

GENETIC VARIABILITY IN MORPHOLOGICAL AND PHYSIOLOGICAL TRAITS WITHIN AND AMONG RICE SPECIES AND THEIR INTERSPECIFIC PROGENIES

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ABSTRACT

This study compares genetic variation in morpho-physiological traits within and among five groups of *Oryza* species. Several morphological and phenological characters were measured in field trials. Results showed that genetic variation exists among and within these groups for the characters measured. More *O. glaberrima* and traditional *O. sativa* possess attributes which indicate they are better adapted to sub-optimal growing conditions that characterize rice cultivation in West Africa, but are poor yielding. The interspecific progenies possess characters that cover the range of both their parents. Cluster analysis amalgamated some as possessing the adaptive morphological traits of their *O. glaberrima* parents, and the panicle and yield attributes of improved *O. sativa* parents. *O. sativa* of temperate origin, but of tropical japonica genetic background did not show characters for adaptability to the West African upland conditions, but was similar to interspecifics and other adapted genotypes groups that possess panicle and spikelet characteristics. Those ones could be exploited for extending present yield levels.

Keywords : Germplasm characterization, *Oryza glaberrima*, *Oryza sativa*, genetic variation, West Africa.

RESUME

VARIABILITE GENETIQUE DES TRAITS MORPHOLOGIQUES ET PHYSIOLOGIQUES CHEZ LES ESPECES DE RIZ ET LEURS DESCENDANCES INTERSPECIFIQUES

Cette étude compare la variation génétique de paramètres morpho-physiologiques au sein et entre cinq groupes d'espèces *Oryza*. Plusieurs caractères morphologiques et phénologiques ont été mesurés dans des essais conduits au champ. Les résultats ont montré qu'il existe, pour les caractères mesurés, une variation génétique au sein et entre les groupes étudiés. Un nombre important d'espèces *O. glaberrima* et *O. sativa* traditionnelles ont des attributs qui indiquent qu'elles sont mieux adaptées aux conditions suboptimales de la culture de riz en Afrique occidentale. Elles ont, cependant, un rendement faible. Les descendants interspécifiques possèdent des attributs qui couvrent la gamme des caractères de leurs parents. L'analyse de groupement a identifié certains comme présentant les caractères morphologiques d'adaptation de leurs parents *O. glaberrima*, et des caractères de panicule et de rendement des parents améliorés *O. sativa*. Les espèces *O. sativa* d'origine tempérée, mais de fond génétique japonica tropical n'ont pas démontré une capacité d'adaptation aux conditions de culture de riz pluvial en Afrique de l'Ouest. Par contre, elles étaient semblables aux descendants interspécifiques et autres groupes de génotypes adaptés quant aux caractéristiques des panicules et des grains. Celles-ci pourraient être exploitées pour l'amélioration des niveaux de rendement actuels.

Mots-clés : Caractérisation de germplasm, *Oryza glaberrima*, *Oryza sativa*, variation génétique, Afrique de l'Ouest.

INTRODUCTION

The conservation, management, distribution and utilization of genetic resources necessitate and pre-suppose that the germplasms are fully

characterized. The Genetic Resources Unit (GRU) at WARDA holds a wide range of rice accessions varying from wild species to improved varieties. They include *Oryza glaberrima* Steud, a native rice of African origin, several improved

varieties and landraces of *O. sativa* introduced from other continents, and the interspecific progenies recently obtained from crosses between *O. glaberrima* x *O. sativa* (Jones *et al.*, 1997). Studies by Singh *et al.* (1996), indicated that genetic variability exists for many useful traits like early maturity, grain quality, secondary branches in panicle in *O. glaberrima*. Jones *et al.* (1997) also revealed wide variation in important morphological and agronomic traits such as seedling vigor, the number of panicles per square meter and growth duration within *O. glaberrima* and traditional *O. sativa* accessions. In characterizing competitiveness among cultivars, Johnson *et al.* (1996) found that by the end of season-long competition with weeds, *O. glaberrima* had less weed than improved *O. sativa* types. The mechanism causing less weeds in *glaberrima* was attributed to larger number of tillers, more leaves, higher leaf area index and specific leaf area (SLA). More information on specific characters, on fundamental differences and similarities among all categories of germplasm viz. traditional landraces, cultivars of *O. glaberrima*, *glaberrima* x *sativa* interspecific progenies and improved *O. sativa* are needed and would contribute in enhancing and accelerating ongoing rice improvement work.

The study reported here was undertaken to characterize upland rice accessions currently available and being distributed through the International Network for Genetic Evaluation of Rice in Africa (INGER-Africa). Because of fast

genetic erosion in this region and the request for germplasm restoration to farmers in war affected areas, this comparative study is necessary to better characterize the available land races and introductions in comparison with improved *O. sativa*, *O. glaberrima* and new *O. glaberrima* x *O. sativa* interspecific progenies in order to facilitate a better utilization. It will help understand differences and similarities between germplasm accessions groups, and determine the magnitude of genetic variation in our gene-bank.

