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YIELD IMPROVEMENT OF EGUSI MELON (*COLOCYNTHIS CITRILLUS* L.) THROUGH INTERGENERIC HYBRIDIZATION WITH WATERMELON (*CITRILLUS LANATUS* L.)

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ABSTRACT

This research was aimed to improve the productivity of ‘egusi’ melon through generic hybridization with watermelon. The experiment was carried out in the Department of Crop Science, University of Nigeria, Nsukka, Nigeria. Parental seeds of ‘egusi’ melon accessions from Taraba (Tar), Abakaliki (Abk), Nsukka (Nsk) and watermelon varieties from Kolos (Kol) and Koalack (Koa) were used for the study. Hybrids from all possible cross combinations between parents of ‘egusi’ melon and watermelon were generated using diallel method of selection. The parents, Kolos and Taraba were the best general combiners for yield and growth attributes, respectively. Crosses; Abk x Nsk, Abk x Koa, Tar x Kol and Kol x Abk were good specific combiners for all the traits measured. Four and three clusters were obtained in the F_1 and F_2 progenies, respectively in all the traits combined. The high diversity obtained underlies prospects for improvement of ‘egusi’ melon through intergeneric hybridization.

Keywords: Genetic diversity, general combining ability, specific combining ability, hybrids.

INTRODUCTION

Melon species are members of the family Cucurbitaceae found mainly in warmer part of all continents (Schipper 2002). Egusi melon **(***Colocynthis citrillus* L**.)** is one of the most important vegetable crops in the tropical, subtropical and Mediterranean zones of the world (Schippers, 2000). The crop is known for its widespread adaptation. Kernels of its seeds can be eaten individually as snacks when roasted and used extensively for cooking purposes, either as a soup additive or as cooking oil source (Bande *et al*., 2012). The ‘egusi’ melon seed like soyabean *(Glycine max*) is rich in oil and protein, about 53.1% and 33.8%, respectively (Ogbonna 2013). It is therefore important to improve the productivity of the crop per unit area to satisfy the demands of dietary needs and raw materials for industrial processing edible oil and livestock feedstuff through vigorous breeding programs.

The main thrust in any crop improvement program is to enhance yield. However, the major constraint in achieving high yield potential is mostly due to low genetic diversity for yield among the existing genotypes. Intergeneric and interspecific crosses were made to introduce new genetic variation into cultivated plants (Van-Tuyi and De-Jeu1997). Although intergeneric hybridization has not been successful in some plant families, it has been widely exploited in improvement of some plant families such as Brassicaceae (Lu *et al*. 2001); Poaceae (Edgar and Connor 2000; Liu *et al*. 1993) and Radish (Gupta 1997). Positive attempts have been reported in intergeneric hybridization of Cucurbitaceae family like cucumber (Kho *et al*. 1980) and *Cucumis melo* (Deakin *et al*. 1971). Despite many indications of successful intergeneric hybridization made in some crop families, no or little attempts have been made in intergeneric hybridization in ‘Egusi’ melon. Among the Cucurbitaceous family, watermelon has close resemblance to egusi melon in terms of phenotypic and genetic attributes (Idehen *et al*., 2006). Thus, watermelon *(Citrullus lanatus)* that has the same chromosome number with ‘egusi’ melon (Idehen *et al*., 2006) and third most popular consumed fruit vegetable in the world (Zhao *et al*., 2013) can be useful breeding material for improving important agronomic traits especially seed yield in egusi melon crop.

Estimating combining ability following the hybridization of egusi melon and watermelon is very useful in identifying superior parents because the performance of a hybrid is related to the general (GCA) and specific (SCA) combining abilities of the inbred lines involved in the cross. One of the most used procedures in the diallel analysis is Griffing's (1956) method that estimates the general (GCA) and specific (SCA) combining ability of the parents (Machado *et al*., 2009). In this present study, diallel cross following Griffing (1956) method was employed for to study the possibility of improving egusi melon through generic hybridization with watermelon. Therefore, the objectives of this study were to improve genetic diversity in yield and other agronomic parameter of ‘egusi’ melon through intergeneric hybridization with watermelon and identify the potential genotypes for future utilization in “egusi” melon breeding programs.

