

COMPARATIVE EVALUATION OF COWPEA GENOTYPES AND BREEDING FOR SHORTER COOKING TIME

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Introduction

Critical constraint to consumption of cowpea is the long cooking time caused by storage environments of relative humidity and high temperature (Phillips et al., 2003). This occurrence is called the hard-to-cook (HTC) deficiency besides has been experiential on different legume species.

Long-time in cooking is an undesirable characteristic for consumer because of the relatively large amount of energy required to soften grains of these cultivars (Yeung et al., 2009).

Decreasing the cooking times and improving palatability are good qualities for cowpea grains demand, and would be especially important in areas cowpea are eaten as primary sources of protein. However, the genetic disparity for cooking times and palatable quality are less

Objectives

To evaluate the diversity of cooking time in cowpea accession

To determine the mode and mechanism of inheritance of genes for cooking time on cowpea. To estimate the combining ability of putative parents for cooking time in cowpea

Methods

Screening and Evaluation of 101 Cowpea Accessions

This research work was carried out between 2018 and 2020. Seeds were sourced from Gene Bank, International Institute of Tropical Agriculture. The 101 accessions were grown in November, 2018 - January of 2019.

Cowpea Cooking

The harvested cowpea from 2018 field work were taken to the laboratory and analyzed based on cooking time. This was achieved by cooking the bean of the different 101 accessions. This laboratory work was done in 2019. Two seeds from each of the accessions in 2018 were planted, and crosses were carried out in late May 2019. Parental lines crossed are as follows: TVU 2, TVU 45, TVU 43, TVU 8, TVU 23, OK 3 as males and TVU 34, TVU 52, OK1, TVU 50, TVU 21, TVU 39, TVU 36, TVU 29, OK 4 as females. The harvested F1 hybrids were planted alongside their parents for evaluation in September 2020.

Hybridization

Partial Diallel mating design was used to perform crosses (Kempthorne and Curnow, 1961).

A total of 54 crosses were made with each female crossing with each male. 16 crosses were successful in forming fruits. Emasculation was carried out on all the female plants post booting of plant flower



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Performance of some Agronomic Traits measured in the parents and selected F1 population.

Results and Discussion

Table 4.1 Shows the means for some agronomic traits measured in the parents and selected F1 population. From the table the F1 TVU 43 x TVU 21 gave the highest mean value for plant height (184.60) whereas the lowest mean value plant-height was given by Check OK 4 (9.00). Other F1 progenies that recorded high mean values in plant heights. The parent TVU 50 gave highest leave area index (2.19) while the F1 progeny TVU 45 x TVU50 gave lowest mean value (0.14) of leave index.

Analysis Variance for Combining Ability Effects in Thirty F1 and Parents for Various traits

Table 4.2 shows analysis variance combining effects in parents and F1 progenies from the table, highly significant values recorded plant height per plant male parents (9.95), female parents (97.01) Male x Female (65.31) A significant but negative value was recorded by female x male variants (-5.087) also from the table below, female parents, male and female variance all gave highly significant values for leave area index LAI 0.220, 0.024 and 0.027 respectively.

Performance general combining GCA measured on fifteen selected studied traits of cowpea parents.

Table 4.4 shows general combining ability GCA measured on selected studied traits of Cowpea parents. Male parents per cross generally was more the female parents. Many of selected promising parents did better than check varieties OK1, OK 3, and OK4 as seen in table 4.3. The parents TVu 23 gave the highest significant plant height per plot (97.89) whereas the parents TVu 29 gave (2.45) while a high negative significant value (13.55) was recorded for TVu 50. Male parents TVu 52 and TVu 36 recorded negative but not significant values (-9.05 and 28.55) parents which recorded highly significant values.



TABLE 1: Mean Performance for Agronomic Traits of selected Parents, checks varieties and F1 population evaluated in 2019.