MATERIALS AND METHODS

Trials were conducted in an upland rice field during 1998 growing season at the WARDA main research center, Mbe, Cote d'Ivoire. Mbe is located in the guinea-savanna zone (5° 06' W, 7° 52' N), and is characterized by an annual rainfall of 1146 mm and average daily temperature of 25 °C. The soil in the area is an alfisol, with a loamy sand texture and frequent iron concretions.

TREATMENTS

Three hundred and ninety three (393) rice genotypes originating from different countries and institutions in Africa, Asia, and The Americas (table 1) were used as treatment entries in the trial. Genotypes were in five treatment groups in which all entries of a species, subspecies are clumped to form a treatment. Number of entries per treatment group and a brief description of group members are in table 1.

Table 1 : Arbitrary classification of 393 rice genotypes characterized for morpho-physiological traits during 1998 at WARDA, Mbe Cote d'Ivoire

Classification arbitraire de 393 génotypes de riz caractérisés pour leurs caractères morpho-physiologiques. ADRAO, 1998, Mbé, Côte d'Ivoire

Genetic Description	Group code	No. of Entries	Remarks
<i>O. glaberrima</i>	G	11	Native <i>O. glaberrima</i> lines collected in West Africa, including parents of the interspecifics in group-2.
<i>O. glaberrima</i> x <i>O. sativa</i> interspecific progenies	P	20	Obtained from the interspecific hybridization project at WARDA.
Temperate <i>Oryza sativa</i> , with tropical japonica genetic background	U	9	Introduced in the year 1998 from the USDA germplasm enhancement center in Arkansas, USA.
Improved <i>O. sativa</i> lines	W	319*	A large number of <i>O. sativa</i> already released and largely cultivated by farmers in different West African countries, and lines developed or selected at WARDA, including parents of the interspecific progenies in group-2.
Traditional <i>O. sativa</i> / landraces	T	34*	Received in the year 1996 from the national research institute (IDESSA) in Côte d'Ivoire

*A subset of 20 genotypes representative of the group was used in cluster analysis.

* un sous-échantillon de 20 génotypes représentatifs du groupe a été utilisé dans l'analyse de groupement.

TRIAL SET-UP AND EXPERIMENTAL DESIGN

Experimental area has been disc plowed and harrowed twice. One hundred and fifty (150) kg/ha of compound fertilizer (NPK 15-15-15) was applied as basal. Top dressing was done with two split applications of 50 kg/ha each of urea (46 %) at 35 and 65 days after sowing (DAS). Experiment was conducted on 27 July 1998 on plots 5m long x 1m wide. Two-three seeds were dibbled at hill spacing of 0.2 m on row. A distance of 0.5 m was maintained between plots. The experiment design was completely randomized, with three replications.

During the dry spell, supplementary irrigation was provided from an overhead sprinkler source to maintain soil moisture at field capacity.

DATA COLLECTION AND ANALYSIS

Data were collected on the two middle rows, a border row on either side being left. Tillers production (number /plant), specific leaf area (SLA, calculated as leaf surface area dry weight of the same leaf [m^2/kg]) and seedling vigor were measured at 30 DAS. Occurrence of diseases including leaf blast, neck blast, brown spot, stalk rot and insect pest (stem borers and gall midge) were also noted. The characterization of seedling vigor and reaction to diseases/insect pests were based on a 1-9 scoring scale (1 = best ; 9 = poorest) as described in the Standard Evaluation System (SES) for rice (IRRI, 1998). Date of 50 % of flowering were also recorded when occurred, while at physiological maturity, plant height (cm) was measured. Grain yield and yield components including 1000-grain weight (g), grain-to-shoot dry matter ratio or harvest index (g grain/g shoot weight), panicle length (cm), panicle exertion (cm), primary and secondary branching (number/panicle), and spikelet count (number/panicle) were measured at harvest.

Data collected were subjected to appropriate statistical analysis using SAS to describe means and variability within and between groups. Hierarchical cluster analyses were carried out to measure the extent of the inherent diversity within and across all the rice groups, using the various characteristics measured. The amalgamation method used was «Complete linkage». In the procedure, the distance between two clusters is computed from the maximum euclidean distance between an observation in one cluster and an observation in the other cluster. This method was used because the genotypes actually belong to five (5) clumps as presented in table 1. For group T (n = 34) and group W (n = 319) only a subset of 20 entries, representative of the members of a group was used for the cluster analysis.

K-means clustering, with K = 5 was also carried out. The purpose is to crosscheck if the genotypes can be amalgamated as described in table 1. Cluster analysis was performed with STATISTICA (SPSS, 1995).

RESULTS AND DISCUSSION

Variability in the different morphological and physiological traits is summarized in table 2. Means and coefficient of variability (CV %) were calculated with regard to actual sample size (n) in each group.

