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RESEARCH ARTICLE

Genetic Diversity of *Gora* Rice (*Oryza sativa* L.) Landraces of Chotanagpur Plateau Region in Eastern India

Somnath Roy*, Amrita Banerjee, Jitendra Kumar, Bibhash Chandra Verma and Nimai Prasad Mandal
Central Rainfed Upland Rice Research Station, ICAR-National Rice Research Institute, Hazaribag-825301, Jharkhand, India

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The rice cultivars grown in the uplands of the state of Jharkhand, India are traditionally known as *gora* rice. These cultivars possess many important traits such as high seedling vigour, deeper roots and drought tolerance. In this study, a collection of *gora* landraces were assessed for morpho-genetic diversity using SSR markers. Morpho-agronomic analysis indicated that although seed morphological features are traditionally used for differentiating landraces, based on overall morpho-agronomic features also the cultivars could be differentiated as found in case of black gora. A genetic diversity analysis using 39 SSR markers detected considerable gene diversity (0.52) within *gora* cultivars. The white gora accessions were classified as *indica,* and rest including black gora, brown gora and other gora accessions belonged to *aus* group. This germplasm set provides scope for further genetic studies on multiple abiotic stress tolerance traits such as drought, submergenece and phosphorus starvation and traits for aerobic adaptation.

Key Words: Eastern India, genetic diversity, Gora rice, population structure

Introduction

The Chotanagpur plateau region in eastern India which covers much of Jharkhand state and adjacent parts of Chhattishgarh, Odisha and West Bengal (22.0-22.5^{o}N latitude; 83.95-88.0^{o}E longitude; 140-1200 m above msl). This region has a rich rice agroecological diversity due to variable soils and landscapes. The region is also endowed with diverse traditional cultivars and wild genetic resources of rice largely cultivated by the tribal communities inhabiting in the inaccessible areas (Chauhan *et al.,* 1995). In the state of Jharkhand, rice is grown in around 60% of total cropped area and approximately 33% of rice growing area in the state is upland. Jharkhand is the homeland of thirty two tribes including eight primitive tribes. These indigenous communities have selected diverse rice cultivars based on their food habits, suitability to environments and soil conditions, and tolerance to biotic and abiotic stresses. It is well documented that there is an inextricable link between cultural and biological diversity (Maffi, 2001; Gavin *et al.,* 2015). However, the harmonious link between biological and cultural diversity has become vulnerable due to homogenizing effects of climate change, urbanization and modern agriculture, among other influences (Liu *et al.,* 2002). Nevertheless, the tribal communities inhabiting remote areas still cultivate traditional cultivars because of cultural values, quality and individual preferences (Sinha & Xaxa, 2014).

As per revenue class, the land types in Jharkhand are classified in two broad classes: *tanr* (upland) and *don* (lowland). The uplands/ *tanr* is further classified based on fertility and slopes into *tanr*-I (homestead/ *bari* land), *tanr*-II (typical upland/ *gora* land) and *tanr*-III (sloppy and gravelly land). So, basically *gora* is a land type and any rice cultivars grown in *tanr*-II or *gora* land are popularly known as *gora* rice (Mandal *et al.,* 2011). Though the productivity is quite less, these rices provide sustenance to the poor and marginal farm families living in the most fragile environments. *Gora* rices are traditionally categorized based on husk colour (*karanga*/ black gora, *bhura*/brown gora, *charka*/white gora, etc.) and grain shape and sizes: *chhote*/*saria* (small-grained) gora, and *barka*/ *dani* (large-grained) gora (Sinha *et al.,* 1990).

Gora cultivars have evolved under marginal environments where the crop is challenged by a plethora of abiotic (such as drought and phosphorus starvation) and biotic stresses (such as high crop-weed competition, blast, brown spot and insect pests). Hence, these cultivars represent a valuable genetic resource for

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**Author for Correspondence: Email- somnath.roy@icar.gov.in; sroypbr@gmail.com* rice breeding. For example high seedling vigour and deep roots have been reported in black gora (Shrestha *et al.,* 2014; Redoña and Mackill, 1996). Earlier studies with molecular markers have classified *gora* cultivars within *aus* (Courtois *et al.,* 1997; Ali *et al.,* 2011) and *indica* (Garris *et al.,* 2005). However, these studies, conducted on a global-scale, are often limited by the relatively small number of accessions obtained from a specific geographic region. In contrast, studies with rice germplasm from a narrow geographical region, are also important to understand rice genetic diversity at micro level which is often shaped by intricate influences of the environment and cultural references of human communities. A study with 511 rice cultivars, including 5 *gora* accessions collected from Assam, Bangladesh and West Bengal reported two distinct groups within the *aus* sub-population (Travis *et al.,* 2015). Genetic diversity analysis of 69 imporved and traditional drought tolerant cultivars of India using SNP markers clasisifed accessions into *indica* and *aus* specific groups, and two *gora* acessions identified as *aus* (Vikram *et al.,* 2016).

