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Inheritance Of Amylose Content And The Relationship Between Grain Appearance Quality Traits And Amylose Content In Rice Genotypes In Uganda

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Abstract: *Amylose content and grain appearance quality of rice (Oryza sativa L.) represent a major problem of rice marketing in many rice producing areas in the world. In Uganda cooking and eating quality and that of the appearance quality remain undefined in the rice breeding program. The objective of this study was to determine the amylose content and to understand the inheritance patterns of amylose content and possible relationships between grain appearance quality traits and amylose content in rice in Uganda. Forty genotypes were planted in two seasons (2015B and 2016A) in alpha lattice design at national crop resource research institute with three replications to characterize for amylose content and grain appearance quality traits. Seven parents involving 3 low, 4 intermediate amylose content genotypes were crossed in a half diallel and the F1 were advanced to F_2 generation which together with parents were planted in the field in alpha lattice design in three replications.*
The results showed that amylose content (AC), Kernel width (KW) and kernel length to width ratio (K/L) were affected by both genetic effects and genotype by season (G x S) interaction while kernel length (KL) was mainly affected by genetic factors. Genotypes were grouped into low, intermediate and high amylose content categories. AC correlated weakly negatively with the physical appearance quality traits of the grain implying that improvement of amylose content in grains would not affect grain size and shape. There were significant differences ($P \leq 0.001$) among the parents for general combining ability (GCA) and crosses for specific combining ability (SCA) ($P \leq 0.5$) for amylose content, indicating that both additive and non-additive gene actions were responsible in the inheritance of AC, however, the variance component for GCA was larger than the variance component for SCA implying that the inheritance of amylose content was more conditioned by the additive gene effect.
Key words: *Kernel length and width, amylose content, combining ability, additive gene effects and inheritance*

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I. Introduction

Uganda has grown lowland rice since 1974 especially in Eastern region [1]. High yielding, lowland rice production requires a lot of water, knowledge and labor. These factors had slowed down the adoption of rice in Uganda. However, with the introduction of NERICA and other upland rice varieties, rice has been widely adopted by farmers and now rice is grown throughout the country mainly by small-scale farmers [1].

Quality traits in rice comprises of physical appearance, cooking and eating properties and, more recently, nutritional value. The value of each trait, for example, the length of the grain, varies according to local ethnic background of the consumer [2]. Physical properties including yield of edible and marketable polished grain, uniform shape, whiteness and, in most countries, translucence are immediately obvious to consumers and so they are major factors defining market value [3]. Predictable expression of these traits across seasons and years give a variety its reputation. Cooking and eating quality of rice are mostly determined by the amylose content, gel consistency and gelatinization temperature of the grain endosperm. The appearance quality is determined by grain shape as specified by length-width ratio and the translucency of the endosperm [4] The long-grain quality varieties tend to produce dry, fluffy and separated cooked grains, whereas the medium- and short-grain varieties tend to produce clumped, moist and chewy grains after cooking. Rice of low amylose content are waxy, sticky and do not expand in volume when cooked and that of intermediate amylose content rice (<30%) cook moist, tender and does not harden after cooling and high amylose content variety (>30%) [5]has high expansion volume and non-sticky but become hard on cooling [6]. While other varieties with long grain cook soft.

Appearance quality of the rice grain represents a major problem of rice production in many rice-producing areas of the world and this is especially the case in rice production in Uganda [7] Currently, there is a

strong emphasis in Uganda on improving yield and quality of rice varieties [8] especially the quality of locally released varieties. The most serious problems lie in cooking, eating, and appearance qualities and to some extent, in milling quality. Amylose content and grain appearance qualities are highly variable and are highly influence by variety and environment [9]. It is important to breed varieties showing least change in cooking, eating and appearance quality under local environments and to understand the mode of the inheritance of amylose content in the local cultivars.