The CV's of the means are high for the disease/pest resistance rating (e.g. CV for neck blast = 375 %) because data are the scores done on scaling of 1 to 9, therefore need to be interpreted differently. Otherwise, among the quantitatively measured traits, the variability in grain yield (g/plant) varied most (CV = 83 %), followed by the variability in grain-to-shoot dry matter ratio (cv \approx 57 %). Variability in tiller number and SLA was between 23 and 29 %. Plant height, days to flower and panicle length were the least diverse traits (CV \leq 16 %).

COMPARISON OF VARIABILITY WITH SPECIFIC GENETIC GROUPS

Morphology and phenological characteristics

The glaberrimas had the highest mean tiller number and the best seedling vigor, but the CVs associated with these traits were small (12 and 0 % respectively). Genetic variation in plant height and days to flower were also small in the *glaberrima* group while higher variation in seedling vigor and tillering occurred in the traditional *sativas* (table 2).

Genetic means for seedling vigor, tillering ability, SLA, primary and secondary branching were low in the USA varieties. This group had shorter straw height and duration to flowering, but is more varied than the glaberrimas in a few properties (table 2). This indicates that the group could be exploited for those traits which CVs are high. Means show that the glaberrimas and the traditional *sativas* were the tallest among the varietal groups, this can explain the common lodging of these groups (Jones *et al.*, 1997). The lodging of straws in tall varieties, according to Japanese scientists, is due to low tensile strengths of the straw. Shorter straw-height and leaf sheath covering enable rice to tolerate heavier load and avoid lodging (Ookawa and Ishihara, 1993). The US varieties and the Interspecific progenies were similar, and had shorter plant types (table 2). The similarity indicates that interspecific progenies originally developed for low input systems in West Africa (Jones *et al.*, 1997, Dingkuhn *et al.*, 1997) could suit the high-input mechanized harvesting system to which US varieties are adapted.

The variability in SLA of the US varieties was of 27 % and compares to 29 % among the glaberrimas. But the mean of SLA was the lowest among the US varieties and the highest in the glaberrimas, interspecific progenies and traditional *sativas*, which were statistically at par ($p < 0.05$). Glaberrimas and interspecific progenies have been reported in previous studies to possess high SLA which was linked to superior competitiveness against weeds (Jones *et al.*, 1997; Johnson *et al.*, 1997). Relatively low SLA, seedling vigor and tillering capacity observed among the USA group suggest that, although these germplasm possess tropical-japonica genetic background, their evolution elsewhere makes them less adapted to West African environments.

Panicle characteristics and grain yield attributes

Improved *sativas* were superior or at par with the best in grain yield and panicle characteristics except grain yield ($p < 0.05$). The highest plant yields were obtained with glaberrimas, although this group had the smallest CV in this trait. Variability in yield among the improved *sativas* and the US varieties were approximately 84 % showing that considerable gains can be obtained by further improvement of these germplasms for yield per se.

The highest variation in the secondary branching was found among the traditional *sativas* (CV = 40.5 %), although this group did not show the highest means ($p < 0.05$, table 2). The glaberrimas had the lowest number of secondary branches per panicle, with a 38 % of variability in the trait.

Panicle exertion and panicle length, criteria often used by West African rice farmers and women harvesters in adopting a variety, were the best among the improved *sativas*, and this group also varied the most in panicle exertion. Nearly equal but higher amount of genetic variation in panicle length exists in all non-*glaberrima* groups.

Differences in spikelet numbers among glaberrimas, interspecific progenies, US varieties, and improved *sativas* were not statistically significant. However, they had higher mean spikelet number than the traditional *sativas*. Interestingly, the widest genetic variability of the trait occurred in the traditional *sativas* indicating opportunities for further exploitation and improvement.

Grain yield, grain-to-shoot index and 1000-grain weight were high in interspecific progenies. The *glaberrima* and improved *sativa* were either par or lower than the interspecific progenies (table 2). Genetic variability in grain yield was large in all (CV = 73 - 84 %) but *glaberrima* groups (CV = 33 %). Jones *et al.* (1997) have also reported low variability in *glaberrima* grain yield. Glaberrimas due to its long history of cultivation and mass selection in West Africa became fully adapted to local environments and the genetic base is approaching or are already at their highest level for yield. The lack of genetic variability for yield makes it difficult to obtain further genetic gain through varietal improvement of glaberrimas per se.

CLUSTER ANALYSIS AND ACROSS SPECIES GENOTYPIC GROUPING

Figures 1, 2 and 3 present three diagrams of hierarchical clustering of 80 genotypes (cases) across the five groups, based on complete linkage euclidean distances of mean data obtained from 3 replications. The basis of clustering in Figure 1 is the reaction of individual entry to specific diseases / pests - leaf blast, neck blast, brown spot, stem borer and gall midge. Results indicate that at 20 % relative euclidean linkage distance level (Dlink/Dmax *100), 80 genotypes can be amalgamated to 31 clusters.