In this study, we assess the genetic diversity and population structure of a collection *gora* rice accessions grown in the upland ecologies of Chotanagpur Plateau in Eastern India using agro-morphological traits and SSR markers. The genetic relationship between the *gora* accessions is compared by cultivar groups and check varieties from *indica* and *aus* subpopulations. Overall, this study provides an exhaustive examination of the genetic diversity within *gora* rice accessions for further utilization.

Materials and Methods

Plant Materials

A set of 49 *gora* rice accessions was used in the study. The accessions were sampled from rice germplasm collection being maintained at Central Rainfed Upland Rice Research Station (CRURRS), ICAR-National Rice Research Institute, Hazaribag, Jharkhand, India. These genotypes were collected earlier from different parts of the states of Jharkhand and Bihar in the Chotanagpur plateau region of Eastern India (Sinha *et al.,* 1990; Chauhan *et al.,* 1995). In addition to the *gora* accessions, 13 check varieties were used for phenotyping, while, 19 checks were included for genotyping. In this paper, '*gora*' (italics) is used when referring to gora cultivars as a whole, and 'gora' (normal font) for referring to different cultivar types such as black gora, brown gora, and white gora, etc.

Agro-morphological Characterization

Forty-nine *gora* and 13 check varieties were grown at CRURRS research farm during wet season (July-October) as rainfed crop in 2017 and 2018. The experiment was laid out in randomized complete block design with two replications and standard management practices were followed to raise a healthy crop. The entries were line sown in 3 rows having 2 m row length in the third week of July. After germination, the extra seedlings were hand removed to maintain a plant-to-plant distance of ~15 cm. Hand-weeding was done at 25 and 45 days after sowing. A recommended fertilizer dose of 60:30:30 ($N:P_2O_5:K_2O$) was applied. Data were recorded for 26 agro-morphological traits following Standard evaluation systems (SES) for rice (International Rice Research Institute, 2013). Grain yield plant^{-1} was calculated as the average yield of ten randomly selected hills from middle row of the plot.

Genotyping using SSR Markers

Thirty nine SSR markers, distributed across rice chromosomes, were selected from the GCP panel of 50 recommended markers for diversity analysis (Gramene marker database https://archive.gramene.org/markers/microsat/50_ssr.html) were used to assess genetic diversity among the accessions.

DNA was extracted from fresh leaves using the Qiagen DNeasy plant mini kit (Qiagen, CA, USA) following the manufacturer's instructions. Polymerase chain reaction (PCR) was carried out in a total volume of 10 µl reaction mixture having 25 ng template DNA, forward and reverse primers (5 pM each) and Master Mix (Thermo Fisher Scientific, USA). PCR was done in a thermocycler using following conditions: 5 min at 94°C; 35 cycles of 30 s at 94°C 30 s at annealing temperature and 30 s at 72°C; followed by 7 min at 72°C. Amplicons were visualized in Agarose gels stained with SYBR Safe DNA gel stains (Invitrogen). During scoring, the band with the lowest molecular weight was assigned allele number 1 and the progressively heavier bands were scored incrementally.

Data Analysis

The phenotyping data were subjected to analysis of variance and descriptive statistics using R v.3.4.4. (R Core Team, 2017). A factor analysis of mixed data

(FAMD) was performed in R using 'FactoMineR' and 'factoextra' packages in R to examine the variability including both quantitative and qualitative traits. FAMD algorithm can be seen as mixed between PCA and multiple correspondence analysis (MCA) and it ensures balance between the influences of both continuous and categorical variables to determine the dimensions of variability. Cluster analysis was done using 'cluster' package in R. The mixed data set (untransformed) of qualitative and quantitative traits was also used for cluster analysis by calculating the 'Gower' coefficient. A hierarchical cluster dendogram was generated using the 'Euclidean' distance and 'average' linkage between the objects.

The MCMC (Markov Chain Monte Carlo) population analysis program STRUCTURE (Falush *et al.,* 2003) was used to infer underlying population structure using an initial burn-in of 5,000 iterations, followed by a run length of 50,000 iterations. The population structure in the data was investigated using putative population *K* values ranging from 1-8 (10 replicates per *K* value) with a STRUCTURE model allowing for admixture and correlated allele frequencies. 'Structure Harvester' (Earl and VonHoldt, 2012) was used to determine an optimum *K* value. Subsequently, the SSR data was then reanalysed using STRUCTURE with the optimum $K = 2$, burn-in of 10,000 iterations and run length of 100,000 iterations to generate a STRUCTURE *Q* matrix. Major modes in the STRUCTURE output were identified using CLUMPAK (Kopelman *et al.,* 2015).

The following summary statistics of the SSR markers matrices were estimated: number of alleles (Na), major allele frequency (MAF), observed heterozygosity (Ho), expected heterozygosity (He) and polymorphism information content (PIC). The phylogenetic tree was constructed using Roger's 1972 genetic distance and neighbour joining method using PowerMarker V3.25 (Liu and Muse, 2005). To summarize the patterns of variation in multi-locus dataset, principal coordinate analysis (PCoA) was performed in GenAlex v6.5 software (Peakall and Smouse, 2012) using the genetic distance matrix among the accessions. Separate analyses were conducted by classifying the rice accessions into: cultivar groups (black gora, brown gora, white gora, gora and check) and STRUCTURE subpopulations (K1, K2 and admix). Accessions were only assigned to a STRUCTURE groups if the probablity of their group membership was >75%. Accessions with <75% probablity of a single group membership were classified as 'admix'.

