.42
PH	85.00	73.81	-13.16

*ID: Inbreeding Depression

Note: NP: No of petioles; SL: Shoot length; RWI: Root width; SHWI: Shoulder width; SWE: Shoot weight; RWE: Root weight; RL/SL: Root length to shoot length ratio; RWI/SWI: Root width to shoulder width ratio; RWE/SWE: Root weight to shoot weight ratio; PH: Plant height

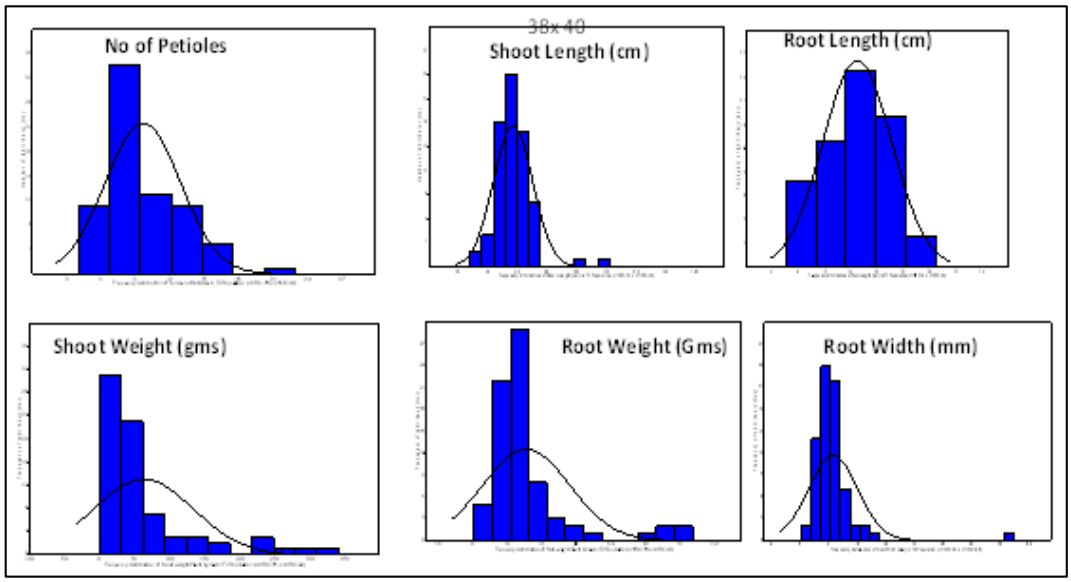

Fig 1a: Frequency distribution of important quantitative traits in F_2 (UHSBC-38 x UHSBC-40) Mapping population