II. Materials and methods

2.1 Genetic materials

Forty rice genotypes (*Oryza sativa* L.) collected from NaCRRI rice breeding program, International Rice Research Institute (IRRI), International Institute of Tropical Agriculture (IITA), Africa Rice Centre (ARC), International Centre for Tropical Agriculture (CIAT), Madagascar and Korea were planted in alpha lattice design with three replications in two seasons in the same site at NaCRRI. The grains were dried in the sun to a moisture content of about 14%, and were dehulled using mortar and pestle. Seven lines were selected from the 40 genotypes after characterization based on the amylose content and were crossed in a half diallel mating design to generate F_1 seed at NaCRRI. Crossing was done by hand pollination using manual emasculation and hooking method [10]. The F_1 seeds were planted in leveled pots in the screen house. The produced F_2 seeds along their parents were planted in the field in alpha lattice design with three replications, 8 blocks x 5 genotypes at spacing of 20x20cm. The F2 plants were harvested individually at maturity and dried in the sun until the moisture content was about 14% and then milled using mortar and pestle to produce brown rice.

1. Amylose content

Amylose content (AC) was determined from the starch according to the simplified method of [11] and modified by [12] and test tubes were used in place of volumetric flasks to prevent upsetting. 0.1g of rice starch was put into a test tube and was wetted with 1 mL of 95% ethanol and 4.6 ml of 1 M sodium hydroxide. The contents were shaken well and heated in a boiling water bath for 10 minutes to gelatinize the starch. After cooling for 30 minutes, the volume of the solution was made up to 10 ml using distilled water. 0.1 ml of the sample was pipette from the 10 ml into test tube in duplicate. 1 ml 1M acetic acid and 2.0 ml I-KI solution were added into each test tube and the volume in the test tubes was made up to 8.25 ml with distilled water. The absorbance of the solution was measured at 620 nm against the blank solution using a spectrophotometer (UNICAM UV300, Thermo scientific, UK). AC was calculated using a standard curve made from pure amylose starch from (Sigma A0512)

2. Measuring the traits of appearance quality

The grains dimension were measured according to the method described by [13]. Paddy rice was de-husked using mortar and pestle. Ten randomly selected unbroken brown rice grains of each genotype were lined up length-wise along the x-axis of a graph paper to measure the length, after which the grains were arranged in the breadth to measure the width. The values were averaged and used as the measurements for length and width of individual grains. The length to width ratio of the grains was calculated and the results which reflected the shape of the grains recorded [3].

3. Statistical analysis

Data were analyzed individually for each season and combined across season using linear mixed model (REML) option of GenStat 12th Edition (VSN International Ltd., UK) with genotypes being considered as fixed effects while season, replications and blocks within replications as random effects. The statistical procedures followed a statistical model of lattice incomplete block analysis with adjusted blocks within unadjusted replications [14].

$Yijk = \bar{\bar{Y}} \ldots + Gi + Rj + (B/R)jk + eijk$……..(1)

Where Yijk = observation of genotype in replication j, and block k; $\bar{\bar{Y}}$= the general mean; Gi= effect of genotype i; Rj = effect of replication j and (B/R)ij = the interaction effect between replication j and block k; eijk = error of observation ijk.

After analyzing for season one and two, a combined season analysis was performed following the model:

$Y_{ijk} = \bar{\bar{Y}} + Gi + Sj + GxSij + S/Rjk + eijk$ …… (2)

where; $\bar{\bar{Y}}$ is grand the mean, Gi is the effect of the i^{th} genotype, Sj is the effect of the j^{th} season, GxSij is the interaction of the i^{th} genotype with the j^{th} season, S/R_{jk} is the effect of the k^{th} replication in the j season, and e_{ijk} is the random error.

For the analysis of combining ability and gene action in relation to half diallel mating design,

Alpha lattice design consisting of 3replications 8 blocks five plots was used. In each block, each plot contained 15 F2 plants. The genotypic difference among F2 was tested by F test [14].

F[(a-l), m)]= MSg,/MSe ……..(4)
Where (a-I) and m are the degrees of freedom associated with the numerator and denominator of the F ratio, and MSg and MSe are the genotype and error mean squares respectively.
combining ability analysis was performed following Method 4 Model 1 of [15] option of GenStat (VSN International Ltd., UK) following the model:
Yij = Y… + Gi + Gj +Sij +Bk + eijk…… (5)

Where $\bar{\bar{Y}}$ is the general mean; Gi is the general combining ability effect of i^{th} parent, Gj is the GCA effects of j^{th} parent, Sij is the SCA of ij^{th} cross, Bk is the effect of kth block and eijk is the error effect particular to the ijk^{th} observation. The mean square error was used as denominator in the F-values for testing combining abilities [15] as; F[(p-l),ml = Mg/Me, F[p(p-3)/2, ml = Ms/Me; where Mg, Ms and Me are mean square due to GCA, SCA and error. While [(p-1),m] and [p(p-3)/2,m] are degrees of freedom associated with the numerator and denominator of the F ratio respectively. Component due to GCA and SCA was calculated according to [16].