Results and Discussion

Variability in Morpho-agronomic Traits

The *gora* accessions were classified into four groups: black grora, brown gora, white gora, and gora (other gora genotypes) based on traditional name. Overall, considerable variations were observed for seedling vigour (Vg), leaf blade pubescence (LBP), basal leaf sheath colour (BLSC), leaf angle (LA), apiculus colour (ApC), lemma and palea colour (LmPC) and seed coat colour (SCC). Frequency distribution indicated that seedlings of 85% *gora* accessions were extra-vigorous to vigorous. Awing was present in black gora accessions. Significant variations were also observed for LmPC within brown gora, white gora and gora subgroups. The LmPC of brown gora accessions varied from gold furrows on straw to brown furrows on straw. Majority (61%) of *gora* accessions had brown and red pericarp, with a few exceptions in white gora and gora where SCC varied from white to red (Fig. 1). The *gora* accessions predominantly had medium brown rice length and medium brown rice shape. Three black gora accessions (HRC82, HRC86, HRC88) had short-bold kernels.

Descriptive statistics of eleven quantitative traits revealed that all the traits showed significant variation within current germplasm collection (Table 1). Days to 50% flowering (DF) varied from 54 days (N22) to 95 days (Apo). Among the *gora* accessions, highest average DF was observed in white gora (66.56 days) followed by black gora (66.4 days). The highest average plant height (Ht) was observed in white gora (115.9 cm) followed by brown gora (113.5 cm) accessions. Most of the rice accessions had intermediate (90-125 cm) plant height. White gora cultivars recorded Panicle length (PnL) varied from 16.45 cm (HRC92) to 25.50 cm (HRC220) with an average value of 21.27 cm. The highest average brown rice length (BrRL) was observed in brown gora (6.23 mm) followed by white gora (5.99 mm). On an average, brown rice width (BrRW) was lowest in white gora (2.47 mm), and highest in brown gora and gora. The 100-grain weight (GW) varied from 1.54 g (Karhani) to 2.84 g (HRC94). Among the *gora* accessions, the gora group recorded the highest (2.12 g) GW, while black gora accessions had the lowest value (1.99 g). Grain yield plant^{-1} (Yld) under rainfed DSR varied from 0.72 g (HRC95) to 12.60 (Karhani).

Table 1. Range of variation in agro-morphological traits of *gora* rice landraces.

Groups	Stat	DF	Ht	PnN	PnL	GrL	GrW	SLmL	BrRL	BrRW	GW	Yld
All	Mean	64.42	110.82	10.17	21.27	8.35	3.22	2.56	5.98	2.59	2.09	5.97
n = 62	SD	6.91	12.28	2.61	2.49	0.52	0.20	0.29	0.39	0.20	0.23	2.77
	Min	54.00	69.00	4.67	16.45	6.62	2.36	1.83	4.67	1.99	1.54	0.72
	Max	95.00	134.33	16.33	27.50	9.47	3.70	3.25	6.87	3.00	2.84	12.60
	P	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.002	0.037
	%CV	10.73	11.08	25.66	11.71	6.23	6.21	11.33	6.52	7.72	11.00	38.02
Black gora	Mean	66.40	111.82	10.43	20.57	8.46	3.23	2.73	5.76	2.61	1.99	5.67
n = 10	SD	4.26	10.41	2.75	2.69	0.46	0.15	0.37	0.35	0.19	0.25	2.94
	Min	61.00	95.67	6.00	16.50	7.52	2.99	2.08	5.28	2.38	1.56	1.53
	Max	78.00	128.33	16.33	24.30	9.47	3.64	3.25	6.55	3.00	2.54	11.90
	P	0.000	0.104	0.079	0.000	0.231	0.010	0.003	0.000	0.000	0.279	0.795
	%CV	6.42	9.31	26.37	13.08	5.44	4.64	13.55	6.08	7.28	12.56	35.98
Brown gora	Mean	64.75	113.46	10.34	21.01	8.56	3.24	2.63	6.23	2.62	2.07	4.58
n = 12	SD	6.06	10.25	2.23	2.58	0.38	0.20	0.17	0.28	0.19	0.29	2.26
	Min	58.00	80.33	4.67	16.45	7.89	2.86	2.29	5.70	2.15	1.64	0.72
	Max	85.00	132.33	16.33	27.00	9.21	3.56	2.92	6.65	2.87	2.84	9.43
	P	0.000	0.076	0.999	0.000	0.002	0.000	0.000	0.000	0.000	0.257	0.712
	%CV	9.36	9.03	21.57	12.28	4.44	6.17	6.46	4.49	7.25	14.01	39.74
White gora	Mean	66.56	115.85	10.69	20.22	8.36	3.06	2.49	5.99	2.47	2.10	5.24
n = 8	SD	6.16	10.63	2.44	1.89	0.46	0.17	0.35	0.24	0.19	0.24	2.04
	Min	60.00	89.50	6.67	17.20	7.63	2.89	1.93	5.49	2.19	1.61	1.49
	Max	81.00	133.00	14.33	23.20	9.10	3.45	2.95	6.32	2.79	2.49	9.65
	P	0.007	0.173	0.214	0.000	0.001	0.004	0.000	0.000	0.000	0.070	0.265
	%CV	9.25	9.18	22.83	9.35	5.50	5.56	14.06	4.01	7.69	11.43	37.02
Gora	Mean	61.71	112.25	10.16	21.70	8.33	3.24	2.51	5.97	2.62	2.12	6.25
n = 19	SD	4.38	9.80	3.01	2.50	0.52	0.23	0.27	0.35	0.20	0.18	2.64
	Min	55.00	85.17	4.67	16.75	6.81	2.36	1.83	5.16	1.99	1.77	0.86
	Max	79.00	128.33	16.33	27.50	9.41	3.70	3.08	6.87	2.90	2.58	12.08
	P	0.000	0.000	0.267	0.000	0.139	0.000	0.000	0.000	0.000	0.253	0.098
	%CV	7.10	8.73	29.63	11.52	6.24	7.10	10.76	5.86	7.63	8.49	32.64
Checks	Mean	65.23	102.44	9.50	22.08	8.08	3.27	2.49	5.92	2.60	2.13	7.52
n = 13	SD	10.87	15.92	2.35	2.31	0.62	0.18	0.23	0.52	0.20	0.21	2.95
	Min	54.00	69.00	5.00	18.40	6.62	2.90	2.09	4.67	2.16	1.54	1.67
	Max	95.00	134.33	13.00	26.30	8.97	3.60	3.08	6.58	2.96	2.37	12.60
	P	0.000	0.000	0.004	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.068
	%CV	16.66	15.54	24.74	10.46	7.67	5.50	9.24	8.78	7.69	9.86	31.25