MATERIALS AND METHODS

The experiment was carried out at the Teaching and Research Farm of the Department of Crop Science, University of Nigeria, Nsukka, Nigeria. Nsukka is located at latitude 06°N, longitude 07°24' East and altitude 447.26m above sea level in the derived savanna of the South Eastern Agro-ecological zone of Nigeria.

Table 1.Description of 'egusi' melon accessions and watermelon varieties used for the study.

S/N	Accessions	Melon	Source	Description of Materials
1	Taraba	'Egusi' melon	Taraba State	Thin skin and thick tips.
2	Abakaliki	'Egusi' melon	Ebonyi State	Thin skin and black molded edges.
3	Nsukka	'Egusi' melon	Enugu State	Thin skin flat and oval shape
4	Kolos	Watermelon	IAR, Kaduna State	Thick brown skin, with dark patches
5	Koalack	Watermelon	IAR, Kaduna State	Thick brown skin with dark tips

IAR-Institute of Agricultural Research, Ahmadu Bello University, Samaru Zaria, Nigeria

The genetic materials consist of three accessions of "egusi" melon and two varieties of watermelon (Table 1) collected from different indigenous sources in four agro-ecological zones of Nigeria. Experimental site measuring 14m x 18m was laid out in a randomized complete block design (RCBD) replicated three times. Planting was done at the spacing of 1m x 1m. Seeds were sown at seed rate of 3 – 4 seeds per hole and were thinned down to two vigorous plants per stand at 14 days after planting. The accessions in Table 1 were crossed in all possible combinations without reciprocal to produce ten F_1 hybrids in year 2013. Hybrids were selfed to produce F_2 in year 2014. The hybrid and F_2 were further evaluated for growth and yield attributes.

Data Collection: The following agronomic and yield data were collected; days to first seedling emergence, days to 50% seedling emergence, length of vine at 30 days after planting (cm), number of branches at 30 days after planting, days to first male flowering, days to first female flowering, days to 100% male flowering, days to 100% female flowering, fruit per plant, weight of fruit per plant (kg), average fruit weight (kg), number of seeds per plant, weight of seeds per plant (g), seed yield per fruit (g), 100 seed weight (g), seed yield Ha^{-1}(g).

Data Analysis: The variation among the hybrids obtained from the experiments were partitioned into genetic components attributable to general (GCA) and specific (SCA) combining abilities following the Griffing (1956) Model 11 Method 1 (parents, F_1 with reciprocal) analytical procedures as explained by Singh and Chaudhary (1985). Clustering analysis and principal component analyses were done using the software package GenStat Release 10.3 Discovery Edition 4 (GenStat 2011).

RESULTS AND DISCUSSION

Analysis of variance showed highly significant effect of general combing ability (GCA) ($P \leq 0.01$) in all traits measured (Tables 2, 3) with exception of weight of seed per plant (Table 3), while the effect of the specific combining ability (SCA) was significant in few traits. Significant effect of GCA and SCA obtained in this study were also reported by Souza *et al*. (2012) in watermelon. General and specific combining abilities are important indicators of the potential of parental lines for generating superior breeding populations. The consistent higher GCA over SCA observed in all the traits except days to 50% seedling emergence, weight of seed per plant and seed yield per hectare indicates that the traits are mostly under the control of additive gene actions.

A small or negative combining effect indicates a poor ability to transfer its genetic superiority to hybrids (Cruz and Regazzi, 1994). The largest positive values have the largest effects. On the other hand, the largest negative values have the smallest effects (Tenkouano *et al*. 1998). Thus, the result in Table 4 showed that Taraba parent had high significant ($P \leq 0.05$) negative GCA in all growth and phenological traits recorded except in vine length at 30 days after planting that exhibited positive GCA. Conversely, high significant positive ($P \leq 0.05$) GCA was observed in the parent, Kolos in all the traits, but in vine length at 30 day after planting. The yield and yield components of the GCA estimates presented in Table 5 displayed that the parent, Kolos had a positive and highly significant ($P \leq 0.05$) GCA in all yield and yield related traits measured except in number of fruit/plant. The parent, Nsukka recorded significant ($P \leq 0.05$) relatively low GCA in most of the yield and yield related traits. Abakaliki parent was the least in the number of fruit/plant, average fruit weight and weight of seeds/plant while Taraba parent recorded significantly lower ($P \leq 0.05$) GCA in seed yield/fruit than any other parents. A high positive GCA values means the parental lines has high potential for generating superior offspring (Cruz and Regazzi 1994). This underlies that these traits are heritable. The parent Kolos was a good general combiner for yield and other yield components. However, in respect to earliness *per se*, parents and crosses that have negative GCA and SCA values were good combiners for earliness. Therefore, Taraba parent was best in achieving earliness in key traits such as days to flowering. The parents, Kolos and Taraba could be used as good parental source for improvement of growth and yield attributes in melon plants.