Error (δ^2 e), genotypic (δ^2 g) and phenotypic (δ^2 p) variances were calculated from expected mean squares of analysis of variance according to [15]. Under the assumptions that parents are unrelated, negligible epistasis and negligible maternal effects, additive (σ_a^2) and dominance (σ_d^2) genetic variances can be related to GCA and SCA effects as follows:

$\sigma_a^2 = 4\sigma^2$GCA…… (6)
$\sigma_d^2 = 4\sigma^2$SCA……..... (7)
$\sigma^2P = 2\sigma^2$GCA+ σ^2SCA+ σ^2e ……... (8)

Heritability was estimated according to the relationship between additive (σa^2), genotypic (σ^2g) and phenotypic (σ^2p) variance. Broad sense heritability (H^2) was determined as the ratio of genetic variance to phenotypic variance and narrow sense heritability (h^2) determined as the ratio of additive to phenotypic variance.
Baker's ratio was used to determine the progeny performance based on the relative importance of GCA and SCA mean squares according to fixed effects model 1[17].

4. Amylose content in selected rice genotypes

The results of analysis of variance (ANOVA) for amylose content in seasons 2025B, 2016A and across seasons are presented in Table 1.

Table 1: Analysis of variance for Amylose content of selected rice genotype planted at NaCRRI 2015B and 2016A

		Seasons		
Source of Variation	**d.f.**	**2015B**	**2016A**	**Across**
Season	1			349.73***
Genotype	39	29.68***	26.583***	49.30***
Season/Genotype	38			5.24***
Error	91	2.17	1.505	1.83
LEE	79			

df = degree of freedom, , *** significance at 0.001, 2015B = season one, 2016A = season two

The results indicated, strong genotype effect (P <0.001), season effect (P < 0.001) for amylose content and season-by-genotype interaction (P <0.001). The amylose content of the genotypes ranged from 15.01 to 27.68 and from 14.28 to 27.99%, for season 2015B and 2016A respectively (Table 2). The rice genotype grown in 2015B had consistently higher AC than the same genotype grown in 2016A. The result in Table 2 also indicated that the extent of the decrease in AC was cultivar-dependent, suggesting that some cultivars for example 1190 and P62H17 were more stable than others for example ART3-8L6P3-2-3-B. However, in this study the temperature was much lower in growth seasons 2015B 24/20^{o}C day/night than in season 2016A 30/20^{o}C day/night during the grain filling period according to weather station in NaCRRI 2015-2016, suggesting that the high day temperature could be the cause of decrease in amylose content of genotypes in the 2016A season. [18]) noted that AC in rice decreased as the mean temperature increased and that greatest drop in amylose content of milled rice was due to increase in day temperature. In contrast, genotype P24H10, ART3-8L6P3-2-3-B-C and ART3-8L6P3-2-3-B had high AC in season 2016A than in 2015B. [19]) noted high amylose content in two waxy cultivars in year 2 which was hotter than year 1. [21] reported that the extent of increase or decrease in AC % varied with varieties.

There were twenty three genotypes classified with intermediate AC, twelve with low and five with high AC in season 2015B but only fourteen genotypes were classified with intermediate AC, with the remaining

twenty five genotypes falling with low AC and only one with high AC in season 2016A. The results suggested that classification of genotypes, varied from one season to another.

Table 2: Percentage Mean of amylose content of genotypes and their responses to different growth seasons at NaCRRI