DF, Days to 50% flowering; Ht, Plant height; PnN, Panicle number plant^{-1}; PnL, Panicle length; GrL, Grain length; GrW, Grain width; SLmL, Sterile lemma length; BrRL, Brown rice length; BrRW, Brown rice width; GW, 100-grain weight; Yld, yield plant^{-1}; SD, Standard deviation; CV, Coefficient of variation

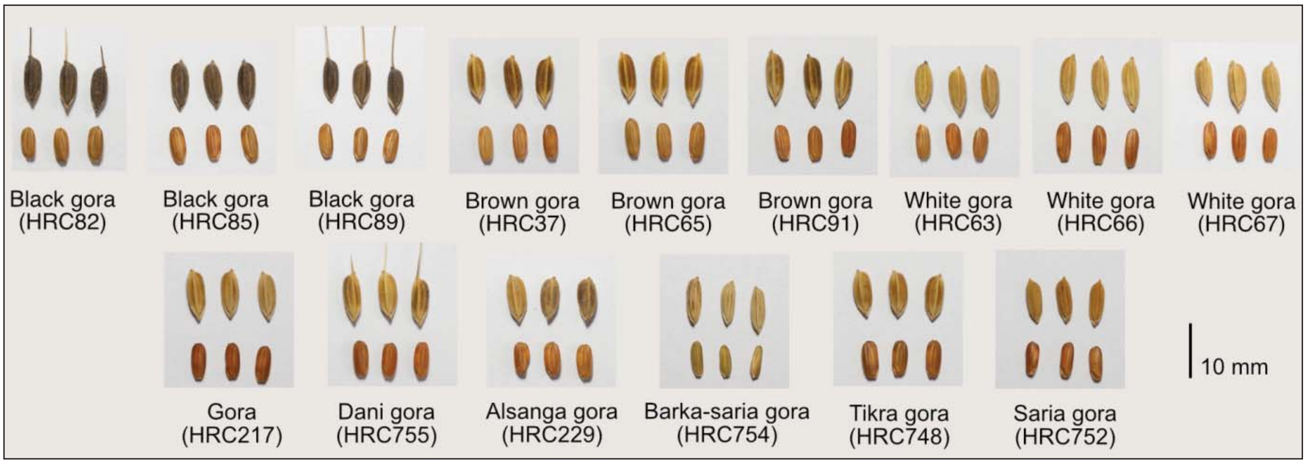

Fig. 1. Grain and kernel morphology of representative *gora* cultivars

The highest average Yld was recorded in checks (7.52 g) followed by gora (6.25 g), and the lowest Yld was observed in brown gora accessions (4.58 g). Considering the mean Yld of individual entries, only three accessions IR64Drt1, N22 and Karhani achieved Yld >10 g. The variation (% CV) for Yld was very high within four *gora* groups as well as within overall panel.