Table6 shows the agronomic traits of the hybrids SCA estimates studied. The result showed that the cross, Abk x Nsk recorded significantly ($P \leq 0.05$) high SCA in all agronomic traits measured except in vine length and number of branches at 30 days after planting. The hybrid, Abk x Koa showed significantly ($P \leq 0.05$) high SCA in vine length and number of branches at 30 days after planting. The crosses Kol x Abk, Kol x Koa, Kol x Nsk, Nsk x Koa, Tar x Abk, and Tar x Kol displayed significantly ($P \leq 0.05$) low SCA in one or more growth traits measured. The yield and yield components obtained in Table 7 showed significant ($P \leq 0.05$) and high SCA in the hybrids; Abk x Koa, Tar x Kol, Kol x Abk and Nsk x Koa. Significant low SCA was recorded in the hybrids Abk x Nsk, Kol x Koa, Tar x Kol, and Tar x Nsk. As earlier reported, the significant effects of GCA and SCA obtained in this study on the measured traits were also reported by Souza *et al*. (2012) in watermelon.

The higher positive specific combining ability obtained in the hybrid, Kol x Abk could have resulted from the influence of the parent (Kolos) that was identified as the best general combiners for yield and yield components. This suggests that either additive x additive and/or additive x dominance genetic interactions were predominant. The superiority of these crosses may be due to complementary and duplicated type of gene interactions. Similar results were reported by Idohosa and Alika (2013). The hybrids; Abk x Nsk, Kol x Abk, and Nsk x Koa have the potentials of producing good segregates for selections for these attributes in the higher generations.

The cluster analysis is an appropriate method for determining family relationships (Mellingers 1972). The analysis of overall pattern of genetic diversity and relationships among germplasm accession facilitates the selection of parents with diverse genetic background (Murphy *et al*. 1986; Souza and Sorrels 1991). Hence, cluster analysis helps to group the genotypes on the basis of their genetic similarities or diversity. The hierarchical clustering of the hybrids (F_1) and F_2 progenies was presented in the Figures 1-2. Four and three clusters were obtained in F_1 and F_2 progenies, respectively in all the traits combined at similarity axis of 0.7. The four and three clusters obtained in F_1 and F_2 generations, respectively in relation to all the traits combined show dissimilarities of the hybrids with Tar x Kol, and Nsk x Koa showing the highest diversity. Thus, selection and crosses between hybrids that showed higher divergence can result in higher heterosis. Therefore, hybrids; Tar x Kol, and Nsk x Koa that showed higher genetic diversity could be selected for further improvement in 'egusi' melon.

Principal component analysis is a useful technique that provides information about the groups where certain traits are more important in allowing the breeders to conduct specific breeding programs (Salimi *et al*. 2012). The traits with the higher vectors irrespective of the sign showed higher contribution to phenotypic variation among the genotypes. Table 7 shows the results of the principle component analysis for the 16 characters of F_1 and F_2 genotypes. Vector 1 accounted for 81.07% in F_1 and 98.32%in F_2 of the total phenotypic variation observed among the population. In F_1, seeds/plant (-0.96547) had the highest contribution to the total phenotypic variation observed in the hybrids, followed by weight of seed/plant (-0.23177), seed yield/fruit (-0.10535), seed yield/ hectare (-0.0496) while days to 50 % seedling emergence was the least (0.00003). Similarly, in F_2, seeds/plant (-0.98196) was the highest contributor to phenotypic variation followed by weight of seed/plant (-0.1488), seed yield/hectare (-0.08818), seed yield/fruit (-0.07337), while the lowest contribution was recorded in number of fruits/plant (-0.00039). The higher phenotypic percentages obtained in F_I (81.07%) and F_2 (98.32%) revealed that most of the variation was captured in the vector 1. Based on the result of the principal component analysis, the important characters responsible for genetic diversity in the F_1 and F_2 generations were in number of seed/plant, weight of seeds/plant, seed yield/fruit and seed yield/hectare, though seed yield/hectare showed lower contribution to phenotypic variation in F_1. Similarly, number of pods/plot, pod yield/plot and seed yield were important contributing variables in distinguishing the accessions (Nwofia *et al*., 2013). The greater diversity in the present materials could be attributed to the four characters especially number of seed/plants that showed consistent higher contributions in the total phenotypic variation obtained in the two generations. These traits will offer a good breeding basis for further improvement of yield in 'egusi' melon.