		% Amylose content		
Origin	**Genotype**	**2015B**	**2016A**	**Across**
Africa Rice	1190	27.65	27.99	27.86
	1191	19.93	18.52	19.12
	ART10-1L15P1-4-8-1	23.40	22.16	22.63
	ART12-L4P7-21-4-B-3	26.04	19.20	20.91
	ART15-11-8-5-2-B-1	26.79	20.13	23.46
	ART16-4-11-13-4	17.82	16.11	16.97
	ART16-5-4-3-3-1-1-1	16.22	14.54	15.38
	ART25-3-29-2-B	22.26	16.76	19.51
	ART3-2L4P19-2-1-B	23.21	17.00	20.10
	ART3-7L9P8-3-B-B-2	24.69	22.63	22.71
	ART3-8L6P3-2-2-B	18.06	16.06	17.07
	ART3-8L6P3-2-3-B	27.55	21.44	24.76
	GSR-1-0057	23.59	20.69	22.14
	Jaribu 220	22.50	19.55	21.03
	Nerica 4	22.50	21.39	21.94
	Nerica 6	24.21	21.68	22.94
	TXD306	22.74	18.22	20.03
	WAB788-16-1-1-2-HB	22.17	20.76	21.46
CIAT	CT11891-3-3-3-M-1-2-1-M	17.57	16.09	16.68
CIAT	PAC-4/0/0/0>19-M-1-1-5-1-M	23.42	19.54	21.48
IRRI	1052	16.75	18.79	17.76
Korea	326104	22.51	20.45	21.28
MGC	Scrid006-2-4-3-4-5	19.82	18.72	19.51
MGC	Scrid 006-2-4-3-5	20.68	15.86	17.45
MGC	Scrid037-4-2-2-5	15.50	14.85	15.11
NaCRRI	Namche 1	22.00	21.66	21.84
	Namche 2	18.16	15.33	16.74
	Namche 3	15.01	14.28	14.64
	Namche 5	23.17	22.38	22.77
	P24H1	21.33	14.30	14.81
	P24H10	16.51	20.64	23.04
	P24H11	25.43	18.91	20.12
	P26H1	16.12	14.75	15.30
	P27H3	23.26	20.50	21.57
	P29H1	19.63	16.93	18.28
	P5H12	20.83	17.84	19.33
	P5H14	20.73	18.54	19.42
	P5H6	17.28	15.42	16.13
	P62H17	20.96	20.78	20.86
	Mean	**21.23**	**18.75**	**19.84**
	LSD	**2.83**	**2.19**	**2.54**
	CV%	**6.94**	**6.97**	**10.65**

LSD = least significant different, CV = coefficient of variation, 2015B = season one and 2016A season two

[22] reported that the classification of amylose into high, intermediate or low depended on the environment where the rice cultivars were grown. The growth season variation in temperature could affect the level of amylose in rice [23] [24] reported that AC of genotype grown in hot environments was low compare to the AC of the same genotype grown in low temperature environments.

The range of variation in AC within the low, intermediate and high amylose group were 7.06%, 6.69% and 6.1% which was attributed to seasonal effects. Based on this, the forty varieties were grouped into three categories. The first category shows no genotype by season interaction as seen in three genotypes: Namche 1 of low AC, P62H17 of intermediate AC and 1190 of high AC. These genotypes were expected to show no significant changes in amylose content in different grwoing seasons. [25] reported that genotypes that showed no genotype by temperature interaction were not expected to show any siginificant change in their amylose content. The second category showed average response to season as observed in thirteen genotypes of low AC and eight of intermediade AC group. The third category was the high responsive genotypes as observed in six genotypes; ART25-3-29-2-B, and P24H1 of low AC, and ART15-11-8-5-2-B-1, ART12-L4P7-21-4-B-3, ART3-8L6P3-2-3-B and P24H11 from the intermediate amylose group. There was drastic fluctuation in amylose content of these genotypes in the two seasons. Genotype P24H1 had the largest drop in amylose content from 21.33% in season 2015B to as low as 14.30% in season 2016A. [9] reported a drop of 5% in non-

wax rice due to increase in day temperature but there could be a reduction of as much as 16% in amylose content among high responsive genotype due to temperature difference [25] suggesting that unstable genotype could change group depending on temperature.

Table 3: Analysis of variance for grain quality traits of selected rice genotype planted over two seasons in NaCRRI

SOV	Df	GW(g)	L/W	KL(mm)	KW(mm)
Season	1	0.40*	1.83*	0.03ns	0.94*
Genotype	39	0.14***	0.38***	0.48***	0.28***
Genotype x season	38	0.03***	0.11*	0.12ns	0.09*
Error	91	0.02	0.11	0.18	0.10
Lee	81	0.01	0.07	0.11	0.06

Gw = grain weight, L/W = kernel length to width ratio, Kl = kernel length, Kw = kernel width, source of variation and Df= degree of freedom, g = gram and mm = millimeter

The result indicated strong genotypic effect ($P < 0.001$) for all the traits of appearance quality and strong seasonal(< 0.05) effect for GW, L/W and KW and high genotype-by-season interaction ($P < 0.001$) effect for GW with that of L/W and KW being significant ($P < 0.05$), indicating influence of environment on these traits. However, seasonal effects and genotype by season interaction effects did not affect KL, suggesting that KL is a grain appearance quality trait which is controlled by genetic factors and not by environmental factors.