Ago-morphological Diversity within Gora Rices

The factorial analysis of mixed data (FAMD) using 26 traits extracted five factors (eigen value = 3.67 - 5.64) which collectively explained 33% of the total phenotypic variance. Among the traits, BrRL, An, AnC, ApC, LmPC and Len recorded higher contributions to factor 1 (Dim.1), while SLmL, Vg, An, ApC, LmPC and SCC showed greater contributions to factor 2 (Dim. 2). Overall, LmPC, ApC, SCC, An, AnC, Len, BrRL and Vg had contributed 69.19% to first two factors (Fig. 2a). Biplot of Dim.1 and Dim.2 explained about 16% of the total variance and separated the accessions mainly based on grain and kernel traits (Fig. 2b). The black gora accessions having morphologically distinct grains, formed separate group from the rest of the accessions. Similarly, the brown gora accessions formed a distinct group in the biplot. The white gora accessions along with improved check varieties grouped differentially

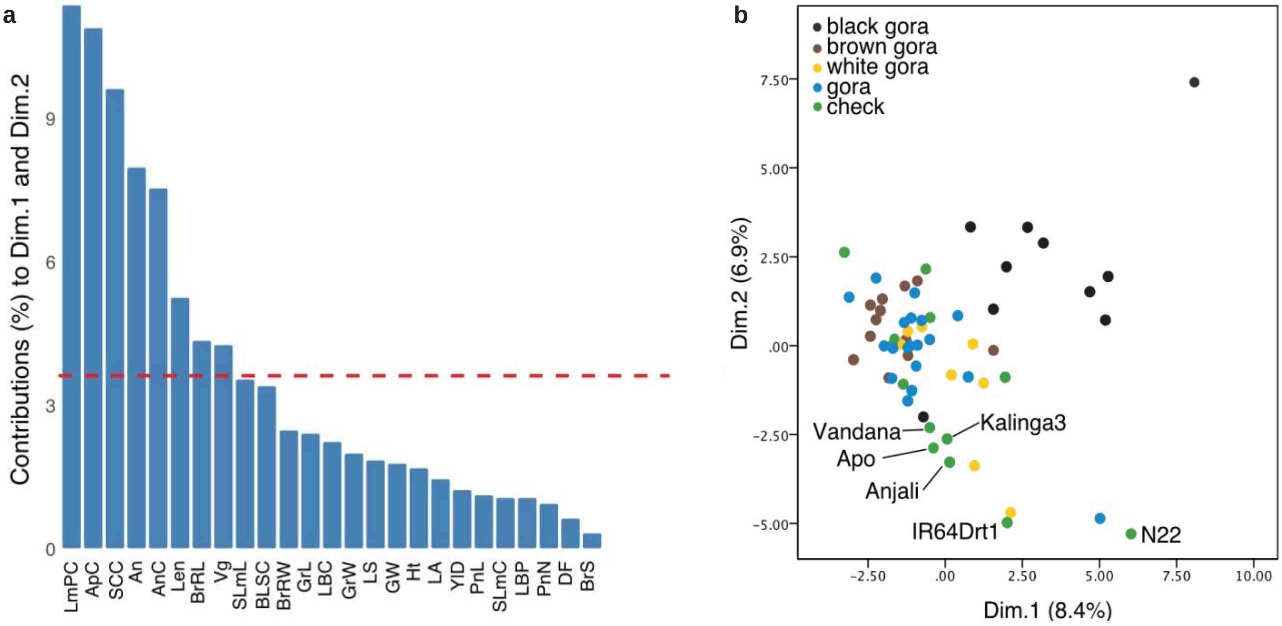

Fig. 2. Factorial analysis of mixed data. a. Percent contribution of the traits on factor 1 and 2; b. Biplot showing distribution of rice accessions based on trait loadings on first two factors

from the brown gora and gora and traditional checks. However, some overlapping between the cultivars of white gora and gora groups was found mostly due to their similarities in LmPC, ApC, SCC, and An.

Cluster analysis also supported the findings of FAMD. Dissimilarity (Gower's coefficient) among the accessions varied between 0.102 to 0.584 with an average value of 0.324. The dendogram depicting the morphological similarities of rice accessions have been drawn using 'average' linkage, due to having the highest cophenetic correlation (0.77) as obtained in the Mantel test (Fig. 3). Analysis of the optimal clusters following 'average silhouette' 'elbow' and 'Kelly-Gardener-Sutcliffe' methods suggested optimum cluster number of 2, 4 and 9. At *K* = 2, only N22 diverged from the rest of the genotypes. At *K* = 4, seven black gora accessions formed separate group from the rest of *gora* accessions. While, at *K* = 9, cluster 3 - 7 were represented by black gora accessions along with a traditional check Widd jong. The cluster 8 comprised two check varieties Kalinga III and IR64 Drt1. Finally, 48 accessions of brown gora, white gora, gora and check varieties formed cluster 9 with some sub-grouping. The white gora accessions distributed in three sub-clusters indicating considerable morphological variability within the white gora cultivars. However, it is apparent from both FAMD and clustering that most of the brown gora, gora and traditional checks are morphologically similar.