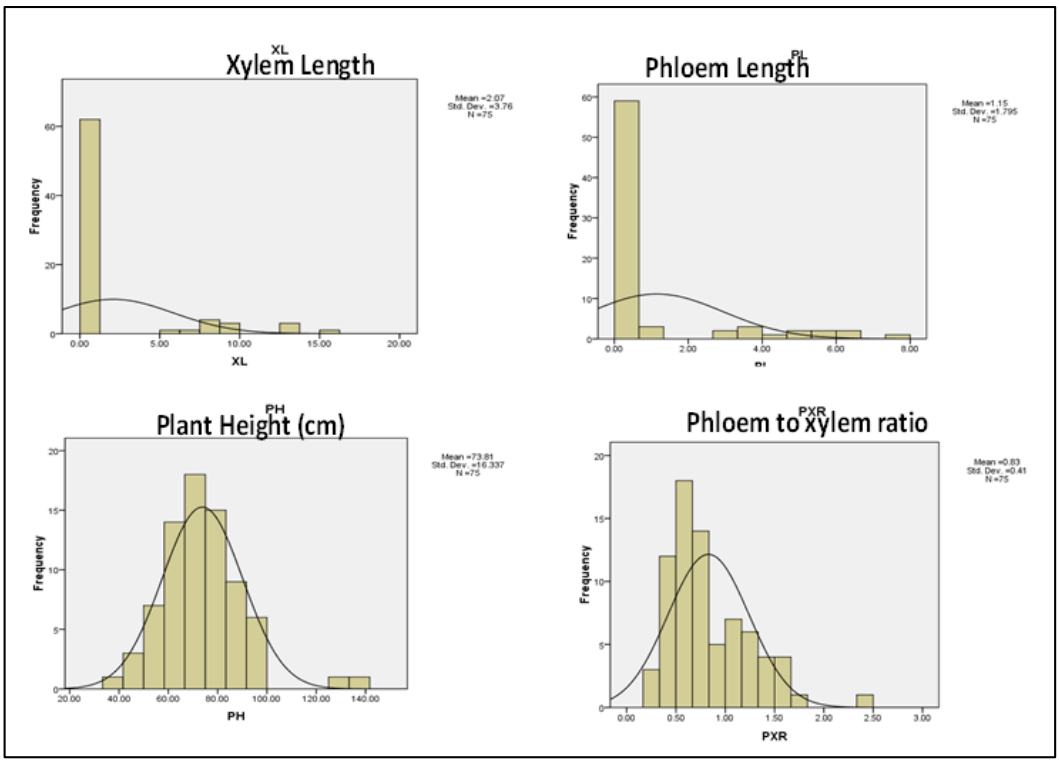

Fig 1b: Frequency distribution of important quantitative traits in F_2 Mapping population (UHSBC-38 x

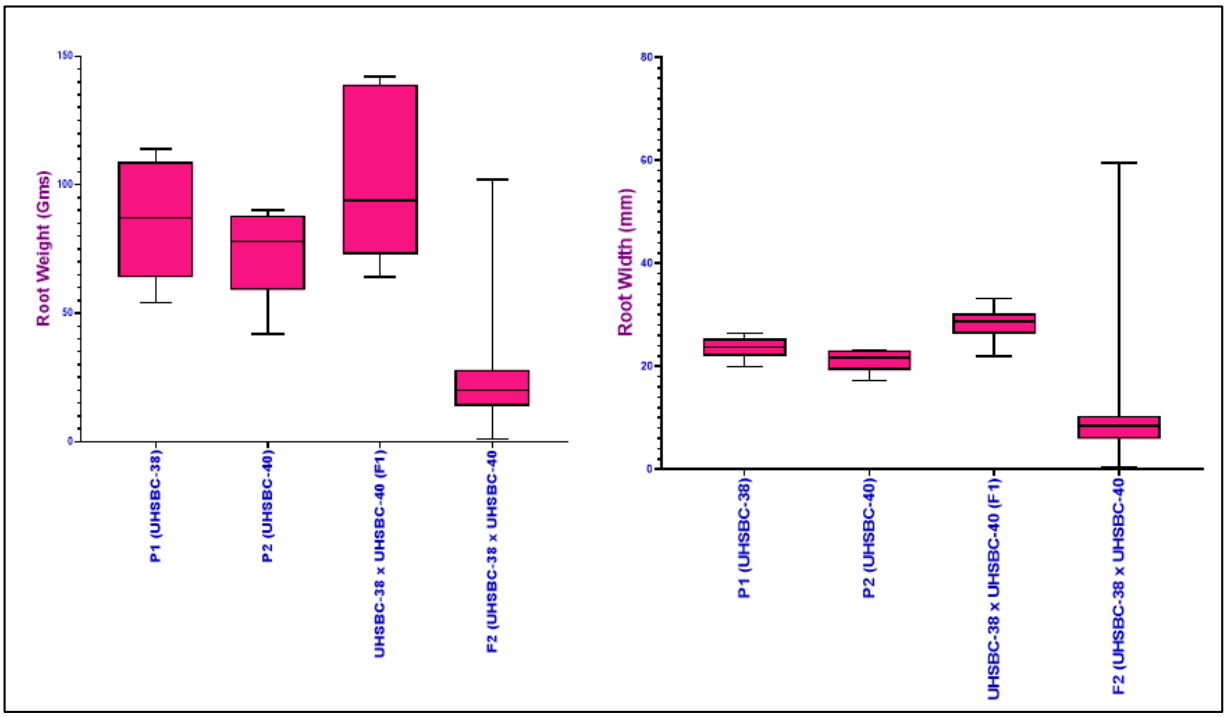

Fig 2: Comparison of parents, hybrid and F_2 population (UHSBC-38 x UHSBC-40) for root weight (Gms) and root width (mm)