The number of clusters can be synthesized to only 7 at 60 % level, and three at 80 % level. Of these, genotype T25 is obviously an out-lier with respect to overall reaction to stresses. T25 amalgamated only at 100 % level. Table 3 shows that genotype T25 (IR644-1-63-1-1) is a lowland variety developed with Asian parents (IR8 and TN1) and introduced from the USA. This variety was seriously affected by stalk rot (score = 9), brown spot (score = 5), and stem borers (score = 3). Its panicle exertion and plant yield were also very poor.

Clustering based on morphological and physiological traits: plant height, days to flower, seedling vigor and SLA (figure 2) revealed that the 80 entries can be amalgamated to 21 clusters assuming that a relative euclidean linkage distance level is of 20 %. At the 80 % linkage level, the 80 entries are amalgamated into three groups of which groups the first and the third are more or less of the same size.

Figures 2 and 3 clearly show that diversity in morphological traits are larger than those observed in yield and panicle characteristics. This means that faster genetic gains in rice improvement could be achieved by exploiting the wide diversity that exists in morpho-physiological characteristics of breeding materials, rather than in focus directly on their yield. In a breeding program, chances of producing individuals with similar attributes are higher when yield and panicle attributes are considered as priority than in the one where morpho-physiological attributes and disease reaction are considered.

The first group contains mainly *glaberrima* entries (G8, G7, G3, G2, G1, G5), T26 and W82. All *glaberrimas* are TOG from Nigeria. T26 (ALAKO),

(table 3) is an introduction from Gambia, where *O. glaberrima* is believed to have originated from Casamance area in Senegambia river valley. T26 (ALAKO) is likely to be genetically linked to *glaberrima*. The variety W82 (IR47686-09-2-4) on the other hand, was developed in Asia by using as parent IRAT104, an improved *sativa-japonica* adapted to West African upland rice conditions (Abamu *et al.*, 1992) and Palawan a traditional upland rice in the Philippines. Therefore, the presence of W82 (IR47686-09-2-4) in this group may be due to IRAT104.

The second group contains progenies P14, P10, P9, P12, P11, P2, P13, P4, P3, W1, and U7 (figure 2). W1 (AMISTAD) originates from Cuba, whereas U7 is NORIN20 from Japan. These two plants are similar but different from interspecific progenies (amalgamated point = 38 %). W185 (UPR103-80-1-2) though statistically linked to interspecific progenies by its morphology, is a lowland variety developed in India. The third and largest group at 80 % level contains most traditional and improved *sativas*, two interspecific progenies, three *glaberrimas*, and eight American varieties.

The classification based on yield and panicle parameters (figure 3) gave more agglomeration and fewer clusters. At 20 % relative linkage level for example, the 80 genotypes can be amalgamated into 10 groups, whereas at 40 % and 80 % the data are respectively synthesized to 4 and 2 groups.

The figure 2 also shows that 11 traditional *sativas* (including T25, T15, T3 ... T5) and W124 are grouped together. This group consists of all varieties but two introduced from national program in Côte d'Ivoire. T25 is a lowland variety developed in Asia and introduced from the USA. Varieties from Côte d'Ivoire not clustered with this group are T2 (IS766) and T11 (IS914). Yield and panicle characteristics of T11 are similar at 5 % linkage level to those of progenies P10 (WAB450-B-16A1-7) and P6 (WAB450-4-1-A20), whereas T2 is similar to *glaberrima* G11 (CG20), traditional *sativa* T32 (TAMBA YEGUETI) and W27 (CT6946-9-1-2-M-1P) at 10 % linkage level (Figure 3).

To provide insight into the arbitrary groupings shown in table 2, the K-means clustering was performed if the genotypes can be amalgamated in keeping with the table. This information has relevance to programs such as INGER, which has responsibility for germplasm support to a wide range of NARS. Due to their resource constraints, NARS often request for fewer sets



Figure. 1 : Relative euclidean linkage distances (Dlink/Dmax*10) and amalgamation of 80 divers rice genotypes, based on their resistance to different diseases and insect pests. Mbe, Cote D'Ivoire.

*Distances euclidiennes relatives de liaison (Dcla./Dmax*10) et regroupement de 80 génotypes de riz sur la base de leur résistance aux différentes maladies et insectes. Mbé, Côte d'Ivoire.*



Figure. 2 : Relative euclidean linkage distances (Dlink/Dmax*10) and amalgamation 80 divers rice genotypes, based on several morphological and phenological attributes. Mbe, Cote D'Ivoire.

*Distances euclidiennes relatives de liaison (Dcta/Dmax*10) et regroupement de 80 génotypes de riz sur la base de leurs attributs morphologiques et phénologiques Mbé, Côte d'Ivoire.*



Figure. 3 : Relative euclidean linkage distances (Dlink/Dmax*10) and amalgamation 80 divers rice genotypes, based on panicle characteristics, plant yield and yield components. Mbe, Cote D'Ivoire.