A comparison of phenotyping results revealed that the extent of variability in different agro-morphological traits is in line with the previous reports (Srivastava *et al.,* 1977; Sinha *et al.,* 1990, 1999). Most of the *gora* rice had intermediate to tall plant height. In general, drought-tolerant cultivars are tall mostly due

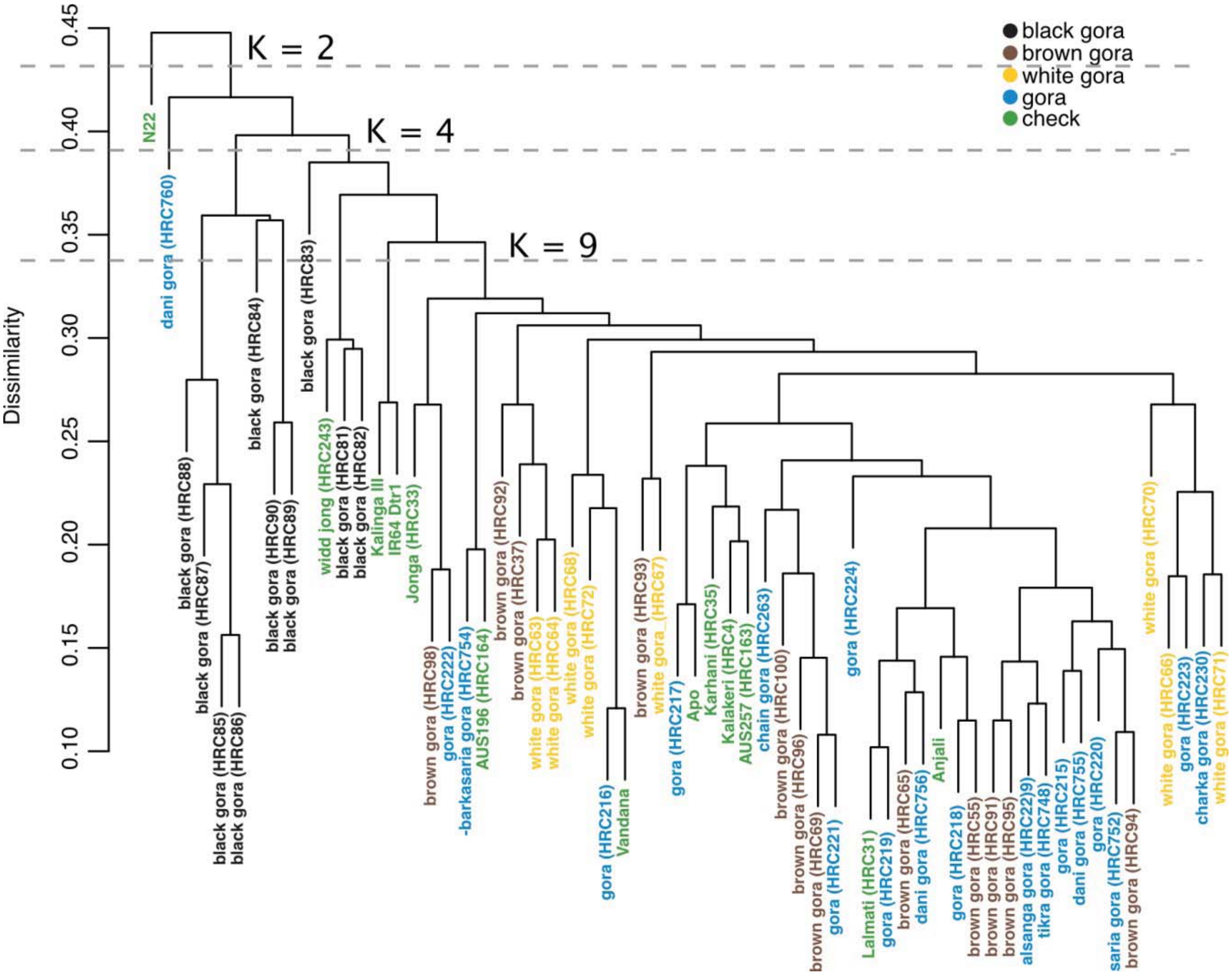

Fig. 3. Agro-morphological similarity among the *gora* rice landraces assessed using Gower's coefficient and clustering

to the tight linkage between the *sd1* gene and drought tolerance (Vikram *et al.,* 2015), and the 'tall' allele of *sd1* is present in most the drought tolerant landraces (Vikram *et al.,* 2016). Grain shape and size seem to vary appreciably in brown gora and white gora accessions as compared to black and gora rices, similar to earlier reports (Chauhan *et al.,* 1997). Among the different *gora* types brown gora was the most widely cultivated by upland farmers of Chotanagpur plateau and maximum number of collections were also made for this type. The lowest average grain yield per plant was registered in brown gora, while yield of all *gora* cultivars was lower than that of the checks. Sinha *et al.* (1998) also obtained very less yield for *gora* varieties and have the opinion that only a few good high yielding varieties could be sufficient to replace the *gora* cultivars. Multivariate analyses indicated that lemma-palea colour, apiculus colour, seed coat colour, awning, awn colour, grain length and grain width are the most influential traits in differentiating the accessions (Srivastava *et al.,* 1977; Sinha *et al.,* 1998). It is well documented that seed morphological features are generally been used as keys in cultivar identification and maintaining genetic purity of rice landraces by traditional farming communities (Roy *et al.,* 2016; Zapico *et al.,* 2020). The cluster analysis revealed that black gora cultivars are morphologically most distinct, while rest of the *gora* accessions are similar to each other and with improved drought tolerant varieties such as Anjali, Apo and Vandana. Hence, under typical upland ecologies, breeders also selected for similar sets of morphological traits that were favoured by traditional farmers over time.