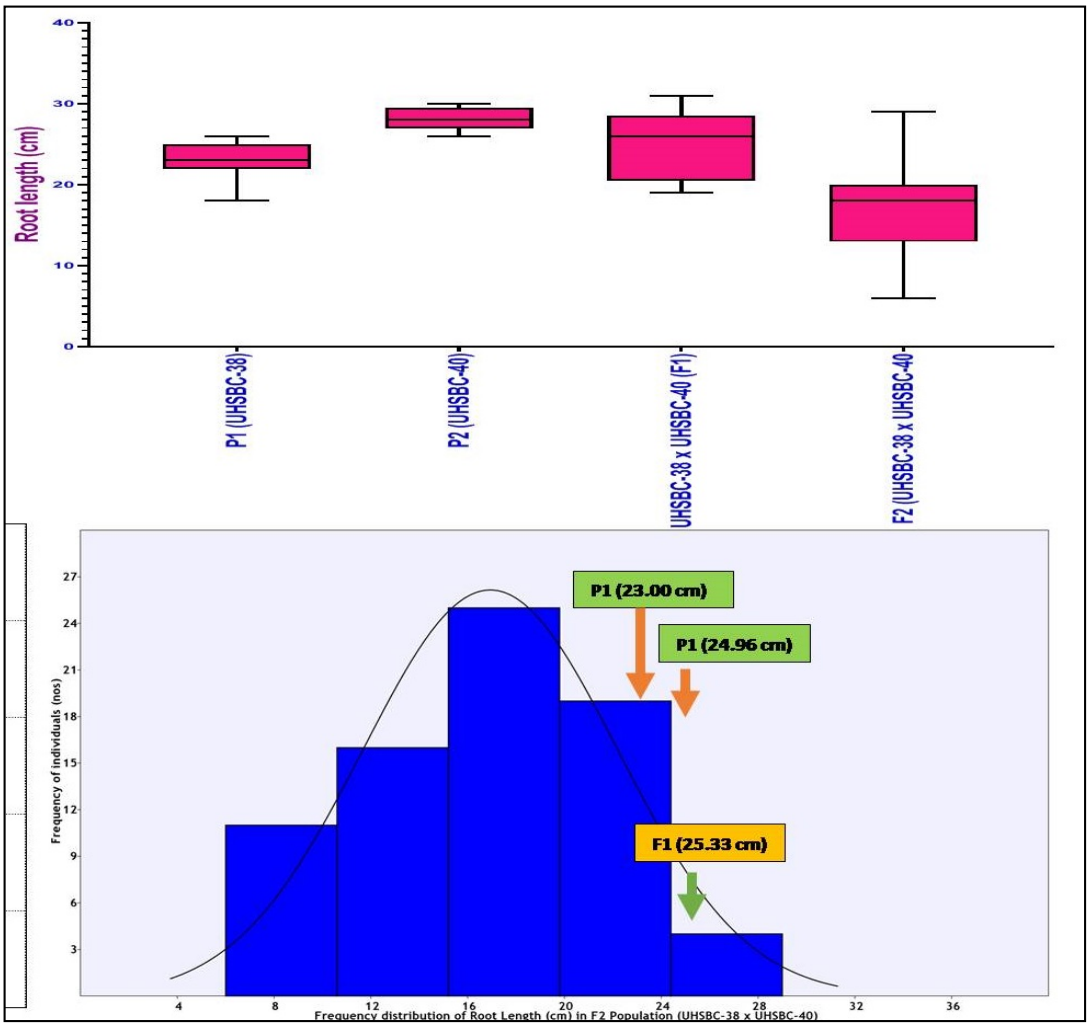

Fig 3: Comparison of parents and F_2 population for root length (UHSBC-38 x UHSBC-40) and frequency distribution of root length in F2

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