*Distances euclidiennes relatives de liaison (Dcla/Dmax*10) et regroupement de 80 génotypes de riz sur la base des caractéristiques de leurs panicules, rendements et composantes de rendement. Mbé, Côte d'Ivoire.*

Table 3 : Entry name, parentage, sources and recommended ecology for cluster analysis.
Désignation, parentée, origines et écologie recommandée pour les 80 génotypes de riz utilisés dans l'analyse de groupement.

Entry code*	Parentage	Source	Recommended ecology	Entry Code*	Parentage	Source	Recommended ecology
G1	WA 1385 / CC 11	WA 1385	WA 1385				
G2	WA 1385 / CC 11	WA 1385	WA 1385				
G3	WA 1385 / CC 11	WA 1385	WA 1385				
G4	WA 1385 / CC 11	WA 1385	WA 1385				
G5	WA 1385 / CC 11	WA 1385	WA 1385				
G6	WA 1385 / CC 11	WA 1385	WA 1385				
G7	WA 1385 / CC 11	WA 1385	WA 1385				
G8	WA 1385 / CC 11	WA 1385	WA 1385				
G9	WA 1385 / CC 11	WA 1385	WA 1385				
G10	WA 1385 / CC 11	WA 1385	WA 1385				
G11	WA 1385 / CC 11	WA 1385	WA 1385				
P1	WA 1385 / CC 11	WA 1385	WA 1385				
P2	WA 1385 / CC 11	WA 1385	WA 1385				
P3	WA 1385 / CC 11	WA 1385	WA 1385				
P4	WA 1385 / CC 11	WA 1385	WA 1385				
P5	WA 1385 / CC 11	WA 1385	WA 1385				
P6	WA 1385 / CC 11	WA 1385	WA 1385				
P7	WA 1385 / CC 11	WA 1385	WA 1385				
P8	WA 1385 / CC 11	WA 1385	WA 1385				
P9	WA 1385 / CC 11	WA 1385	WA 1385				
P10	WA 1385 / CC 11	WA 1385	WA 1385				
P11	WA 1385 / CC 11	WA 1385	WA 1385				
P12	WA 1385 / CC 11	WA 1385	WA 1385				
P13	WA 1385 / CC 11	WA 1385	WA 1385				
P14	WA 1385 / CC 11	WA 1385	WA 1385				
P15	WA 1385 / CC 11	WA 1385	WA 1385				
P16	WA 1385 / CC 11	WA 1385	WA 1385				
P17	WA 1385 / CC 11	WA 1385	WA 1385				
P18	WA 1385 / CC 11	WA 1385	WA 1385				
P19	WA 1385 / CC 11	WA 1385	WA 1385				
P20	WA 1385 / CC 11	WA 1385	WA 1385				
U1	WA 1385 / CC 11	WA 1385	WA 1385				
U2	WA 1385 / CC 11	WA 1385	WA 1385				
U3	WA 1385 / CC 11	WA 1385	WA 1385				
U4	WA 1385 / CC 11	WA 1385	WA 1385				
U5	WA 1385 / CC 11	WA 1385	WA 1385				
U6	WA 1385 / CC 11	WA 1385	WA 1385				
U7	WA 1385 / CC 11	WA 1385	WA 1385				
U8	WA 1385 / CC 11	WA 1385	WA 1385				
U9	WA 1385 / CC 11	WA 1385	WA 1385				
W1	WA 1385 / CC 11	WA 1385	WA 1385				
W3	WA 1385 / CC 11	WA 1385	WA 1385				
W6	WA 1385 / CC 11	WA 1385	WA 1385				
W17	WA 1385 / CC 11	WA 1385	WA 1385				
W27	WA 1385 / CC 11	WA 1385	WA 1385				
W36	WA 1385 / CC 11	WA 1385	WA 1385				
W62	WA 1385 / CC 11	WA 1385	WA 1385				
W68	WA 1385 / CC 11	WA 1385	WA 1385				
W78	WA 1385 / CC 11	WA 1385	WA 1385				
W82	WA 1385 / CC 11	WA 1385	WA 1385				
W124	WA 1385 / CC 11	WA 1385	WA 1385				
W139	WA 1385 / CC 11	WA 1385	WA 1385				
W185	WA 1385 / CC 11	WA 1385	WA 1385				
W197	WA 1385 / CC 11	WA 1385	WA 1385				
W235	WA 1385 / CC 11	WA 1385	WA 1385				
W240	WA 1385 / CC 11	WA 1385	WA 1385				
W271	WA 1385 / CC 11	WA 1385	WA 1385				
W313	WA 1385 / CC 11	WA 1385	WA 1385				
W317	WA 1385 / CC 11	WA 1385	WA 1385				
T1	WA 1385 / CC 11	WA 1385	WA 1385				
T2	WA 1385 / CC 11	WA 1385	WA 1385				
T3	WA 1385 / CC 11	WA 1385	WA 1385				
T5	WA 1385 / CC 11	WA 1385	WA 1385				
T8	WA 1385 / CC 11	WA 1385	WA 1385				
T11	WA 1385 / CC 11	WA 1385	WA 1385				
T14	WA 1385 / CC 11	WA 1385	WA 1385				
T15	WA 1385 / CC 11	WA 1385	WA 1385				
T17	WA 1385 / CC 11	WA 1385	WA 1385				
T20	WA 1385 / CC 11	WA 1385	WA 1385				
T22	WA 1385 / CC 11	WA 1385	WA 1385				
T24	WA 1385 / CC 11	WA 1385	WA 1385				
T25	WA 1385 / CC 11	WA 1385	WA 1385				
T26	WA 1385 / CC 11	WA 1385	WA 1385				
T27	WA 1385 / CC 11	WA 1385	WA 1385				
T29	WA 1385 / CC 11	WA 1385	WA 1385				
T30	WA 1385 / CC 11	WA 1385	WA 1385				
T32	WA 1385 / CC 11	WA 1385	WA 1385				
T33	WA 1385 / CC 11	WA 1385	WA 1385				
T34	WA 1385 / CC 11	WA 1385	WA 1385				