SSR Polymorphisms

Altogether 154 alleles were identified from 68 tested germplasm using 39 SSR markers. On average 3.95 alleles were detected per marker. The highest number of alleles were identified for RM9 (AN = 9) followed by RM125 (AN = 7). The polymorphism information content (PIC) varied from 0.11 (RM25) to 0.73 (RM55) with an average of 0.47. Higher PIC (>0.60) was recorded for RM209, RM471, RM152, RM9, RM452, and RM19.

Population Structure and Genetic Diversity within Gora Rice Accessions

The results of the model-based STRUCTURE analysis (Fig. 4a), phylogenetic analysis (Fig. 4b) and principal coordinate analysis were consistent and 68 (49 *gora* plus 19 checks) accessions clearly separated into two clusters corresponding to *indica* and *aus*. Fifteen accessions including 13 *gora,* N22 and Kali aus were classified as admix, while, 18 (7 white gora and 11 check) and 35 (6 black gora, 8 brown gora, 15 gora, and 6 check) accessions were classified as *indica* and *aus,* respectively. When the NJ tree and PCoA were annotated based on cultivar groups, the distinctiveness of white gora accessions from the rest of the *gora* cultivars was obvious.

Assessment of genetic diversity indicators within the tested accessions revealed a higher level of genetic diversity within *aus* (He = 0.55) group compared to *indica* (He = 0.51) and admix (0.41) (Table 2). A similar pattern was observed for PIC. Gene diversity (He) at the cultivar level ranged from 0.41 (gora) to (0.57) checks. Among *gora* cultivars, brown gora recorded the highest genetic diversity (He = 0.45) (Table 2).

Although *gora* cultivars are generally classified under the *aus* subpopulation of rice, till date no molecular analysis has been done with a larger set of *gora* germplasm. Population structure analysis divided the current set of germplasm into two groups, K1 and K2, corresponding to *aus* (60%) and *indica* (40%) with average F_{st} of 0.349 and 0.035, respectively. The *gora* accessions were distributed in both the subpopulations, and interestingly seven out of eight white gora accessions were classified as *indica*. Rest of the 41 accessions were identified as *aus* (71%) and admix (29%). These findings are supported by the previous reports that *gora* rice is genetically *aus* (Courtois *et al.,* 1997; Ali *et al.,* 2011; Travis *et al.,* 2015). In the present study, four sub-clusters have been detected within the *gora* accessions falling under *aus* subpopulation, indicating considerable genetic diversity within them. A study with 183 rice landraces of East Kalimantan on the island of Borneo, Indonesia reported high population genetic structure even though there is little or no geographic differentiation within the landraces (Thomson *et al.,* 2009). Five groups were detected within the *japonica* accessions. A few other studies have also indicated that regional genetic diversity analysis with cultivars from a small geographic area (local-scale) often depict rich genetic diversity at micro-level (Barry *et al.,* 2007; Zhang *et al.,* 2007). Travis *et al.* (2015) reported two major groups within a large collection of *aus* germplasm originating from Eastern India and Bangladesh, and classified five *gora* accessions into *aus-1* (brown gora), *indica* (black gora) and *aus*-admix (black gora, dudhi gora and gora dhan). Courtois *et al.* (1997) observed