VARIETY	PHT	LAI	NOL	DTF
TVU 2 X TVU 34	90.50 ^{a-h}	0.265 ^{e-j}	6.50 ^{b-d}	47 ^{a-c}
TVU 2 X TVU 52	111.50 ^{a-f}	0.465 ^{a-q}	7.00 ^{b-d}	48 ^{ab}
TVU 2 X OK1	95.00 ^{a-d}	0.315 ^{a-k}	10.00 ^{a-d}	47 ^{a-c}
TVU 43 X TVU 21	184.60 ^{a-h}	0.325 ^{a-q}	6.50 ^{b-d}	49 ^{a-c}
TVU 43 X TVU 39	145.90 ^{d-i}	0.470 ^{a-o}	11.50 ^{a-d}	45 ^{a-c}
TVU 8 X TVU 36	20.00 ^{b-f}	0.305 ^{b-i}	6.00 ^{b-d}	48 ^{a-c}
TVU 45 X TVU 50	91.00 ^{b-i}	0.140 ^{a-i}	9.00 ^{c-d}	50 ^{a-c}
OK3 X TVU 39	85.50 ^{b-i}	0.495 ^{a-p}	10.00 ^{a-d}	48 ^{a-c}
OK3 X TVU 36	79.00 ^{a-g}	0.295 ^{a-n}	11.00 ^{a-d}	50 ^{a-c}
TVU 23 X TVU 29	117.50 ^{a-g}	0.445 ^{a-o}	10.50 ^{a-d}	50 ^{a-c}
TVU 23 X OK 4	117.00 ^{a-f}	0.740 ^{a-q}	11.00 ^{ad}	50 ^{a-c}
TVU 2	13.6 ^{a-j}	1.56 ^{a-q}	11.0 ^{b-d}	36 ^{ab}
TVU 8	10.5 ^{b-i}	1.17 ^{a-q}	7.00 ^{cd}	48 ^{ab}
TVU 21	18.5 ^{a-h}	1.98 ^{a-l}	22.00 ^{a-d}	48 ^{ab}
TVU 23	16.3 ^{a-g}	1.89 ^{a-o}	21.50 ^{a-d}	49 ^{ab}
TVU 29	14.75 ^{a-j}	1.32 ^{a-q}	10.50 ^{b-d}	48 ^{a-c}
OK 4	9.0 ^{e-j}	0.7 ^{e-q}	11.00 ^{b-d}	46 ^{a-c}
TVU 36	34.5 ^{c-f}	2.01 ^{a-n}	14.00 ^{a-d}	49 ^{ab}
TVU 39	18.0 ^{ef}	1.90 ^{a-o}	8.50 ^{b-d}	48 ^{a-c}
TVU 43	13.5 ^{a-j}	1.43 ^{a-q}	10.00 ^{b-d}	49 ^{a-c}
TVU 45	20.0 ^{a-j}	1.62 ^{a-q}	4.00 ^{cd}	47 ^{a-c}
TVU 50	15.25 ^{a-i}	2.19 ^{a-i}	24.00 ^{a-d}	50 ^{a-c}
TVU 52	11.5 ^f	1.60 ^{a-q}	7.00 ^{cd}	47 ^{a-c}
OK 1	21.0 ^{ef}	2.15 ^{a-k}	12.60 ^{a-d}	47 ^{a-c}
OK 3	17.0 ^{a-f}	1.85 ^{a-p}	18.00 ^{a-d}	47 ^{a-c}
MEAN	12.7	1.06	11.25	47
SE	1.03	0.06	0.87	3.08

PHT= plant height; LAI=leave area index; NOL=number of leaves; DTF= days to flowering;
^{a-q} = means with same letters are not significantly different.

TABLE 2: Analysis of Variance for Combining Ability Effects in F1 and Parents for Various Traits

Mean sum of squares							
Source of variation	DF	PHT	LAI	NOL	DTF	GWTPP	CT
Male parents	8	9.95 ^{**}	0.117 [*]	67.95 ^{**}	65.95 ^{**}	39.34 ^{**}	3788.3 [*]
Female parents	5	97.01 ^{**}	0.220 ^{**}	80.62 ^{**}	3.931 [*]	2.31 [*]	1169.5 ^{**}
Male x Female	22	65.31 ^{**}	0.198 [*]	70.34 [*]	37.133 ^{**}	17.96 [*]	2129.3 ^{**}
Error	53	75.48 [*]	0.417 [*]	70.10 [*]	1.967 ^{**}	29.20 [*]	0.01 ^{ns}
Variance female x male σ^2_{fm}		-5.087 [*]	-0.109 ^a	0.12 [*]	17.58 ^{**}	-5.62 [*]	1064.65 ^{**}
Female variance σ^2_f		5.95 ^{**}	0.024 ^{**}	4.77 ^{**}	-1.73 ^{ns}	0.753 ^{**}	-53.3 ^{ns}
Male variance σ^2_m		1.68 [*]	0.027 ^{**}	5.66 ^{**}	2.56 [*]	4.21 ^{**}	138.25 [*]
Replication	1						

*=0.05 level of significances; **=0.01 level of significances; ***=0.001 level of significance. Ns= not significant. DF= degree of freedom; PHT= plant height; LAI= Leave area index; NOL=number of leave; DTF=days to flowering; GWTPP=grain weight per plant; CT= cooking time.

Conclusion

Significant genotypic variability observed cooking time eleven-cowpea varieties evaluated inheritance of cooking time.

Presences of transgressive segregants within the F1 cross TVu 2 x OK1, OK3 x TVu 39 and OK3 x TVu 36 could show that a replacement varieties identified. Notably, these crosses were between short to long cooking parents (TVu 2= 82minutes, Tvu 39=78minutes, OK1=51minutes, OK3=51minutes, TVu 36=50minutes,) The non-significant difference reciprocal crosses suggests genes controlling cooking time trait were nuclear and cytoplasmic genes with no effect within inheritance of cooking time. The huge genotypic effect on cooking time combined with high heritability for it suggests, selection supported trait itself leaves progress in breeding. This may have caused the eventual fast cooking time of cowpea cultivar acceptable to consumers.

Reference

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