Table 2. Combining ability analysis for growth and phenological traits in five-parent diallel crosses of 'egusi' and watermelons.

Sources of Variation	DF	Days to Seedling Emergence	Days to 50 % Seedling Emergence	Length of Vine/ 30days	Number of Branches/ 30days	Days to first flower initiation in male	Days to first flower initiation in female	Days to 100%Male flowering	Days to 100% Female flowering
GCA	4	1284.85**	104.24**	584.25**	584.25**	1047.17**	25388.43**	1423.37**	5658.13**
SCA	10	-106.34ns	210.70**	39.86**	-32.6^{ns}	-7197.81^{ns}	-8613.87^{ns}	-11614.36^{ns}	-14046.35^{ns}
Error	48	0.08	0.07	0.17	0.17	70.34	2.44	0.754	3.41
GCA/SCA		-12.08	0.49	0.45	0.45	-0.15	-2.95	-0.12	-0.4

*,**Significant at p≤0.05 and p≤0.01, respectively, GCA: General combing ability, SCA: Specific combining ability, DF: Degree of freedom

Table 3. Griffing analysis of variance for yield and yield component in five-parent diallel crosses of 'egusi' and watermelons.

Sources of Variation	Wt. of fruits/plant	Average fruit weight/plant	Number of Seeds/plant	Wt. of Seeds/plant	Seed yield/fruit	100 Seed Wt.	Seed yield/ha
GCA	5.28**	453.26**	18862.15**	-6708.41^{ns}	1647.15**	137.96**	12297.31**
SCA	-44.37^{ns}	-7.17^{ns}	63797715.34**	-25078.31^{ns}	-6941.10^{ns}	-1120.85^{ns}	21646.63**
Error	0.053	0.057	8124.6	630.82	57.76	9.13	913.51
GCA/SCA	-0.12	-63.22	0.00	0.27	-0.24	-0.12	0.57

*,**Significant at p≤0.05 and p≤0.01, respectively, GCA: General combing ability, SCA: Specific combining ability.

Table 4. General combining ability (GCA) estimates of growth and phenological traits of melon parents used for the study.

Parents	Days to Seedling Emergence	Days to 50 % Seedling Emergence	Length of Vine/ 30days	Number of Branches/ 30days	Days to first flower initiation in male	Days to first flower initiation in female	Days to 100% Male flowering	Days to 100% female flowering
Taraba	-2.9	-3.28	2.82	-0.98	-13.92	-15.26	-16.52	-17.44
Kolos	3	3.12	1.87	0.84	14.28	12.64	17.18	19.5
Abakaliki	0.1	0.52	-1.14	0.01	1.18	1.24	0.48	1.38
Nsukka	0.4	-0.08	0.33	0.64	-1.12	1.04	-0.12	-0.2
Koalack	-0.6	-0.28	-1.46	-0.5	-1.02	0.34	-1.02	-3.1
S.E	0.13	0.2	0.21	0.12	3.75	0.7	0.39	0.83
Critical value (P≤0.05)	0.26	0.38	0.41	0.24	7.58	1.41	0.79	1.67

S.E: standard error

Table 5. General combining ability (GCA) estimates of yield and yield component traits of melon parents used for the study.

Parents	Number of fruits/plant	Wt. of fruits/plant	Average fruit weight/plant	Number of Seeds/plant	Wt. of Seeds/plant	Seed yield/fruit	100 Seed Wt.	Seed yield/ha
Taraba	115.51	-0.17	-0.74	-56.07	8.13	-1.52	-2.26	-22.54
Kolos	85.91	1.23	1.91	241.94	39.49	28.21	4.55	45.47
Abakaliki	42.32	-0.26	-0.05	-73.27	-5.72	14.85	2.27	22.71
Nsukka	112.43	-0.11	-0.5	-24.25	-11.42	-2.23	-0.3	-3.01
Koalack	48.92	-0.69	-0.63	-88.37	-30.47	5.53	-4.26	-42.65
S.E	0.44	0.11	0.22	40.31	11.23	3.4	1.35	13.52
Critical value (P≤0.05)	0.89	0.21	0.22	81.47	22.77	6.87	2.732	27.32

S.E: standard error

Table 6. Specific combining ability (SCA) estimates of growth and phenological traits of melon hybrids used for the study.