The result showed that kernel width among genotypes ranged from 2.0 mm (326104) to 3.7 mm (ART3-8L6P3-2-3-B) in season 2015B and 2016A respectively with most genotypes grown in season 2016A having low kernel width than in season 2015B. [26], [27] reported that grain width of genotypes grown in hot environment were lower than of those grown in cold environment. The average kernel lengths to width ratio were 2.8 mm and 2.5 mm in season 2015B and 2016A respectively. Genotypes in season 2015B were classified in the medium shaped category except genotype ART3-7L9P8-3-B-B-2 and 326104 which fell within the slender shaped and ART3-8L6P3-2-3-B in the bold shaped categories. However, in season 2016A, eleven genotypes were classified as slender, one as bold and the remaining twenty eight genotypes were of medium shape categories, which might have been due to temperature during the grain filling period in the 2016A season. High temperature during grain filing period reduces kernel width but has no effect on kernel length which could increase kernel L/W ratio [27]. Significant difference in kernel length ($P \leq 0.001$) among the genotypes within seasons in this study suggested that kernel length was appearance quality traits greatly influenced by genetic background of the cultivars. This was in conformatry with the findings of [28] who reported that variation for kernel length among cultivars and environmental interactions were highly significant but the environment interaction contributed only 1% of the total phenotypic variation in the kernel length. [3] classified kernel length as extra-long >7.5 mm, long 6.61-7.5 mm, medium 5.51-6.6 mm and short less than 5.51 mm. Based on this classification, all the studied genotypes were characterized into three categories. the first category was the medium KL (5.51-6.6 mm) with six genotypes from Africa Rice Centre, four from NaCRRI and one from other origin, the second category was the long KL (6.61-7.5 mm) with twenty six genotypes under this category eleven from Africa Rice Centre, ten from NaCRRI and five from other origin and the third category was the extra-long ($7.5 \leq$ mm) group with only two genotype (ART3-7L9P8-3-B-B-2) from Africa Rice Centre and (1052) from IRRI.

Table 4: Mean of grain appearance quality traits of genotypes grown in two seasons at NaCRRI.

		Season 2015B				Season 2016A			
Origin	Genotype	KL(mm)	KW(mm)	L/W	100GW(g)	KL(mm)	KW(mm)	L/W	100GW(g)
	1190	6.3	2.3	2.8	1.9	7.0	2.3	3.1	1.9
	326104	7.3	2.0	3.6	1.8	7.2	2.0	3.6	2.0
	ART10-1L15P1-4-8-1	7.1	2.9	2.5	2.3	6.4	2.4	2.7	2.2
	ART12-L4P7-21-4-B-3	6.8	3.1	2.2	2.4	6.0	1.9	3.0	1.8
	ART15-11-8-5-2-B-1	7.2	2.6	2.8	2.4	7.7	2.4	3.3	2.4
	ART16-4-11-13-4	6.6	3.3	2.1	2.3	7.0	2.5	2.8	2.2
	ART16-5-4-3-3-1-1-1	7.2	2.7	2.8	2.4	7.1	2.9	2.5	2.5
	ART25-3-29-2-B	7.1	2.9	2.5	2.7	7.4	3.0	2.5	2.5
	ART3-2L4P19-2-1-B	6.6	2.6	2.6	2.3	7.4	2.5	3.0	2.2
ARC	ART3-7L9P8-3-B-B-2	7.9	2.5	3.4	2.5	7.2	2.5	2.9	2.3
	ART3-8L6P3-2-2-B	6.8	2.7	2.6	2.4	6.6	2.8	2.3	2.3
	ART3-8L6P3-2-3-B	6.1	3.7	1.7	2.5	6.0	3.7	1.6	2.8
	GSR-I-0057	5.9	2.4	2.4	1.8	6.2	2.0	3.1	1.8
	Jaribu 220	6.9	2.5	2.8	2.3	6.1	2.1	2.9	1.8
	Namche 1	6.9	2.8	2.5	2.6	6.9	2.5	2.8	2.5
	Nerica 4	7.0	2.8	2.5	2.4	7.2	2.7	2.7	2.1
	Nerica 6	6.2	2.8	2.2	2.2	6.3	2.6	2.6	2.2
	TXD 306	6.3	2.7	2.2	2.0	6.7	2.6	2.6	2.1
	WAB788-16-1-1-2-HB	6.9	3.2	2.2	2.5	6.8	2.6	2.7	2.5