*Prefixes in entry codes "G, P, U, W and T" correspond to genetic groups identified in Table 1.

*Les préfixes dans la colonne Entry codes "G, P, U, W et T" correspondent aux groupes génétiques identifiés dans le tableau 1.

of germplasm to screen for specific objectives. The challenge therefore is to ensure that the 'fewer' number of germplasm to be dispatched are diverse enough for the specific breeding objective. K-mean clustering is a useful tool in this regard.

Five clusters created from the K-mean clustering procedure and members of each group distributed following their on disease reaction are presented in table 4. Figure 4 shows the reaction of each group to diseases. *Glaberrimas* are concentrated in clusters 1 and 2, whereas improved *sativas* are nearly spread uniformly across the clusters. Most interspecific progenies (12 out of 29) belong to cluster 2 (table 4).

All the clusters except cluster 4 showed tolerance to leaf blast. Members of cluster 4 are mainly traditional *sativas* (6 out of 12), and three progenies (table 4). Cluster 5 is susceptible to gall midge, brown spot and stem borer attacks. Members of the group are distributed between the improved *sativas* (6 out of 9), 2 interspecific progenies and one USA variety.

K-means clustering based on morpho-physiological properties (table 5 and figure 5) show a neater classification than the one based on diseases reaction. This is perhaps because the traits measured were quantitative and not «subjective» scorings used for diseases and pests. Traditional *sativas* are clumped in cluster 5 (13 out of 20 entries), whereas 6 out of the 9 USA varieties are in cluster 1, along with improved *sativas* (9 entries) and interspecific progenies (6 entries). The *glaberrimas* are concentrated in cluster 2 (8 out of 11 entries). The morphological characteristics of the 5 clusters (cluster means values) are presented in figure 5.

Seedling vigor did not vary much. Cluster means were between 1.5 and 2.5 (not shown on graphs due to scaling). SLA was the lowest in cluster 1, while cluster 5 is characterized by mean time to flowering in 100 days. Plants reaching mean height of 100 - 110 cm were seen in cluster 2 (mainly *glaberrimas*) and cluster 5 (mainly traditional *sativas*). The best and the worst tillering ability were found respectively among genotypes in cluster 2 (mean tiller /plant = 7) and cluster 5 (mean tiller / plant = 5).

In cluster 1 we have entries of which the mean leaf blast scores are < 1. Cluster 3 did not show

any symptom of leaf blast. Members of cluster 4 rated susceptible (mean score of 4) to leaf blast. Six out of the 10 members of this group are improved *sativas*, the other others being 2 interspecific progenies and 2 USA materials. Clusters 2, 3 and 5 are susceptible to all diseases, whereas Cluster 4, consisting mainly of interspecific progenies (11 out of 25 entries) is characterized by high disease resistance (disease scores < 2.0).

Reclassification based on morphological traits and members of each cluster are shown in table 5. Figure 5 shows the characteristics of the clusters amalgated by morpho-physiological attributes. Cluster 1, where most of the traditional *sativas* are grouped (17 out of 29 members), most *glaberrima* (7 out of 11 *glaberrima* located here) and 4 interspecific progenies are characterized by the tallest heights (mean 105 cm), longer days to flower (90 days) and high SLA (52 m² leaf /g leaf). This cluster had also the best seedling vigor compared to other clusters. Cluster 5, comprising mainly of progenies (3 out of 5 members) showed high SLA also (figure 5). Cluster 2, is characterized by a high tillering rate. This is not surprising because this group is predominantly composed of improved *sativas* (11 out of 16 members) and 2 *glaberrimas*.

When classified on panicle and yield attributes, genetic groups are clearly different (Table 6). Nine *glaberrimas*, as well as 7 improved *sativas* and 7 interspecific progenies were found to be similar with respect to yield and panicle characteristics. This cluster had high mean plant yield, moderate spikelet number, and moderately low secondary branching. Cluster 1 and 2 where other improved *sativas*, and interspecific progenies are mainly located are characterized by high spikelet number (means = 100 to 150 per panicle), high secondary branching (mean 27 to 33) (figure 6). Analysis showed that cluster 5, with seven members is composed principally of traditional *sativas* (6 out of 7 members) and one improved *sativa* W124 (ITA330). This cluster was found to have the lowest primary and secondary branching, the lowest panicle length, the lowest spikelet number, harvest index and plant yield.