Hybrids	**Days to Seedling Emergence**	**Days to 50 % Seedling Emergence**	**Length of Vine/ 30days**	**Number of Branches/ 30days**	**Days to first flower initiation in male**	**Days to first flower initiation in female**	**Days to 100% Male flowering**	**Days to 100% female flowering**
Tar x Kol	3.4	3.48	-7.51	0.93	18.32	17.56	23.22	21.54
Tar x Abk	-7.2	8.92	5	1.95	-29.98	-32.54	-36.08	-38.4
Tar x Nsk	-7.5	-8.32	-1.7	-2.6	-27.68	32.34	-35.48	-36.8
Tar x Koa	-6.5	-8.12	-0.56	-1.46	-27.78	-31.64	34.58	-33.9
Kol x Abk	-0.1	0.68	4.42	-8.15	7.22	6.56	6.72	38.5
Kol x Nsk	0.1	0.28	6.67	0.58	13.52	15.26	15.82	54.6
Kol x Koa	-10.5	-12.12	-1.23	-3.28	-42.78	59.54	70.28	-33.5
Abk x Nsk	-12.5	-14.52	-0.77	-3.57	-56.58	-48.84	-52.48	-55.6
Abk x Koa	4	2.88	7.55	2.07	25.62	23.86	28.92	27.8
Nsk x Koa	4.7	3.68	7.44	1.3	28.32	14.56	17.02	16.9
S.E	0.31	0.29	0.43	0.29	9.19	1.71	0.95	2.023
CD(P≤0.05)	0.63	0.57	0.92	0.59	18.57	3.46	1.92	4.09

SE :standard error, CD: Critical difference, Tar x kol:Taraba x kolos, Tar x Abk:Taraba x Abakaliki, Tar x Nsk:Taraba x Nsukka, Kol x Abk:Kolos x Abakaliki, Kol x Nsk:Kolos x Nsukka, Kol x Koa:Kolos x Koalack, Aba x Nsk:Abakaliki x Nsukka, Abk x Koa :Abakaliki x Koalack, Nsk x Koa : Nsukka x Koalack.

Table 7. Specific combining ability (SCA) estimates of yield and yield component traits of melon hybrids used for the study.

Hybrids	**Number of fruits/plant**	**Wt. of fruits/plant**	**Average fruit weight/plant**	**Number of Seeds/plant**	**Wt. of Seeds/plant**	**Seed yield/fruit**	**100 Seed Wt**	**Seed yield/ha**
Tar x Kol	-0.09	0.93	-0.8	-831.2	89.01	36.93	7.27	72.7
Tar x Abk	-2.69	-2.86	-0.92	-457.3	-89.52	-43.35	-16.97	-170
Tar x Nsk	-4.01	-3.01	-3.92	-506.3	-258.04	-26.27	-14.39	-144
Tar x Koa	-2.89	-2.42	-0.35	-442.2	-64.77	-34.03	-10.43	-104
Kol x Abk	0.59	-0.11	0.39	110.56	73.38	26.43	89.06	120
Kol x Nsk	-1.06	0.45	-0.73	-204.9	40.84	-2.92	20.93	114
Kol x Koa	-2.42	-3.83	-3	-740.2	-95.13	-63.94	-7.72	-172
Abk x Nsk	-2.69	-2.93	-1.17	-489.1	-69.98	-42.64	-18.92	-189
Abk x Koa	1.18	2.25	0.89	416.29	53.8	6.84	4.6	45.4
Nsk x Koa	1. 29	1.62	-0.12	311.41	40.98	-0.2	4.45	44.6
S.E	1.07	0.25	0.26	98.74	27.51	8.33	3.31	33.11
CD(P≤0.05)	**1.15**	**0.51**	**0.53**	**199.55**	**55.61**	**16.83**	**6.69**	**66.9**

SE : standard error, CD:Ctritical difference, Tar x kol:Taraba x kolos, Tar x Abk:Taraba x Abakaliki, Tar x Nsk:Taraba x Nsukka, Kol x Abk:Kolos x Abakaliki, Kol x Nsk:Kolos x Nsukka, Kol x Koa:Kolos x Koalack, Aba x Nsk:Abakaliki x Nsukka, Abk x Koa :Abakaliki x Koalack, Nsk x Koa :Nsukka x Koalack.