CIAT	CT11891-3-3-3-M-1-2-1-M	7.1	3.0	2.3	2.5	7.3	2.7	2.6	2.6
CIAT	PCT-4\0\0\0>19-M-1-1-5-1-M	6.5	3.1	2.1	2.4	6.4	2.8	2.3	2.3
IRRI	1052	8.0	2.8	2.8	2.3	7.8	2.2	3.6	2.3
Korea	1191	7.0	3.1	2.3	2.9	6.8	2.2	3.1	1.9
MGC	Scrid006-2-4-3-4-5	6.9	2.9	2.4	2.7	7.3	2.4	3.1	2.4
MGC	SCRID006-2-4-3-5	7.0	2.6	2.7	2.3	7.4	2.0	3.7	2.2
MGC	SCRID037-4-2-2-5	6.8	2.4	2.8	2.1	7.1	2.0	3.6	1.9
	Namche 2	7.3	2.8	2.7	2.5	6.8	2.4	2.9	2.3
	Namche 3	7.0	2.9	2.4	2.4	6.6	2.5	2.7	2.3
	Namche 5	6.8	2.9	2.3	2.5	6.8	2.4	2.9	2.2
	P24 H1	6.8	2.6	2.7	2.3	7.1	2.3	3.1	2.3
	P24 H10	6.4	2.9	2.2	2.4	6.8	2.6	2.7	2.5
	P24 H11	6.9	2.9	2.4	2.6	7.2	3.0	2.4	2.7
NaCRRI	P26 H1	6.7	2.4	2.8	2.4	6.7	2.4	2.0	2.4
	P27 H3	6.6	3.0	2.2	2.4	6.7	3.0	2.2	2.1
	P29 H1	7.1	2.7	2.7	2.3	6.7	2.8	2.4	2.2
	P5 H12	6.5	2.9	2.2	2.4	6.7	2.4	2.8	2.2
	P5 H14	6.5	2.7	2.4	2.3	7.1	2.6	2.8	2.2
	P5 H6	6.4	2.9	2.2	2.3	6.9	2.7	2.6	2.1
	P62 H17	7.0	2.9	2.3	2.2	6.9	2.4	2.9	2.2
	Means	**6.9**	**2.8**	**2.5**	**2.4**	**6.9**	**2.5**	**2.8**	**2.2**
	LSD	**0.9**	**0.7**	**0.7**	**0.4**	**0.7**	**0.5**	**0.6**	**0.2**
	CV%	**8.3**	**12**	**13.7**	**6.32**	**4.2**	**8.1**	**11.8**	**5.1**

LSD = least significance difference, CV% = coefficient of variations, KL = kernel length, KW = kernel width, GW = grain weight, 2015B =season one, and 2016A season two, ARC = African rice center, MGC = Madagascar, g = gram

Kernel length to width ratio ranged from 1.7mm (ART3-8L6P3-2-3-B) to 3.64 mm (326104), with an average value of 2.65 mm. [3] classified rice grain shape as slender 3.0 mm or less than 3.0 mm, medium 2.1 mm to 3.0 mm, bold 2.0 mm or less than 2.0 mm. Among the studied genotypes, ART3-8L6P3-2-3-B from Africa rice center was classified as bold, and SCRID037-4-2-2-5, 326104 and 1052 from other origin was classified with slender category. The remaining twenty five genotypes were all classified with the medium grain category. [28] reported that it was more desired to have a narrow and consistent distribution of grain dimension for ease of processing and consistency in quality.

5. Correlation among grain appearance quality traits and amylose content

The results of correlation coefficients (r) among the various traits measured in this study are shown in **Table 5**.