Table 5 : Rice genotypes amalgamated by K-mean clustering method (with K=5) on the basis of reaction to different morphological and physiological traits.

Génotypes de riz regroupés sur la base de la similarité de leurs caractéristiques morphologiques et physiologiques (groupement par la méthode des nuées dynamiques, K = 5).

Cluster	Genotypes	Cluster	Genotypes	Cluster	Genotypes	Cluster	Genotypes	Cluster	Genotypes							
1	25	C8, C1, D, C11	W5, W10, W17, W18, W22, W23, W24, W25, W26, W27, W28, W29, W30, W31, W32, W33, W34, W35, W36, W37, W38, W39, W40, W41, W42, W43, W44, W45, W46, W47, W48, W49, W50, W51, W52, W53, W54, W55, W56, W57, W58, W59, W60, W61, W62, W63, W64, W65, W66, W67, W68, W69, W70, W71, W72, W73, W74, W75, W76, W77, W78, W79, W80, W81, W82, W83, W84, W85, W86, W87, W88, W89, W90, W91, W92, W93, W94, W95, W96, W97, W98, W99, W100	2	17	C12, C13, C14, C15, C16, C17, C18	W12, W13, W14, W15, W16, W19, W20, W21, W24, W29, W30, W31, W32, W33, W34, W35, W36, W37, W38, W39, W40, W41, W42, W43, W44, W45, W46, W47, W48, W49, W50, W51, W52, W53, W54, W55, W56, W57, W58, W59, W60, W61, W62, W63, W64, W65, W66, W67, W68, W69, W70, W71, W72, W73, W74, W75, W76, W77, W78, W79, W80, W81, W82, W83, W84, W85, W86, W87, W88, W89, W90, W91, W92, W93, W94, W95, W96, W97, W98, W99, W100	3	18	W3, W11, W38, W14, W17, W18, W19, W20, W21, W22, W23, W24, W25, W26, W27, W28, W29, W30, W31, W32, W33, W34, W35, W36, W37, W38, W39, W40, W41, W42, W43, W44, W45, W46, W47, W48, W49, W50, W51, W52, W53, W54, W55, W56, W57, W58, W59, W60, W61, W62, W63, W64, W65, W66, W67, W68, W69, W70, W71, W72, W73, W74, W75, W76, W77, W78, W79, W80, W81, W82, W83, W84, W85, W86, W87, W88, W89, W90, W91, W92, W93, W94, W95, W96, W97, W98, W99, W100	4	15	W1, W2, W4, W6, W7, W8, W9, W10, W11, W12, W13, W14, W15, W16, W17, W18, W19, W20, W21, W22, W23, W24, W25, W26, W27, W28, W29, W30, W31, W32, W33, W34, W35, W36, W37, W38, W39, W40, W41, W42, W43, W44, W45, W46, W47, W48, W49, W50, W51, W52, W53, W54, W55, W56, W57, W58, W59, W60, W61, W62, W63, W64, W65, W66, W67, W68, W69, W70, W71, W72, W73, W74, W75, W76, W77, W78, W79, W80, W81, W82, W83, W84, W85, W86, W87, W88, W89, W90, W91, W92, W93, W94, W95, W96, W97, W98, W99, W100	5	16	W1, W2, W4, W6, W7, W8, W9, W10, W11, W12, W13, W14, W15, W16, W17, W18, W19, W20, W21, W22, W23, W24, W25, W26, W27, W28, W29, W30, W31, W32, W33, W34, W35, W36, W37, W38, W39, W40, W41, W42, W43, W44, W45, W46, W47, W48, W49, W50, W51, W52, W53, W54, W55, W56, W57, W58, W59, W60, W61, W62, W63, W64, W65, W66, W67, W68, W69, W70, W71, W72, W73, W74, W75, W76, W77, W78, W79, W80, W81, W82, W83, W84, W85, W86, W87, W88, W89, W90, W91, W92, W93, W94, W95, W96, W97, W98, W99, W100