Table 8. Latent vectors for 16 characters of F_1 and F_2 generations of 'egusi' and watermelon cross

Traits	Vector 1 (F_1)	Vector 1 (F_2)
Days to seedling emergence	0.00084	0.00128
Days to 50% Seedling Emergence	0.00003	-0.00045
Length of Vine at 30DAP	-0.00408	-0.00439
Number of Branches	0.00206	0.00409
Days to First Flower initiation in Male	0.00462	0.00369
Days to First Flower initiation in female	0.01885	-0.00223
Days to 100% Male Flowering	0.0038	0.00822
Days to 100% Female Flowering	0.01188	-0.01572
Number of Fruits/Plant	0.00116	-0.00039
Weight of Fruits/Plant	-0.00137	-0.00135
Average Fruit Weight/Plant	-0.00027	-0.00141
Number of Seeds/Plant	**-0.96547**	**-0.98196**
Weight of Seeds/Plant	**-0.23177**	**-0.1488**
Seed Yield/Fruit	**-0.10535**	**-0.07337**
100 Seed Weight	-0.00496	-0.00882
Seed Yield/hectare	**-0.0496**	**-0.08818**
Percentage Variation	**81.07%**	**98.32%**

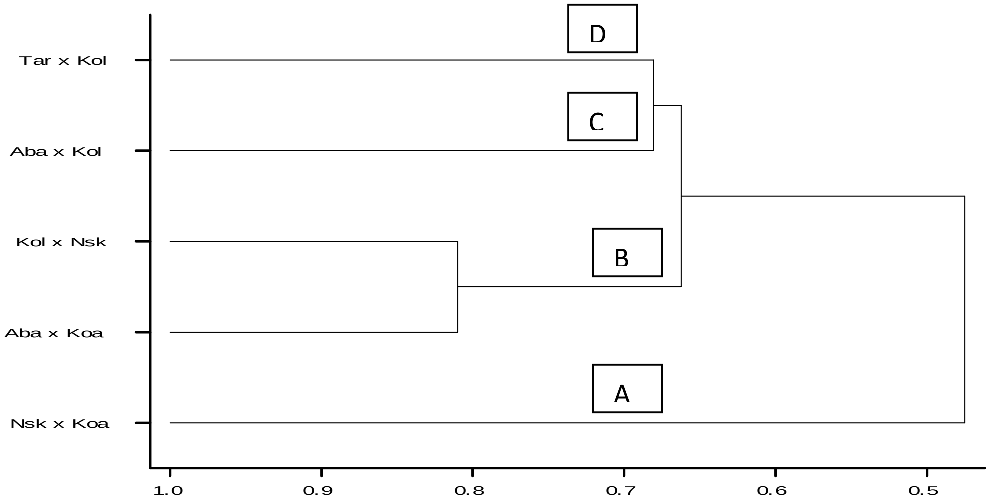

Figure 1. Hierarchical clustering of the five F_1 hybrids in all the traits combined.

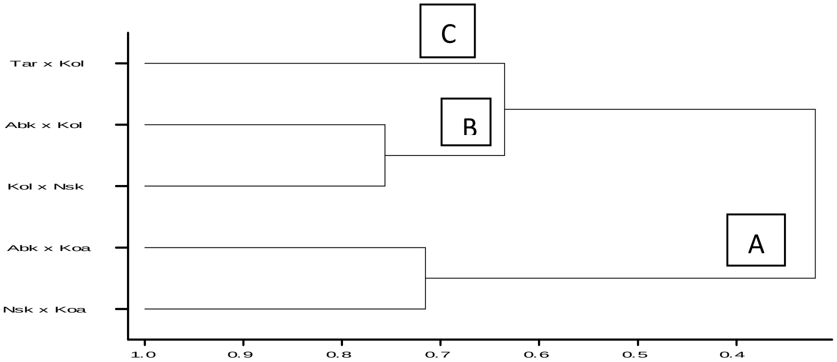

Figure 2. Hierarchical clustering of the five F_2 generations in all the traits combined

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