Table 5: Pearson Correlation Coefficients among grain appearance quality traits and amylose content

	AC%	GW	KL	L/W	KW
AC%	1				
GW	-0.175ns	1			
KL	-0.178ns	0.304*	1		
L/W	-0.003ns	-0.483**	0.579***	1	
KW	-0.028ns	0.715***	-0.233ns	-0.899***	1

AC% = amylose content, GW = grain weight, KL = kernel length, L/W = kernel length to kernel width ratio and KW = kernel width

AC weakly correlated negatively with all the studied grain appearance quality traits implying that breeding for improving the level of amylose content could be achieved without significant change in the quality attributes of the grain characteristics but would not be possible to select for amylose content based on the grain appearance of the genotypes. [29] reported a positive (r = 0.018) but none significant correlation between amylose content and Kernel length but [30], reported that AC correlated significantly positively with KL and negatively with KW. [31], reported that AC exhibited significant positive association with L/W and GW but [32] reported that AC correlated positively but non significantly with L/W ratio. L/W ratio correlated significantly negatively (r = -0.48) with 100Gw and positively (r = 0.58) with KL suggesting that selection for slender kernel shape would reduce GW. The KW correlated significantly positively (r = 0.72) with 100GW and negatively (r = -90) with L/W ratio, suggesting that selection for bold grain would result into increase of GW and reduction to L/W ratio. These results are in conformity with the findings of [33] who reported that Kernel length was negatively correlated to kernel width.

6. Mean performance of F2 populations for amylose content in a 7 X 7 half diallel cross

In comparing the performance of crosses to the corresponding parents mean, two crosses, 326104 x Nam1 (20.23) and 326104 x N4 (21.10), were numerically high **Table 6.**

Table 6: Mean for amylose content for F2 progenies from a 7 x 7 half diallel cross

Parent	1052	326104	Namche 1	Namche 2	Namche 3	Nerica 4	Suparica	arrmn
1052	**17.76**	19.58	18.03	14.92	16.61	18.93	13.89	16.99
326104		**21.28**	20.23	18.14	19.07	21.10	18.13	19.33
Namche1			**21.66**	18.16	17.17	18.46	17.63	17.86
Namche 2				**16.74**	16.54	18.0	15.68	16.74
Namche 3					**14.64**	17.47	17.22	17.35
Nerica 4						**21.94**	17.87	17.87
Suparica							**18.63**	16.74

Arrmn = array mean, figures in bold are the parental mean

The results showed that none of the F2 progeny had higher mean for amylose content than the mean of the high parent or lower than the mean of lowest parent. The lowest mean was observed in a Cross Namche 2 x Suparica (mean = 15.63) (Table 9). [34] reported that AC resulting from crossing of high x high and high x intermediate AC parent were approximately equal to their mid parent and/or High parent. However, parents in this study were of low and intermendiated amylose content.

The results of mean squares of F2 population revealed highly significant ($P \leq 0.001$) differences among the genotypes investigated Table 7.

Table 7: Mean squares from the analysis of variance of amylose content in F2 populations from 7 x 7 half diallel

Source	**d.f.**	**AC%**
GCA	6	5.91***
SCA	14	0.95*
Total	20	2.44
Residual	40	0.44
VCGCA additive component (δ^2_{GCA})		7.29
VCSCA dominant component (δ^2_{SCAj})		0.51
[a]BR = $(2\delta^2_{gcai})/(2\delta^2_{gcai}+\delta^2_{scaj})$.		0.94
[b]BSH= $(2\sigma^2gca + \sigma^2sca)/(2\sigma^2gca + \sigma^2sca + \sigma^2e)$		0.96
[c]NSH = $(2\sigma^2gca)/(2\sigma^2gca + \sigma^2sca + \sigma^2e)$		0.89

AC = amylose content, * and*** significant different at $P \leq 0.001$ and $P \leq 0.00$ probability levels respectively, ns = none significant .a Relative importance of GCA and SCA according to Baker (1978); b Broad sense heritability, C Narrow sense heritability and δ2g, and δ2s, are the respective GCA, and SCA, components; δ2e is the error component averaged over three replications. All MS values are on the basis of the mean of three replications.