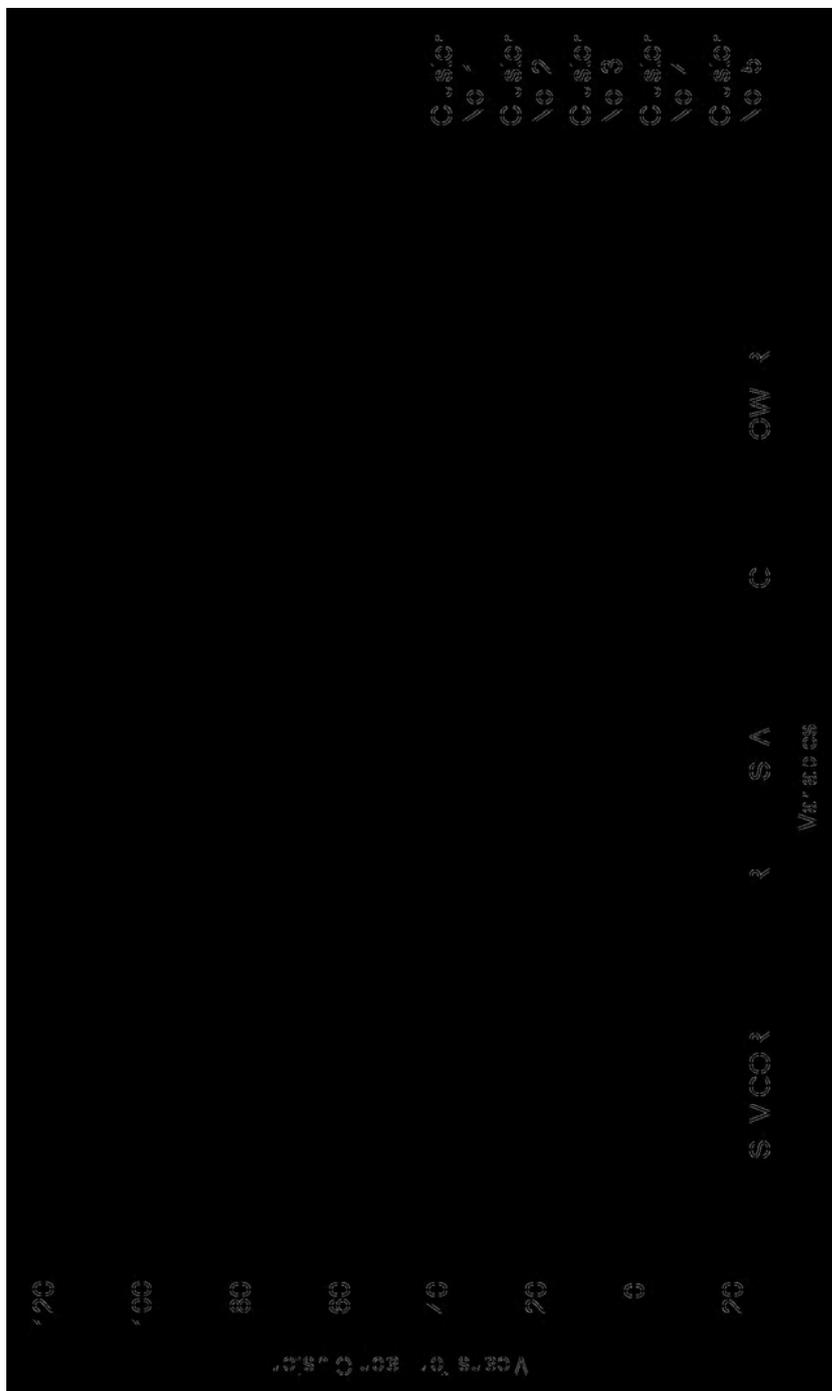


Figure. 5 : Average properties of genotypes lumped together on the basis of K-mean clustering of morphological and phenological characteristics.

Propriétés moyennes de génotypes regroupés par la méthode des nuées dynamiques sur la base de leurs caractéristiques morphologiques et phénologiques.



Figure. 6 : Average properties of genotypes lumped together on the basis of K-mean clustering of panicle characteristics, plant yield and yield components.

Propriétés moyennes de génotypes regroupés par la méthode des nuées dynamiques sur la base des caractéristiques de leurs panicules, rendements et composantes de rendement.

CONCLUSION

Regional and national programs involved in improving rice yields in less favorable rice environments in West Africa, require access to wide range of germplasm for screening, selection and use in their breeding objectives. The germplasm characterization studies reported here clearly showed that a high suitability of a particular genetic group resistant to diseases, morphological type or yield attribute does not equate to wide genetic variability within that group. The studies also showed that the magnitude of variability was not the same for all traits. Some traits are more diverse than others, indicating that breeding programs have different chances of rapidly achieving success with these traits.

Comparison within and between five rice germplasms obtained from tropical and temperate regions revealed an overlap with respect to the traits characterized. Cluster analysis showed for example, that most *glaberrimas* and interspecific progenies possess tolerance or resistance to leaf blast, stem-borer and gall midge attacks. Interspecific progenies and improved *sativas* are diverse with respect to panicle and yield attributes.

The study revealed that interspecific progenies were classified between their two parental groups (the *glaberrimas* and the improved *sativas*), (Jones *et al.*, 1997). Cluster analysis showed progenies spreading between the extremes where both parents occurred. Earlier, Jones *et al.* (1997) reported that progenies inherited from *glaberrima* parents the characters of vigor, high tillering, early growth duration and high SLA. From the *sativa* parents they took characters controlling yield and panicle attributes.

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