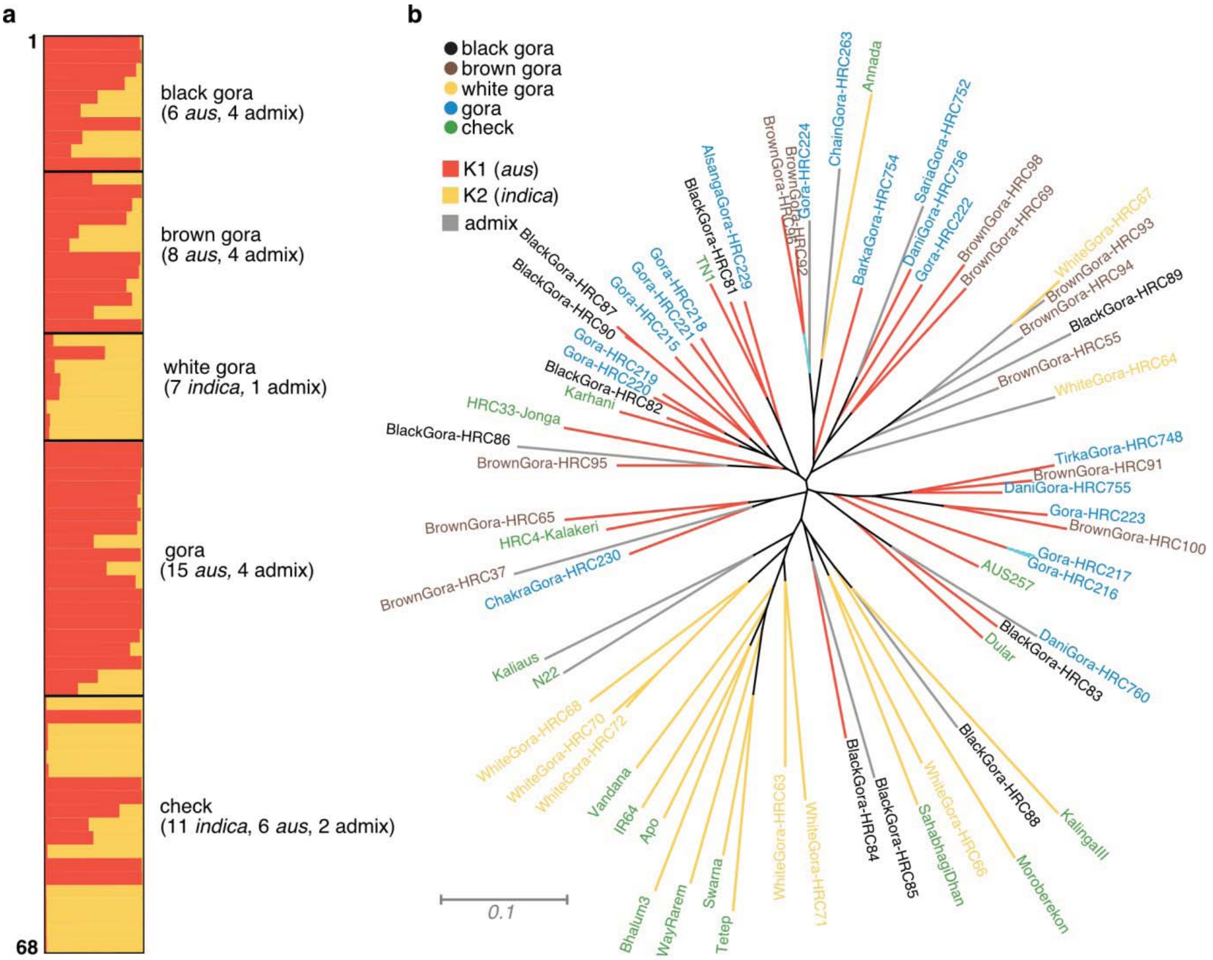

Fig. 4. Genetic diversity within *gora* rice. a. individual ancestry inferred with STRUCTURE. Each individual is represented by a bar partitioned by colour. The proportion of the colour making up each bar/ genotype represents the proportion contributed by the ancestral population. The clustering based on optimal K value divided the accessions into two main groups, corresponding to *indica* and *aus* rice types. b. Unrooted neighbour-joining tree of 68 rice accessions. Accession names and tree branches are colour coded based on cultivar types and STRUCTURE groups, respectively

Table 2. Genetic diversity indicators of *gora* rice landraces at different substructures

Sub-population	n	Na	MAF	He	Ho	PIC
STRUCTURE groups						
K1 (*aus*)	35	3.538	0.553	0.551	0.003	0.496
K2 (*indica*)	18	3.179	0.602	0.509	0.000	0.449
admix	15	3.051	0.704	0.406	0.004	0.353
Cultivar groups						
Black gora	10	2.667	0.682	0.425	0.000	0.369
Brown gora	12	2.769	0.663	0.448	0.006	0.388
White gora	8	2.462	0.667	0.432	0.000	0.370
Gora	19	2.974	0.699	0.408	0.005	0.358
Check	19	3.769	0.539	0.571	0.004	0.521
Mean	68	3.949	0.611	0.521	0.004	0.471

n, Number of genotypes; Na, Average number of alleles; MAF, Major allele frequency; He, Gene diversity; Ho, Observed heterozygosity; PIC, Polymorphism information content that traditional upland cultivars mostly belong to *aus* group and appeared to be less diverse. In the present study, the morphological and genetic similarity of white gora accessions with improved drought tolerant varieties indicates that these cultivars may be some early *indica* cultivars being grown in the adjacent rainfed region and adopted by the traditional farmers for better yield in the specific ecology (relatively favourable uplands) of the region. This study also highlights considerable genetic diversity within the *aus* specific cluster (He = 0.551), as well as within *gora* cultivar types (He > 0.40). Genetic diversity is considered to be a function of ecological and evolutionary history (Thrupp, 2000). The high genetic diversity within *gora* cultivars could be associated with the diverse agro-ecological and ethno-cultural features of the region, as proposed in other studies (Wang *et al.,* 2016; Mbanjo *et al.,* 2019).

Conclusion

Agro-morphological analysis of *gora* rice accessions of Chotanagpur Plateau region in Eastern India indicated that although seed morphological features are traditionally used for differentiating landraces, based on overall agro-morphological features the cultivars could also be differentiated as found in case of black gora. Genetic diversity analysis revealed considerably high genetic diversity within the *gora* cultivars and classified white gora accessions as *indica,* and rest of the black gora, brown gora and other gora accessions as predominantly *aus*. The knowledge on the phenotypic variability and genetic structure of these trraditional upland rice landraces will provide essential foundation of decision making for conservation and utilization in breeding programmes, which is considered as an underexploited set of landraces. This germplasm set also provides scope for further genetic studies on multiple abiotic stress tolerance traits such as drought, submergenece and phosphorus starvation and traits for aerobic adaptation such as early vigour, weed competitiveness and well developed root system.

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