The results indicated significant differences ($P \leq 0.001$) among the parents for general combining ability (GCA) and crosses ($P \leq 0.5$) for specific combining ability (SCA) for amylose content. The significance of GCA and SCA indicated that both additive and non-additive gene effects were important in determining AC [14]. However, the variance component (δ^2_{GCA}) for GCA was greater than the variance component (δ^2_{SCA}) for SCA implying that the inheritance of amylose content is more conditioned by the additive gene effects than the dominance gene effects. These results are in agreement with the results reported by [35]. [17] reported that the closer the ratio of GCA:SCA to unity, the greater the predictability based on general combining ability alone and the GCA:SCA in this study was = 0.94, implying that the performance of a single cross progeny could be predicted fairly accurately based on the GCA of its parent in the study. The broad sense heritability was 0.96 indicating that 96% of the observable amylose content was due to genetic effect [36]. The narrow sense heritability was 0.89 indicating that early selection for AC could give a good response suggesting that the efficiency of rice breeding programs based on cooking quality traits such as AC, would be possible through selection for these traits.

7. GCA effect for amylose content in 7x7 half diallel cross

The results of estimated GCA effects for amylose content are presented in **Table 8.**

Table 8: Estimates of GCA effects for amylose content in 7 x 7half diallel cross.

Parents	**Parental mean**	**GCA effect**
1052	17.76	-0.96*
326104	21.28	1.58**
Namche1	21.33	0.70*
Namche2	16.74	-1.06*
Namche3	14.64	-0.53*
Nerica4	21.94	0.58*
Suparica	18.63	-1.26**

GCA = general combining ability, *, ** = significant different at $P \leq 0.5$, and $P \leq 0.01$ and probability levels respectively; ns = none significant**.**

The GCA effect was significance for all parents. Suparica, Namche 2, Namche 3and 1052 showed significant negative GCA effects whereas 326104, Namche 1, and NERICA 4 showed significant positive GCA effects. Desirable parents are those with significant GCA effects in the right direction for the trait of interest [16]. Parent with a significant negative value would contribute toward low value of amylose content, whereas a parent with significance positive value would contribute towards high value of amylose content [37]. In this regard, Parent 326104 was the best general combiner for high amylose value followed by NERICA 4, and Namche1, Supaica was the best general combiner for reduced amylose content followed by Namche 2, 1052 and Namche 3.

8. SCA effect for amylose content in F2 generations

The results of estimates of specific combining ability (SCA) are presented in **Table 9.**

Table 9: Estimate of SCA effects for amylose content in F2 generations

Parent	1052	326104	Nam 1	Nam 2	Nam 3	Nerica 4	Suparica
1052		1.012ns	0.334*	-1.014*	0.148ns	1.36*	-1.84**
326104			0.574*	0.324ns	0.078ns	-1.21*	-0.13ns
Nam 1				0.568*	-0.95*	-0.768*	0.242ns
Nam 2					-0.182ns	0.534*	0.054ns
Nam 3						-0.524*	1.066*
Nerica 4							0.608*
Suparica							

*, ** and are significance different at $P \leq 0.05$, $P \leq 0.01$ and $P \leq 0.001$ probability levels respectively and ns = none significant different.

The results showed that out of the 21 crosses, 13 crosses were found to be good specific combiners for amylose content. Six of the 13 crosses (1052 x Suparica, 326104 x NERICA 4, 1052 x Namche 2, Namche 2 x Namche 3,Namch 1 x Nerica 4and Namche 3 x NERICA 4), showed significant ($P \leq 0.05$) negative SCA effects indicating that there was reduced AC% in the progenies of these crosses. These results were similar with those obtained by [37]. Seven of the crosses showed positive significant SCA effects for amylose content indicating that there was increase in the AC% of the progenies in these crosses. A similar result was reported by [38]. The superior combination which revealed the significant value for low amylose content was the hybridization between 1052 x Suparica while the cross between 1052 x NERICA 4 revealed a significant value for high amylose content, indicating that such combinations would yield desirable segregants useful for development of improved genotype.

III. Conclusions

The genotypes had wide variation in amylose content (AC) with equally wide variation in grain appearance quality traits. The correlation coefficient (r) among the various quality traits of the grain indicated that amylose content was weakly and negatively correlated with all the studied quality traits of the grain indicating that grain appearance quality was not a reliable means for predicting amylose content among the genotypes.

The results revealed that both GCA and SCA were significantly important in determining amylose content, but the variance component for GCA was greater than the variance component for SCA. Parent 326104, Namche 1 and NERICS 4 had positive GCA effect could be used in breeding program for increasing amylose content and Suparica, Namche 2 1052 and Namche 3 had negative GCA effects and could be used in breeding program for reducing amylose content in rice. The results also showed that the inheritance of amylose content was conditioned by both additive and non-additive gene effects

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