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RESEARCH ARTICLE

GGE biplot analysis in rice landraces grown under rainfed ecosystem

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Abstract

Plant breeders across the world frequently employ GGE Biplot analysis. Purpose of this study was to evaluate the GXE interaction and stable yield performance of 15 rice (*Oryza sativa* L.) landraces of southern India grown under rainfed ecosystem. All the rice landraces were sown in a randomized complete block design with three replications in five consecutive years in rabi season from 2018-19 to 2022-23 at Agricultural Research Station, Tamil Nadu Agricultural University, Paramakudi, Tamil Nadu. The pooled ANOVA over tested years / seasons revealed that both the genotypes and GEI (GXE interaction) significantly influenced grain yield and rice landraces performed contrarily in diverse testing years due to cross over nature of GEI. Biplots with the genotype main effect and GEI were used to study and display the trend of the interaction elements. About 95 % of the overall variation in the GGE model was explained by the first two principal components. (PC1 = 74.8 %, PC2 = 19.9 %). The “what-won-where” polygon was shown that G8 (Kallurundaikar), G11 (Kattanur), G4 (Sivapuchithiraikar) G5 (Kuruvaikalanjium) and G7 (Mattaikar) performed well in each environment and they were the highest-yielding among the landraces tested on the field. In terms of discriminating and representativeness for the environments, rabi 2019-20 was regarded as superior production season as per selectiveness for the testing sites. The rice landraces selected through this study may be utilized as parental lines in breeding for yield enhancement in rainfed situation of southern India or similar agro-ecological zones.

Keywords: GGE biplot; GXE interaction; rice landraces; stability; yield

Introduction

The crop of choice for more than 50 % of the world's population, rice (*Oryza sativa* L.), is known as the "Global Grain" and accounts for around 20 % of the world's caloric intake. Rice is cultivated globally on about 167 million ha of which nearly 45 % area is under rainfed ecosystem, contributing only about 25 % of total production (1). Asia produces and consumes almost 90 % of the world's rice. With 118.87 million metric tonnes produced, India comes in second to China (2). In general, landraces are less productive than commercial cultivars, but in recent years, they have gained significance as sources of genetic diversity in the hunt for genes that can be used to tolerate or resist biotic and abiotic conditions. Farmers have conserved these landraces for their medicinal, nutritional, culinary and cultural values (3).

Research on stable yields and GE interactions is required to assess the consistency of yields of rice grains and create genotypes that perform optimally and consistently throughout years and geographical regions (4). To produce high yielding genotypes coupled with stability, breeding operations sometimes incorporate multi-environment trials (MET) to assess possibly stable and adaptable lines. Numerous statistical techniques have been created to analyze MET data and identify GE interaction (GEI) performance patterns. Among them, the biplot has gained popularity among agricultural researchers and plant breeders as a tool for analyzing and showing MET data (5, 6).

GEI of target traits in various contexts can be found using the statistical technique known as genotypic main effect plus GEI (GGE) biplot. Pictorial GGE biplots illustrate the GEI of several environmental experiments that makes comparing types easier. Using proportionally scaled first two principal components resulting from environment-oriented MET data, GGE biplots are created, streamlining mega-environment demarcation and genotype evaluation (6). A total of 15 rice landraces were assessed in this study for their productivity and stability utilizing the GGE biplot technique in five consecutive years in rabi season at Agricultural Research Station, Paramakudi by adopting pertinent agronomic procedures.

Materials and Methods

The experimental materials included fifteen rice landraces, which were assessed at the Agricultural Research Station of the Tamil Nadu Agricultural University, Paramakudi, during rabi seasons (Sep-Oct to Jan-Feb) of 2018-19, 2019-20, 2020-21, 2021-22 and 2022-23 (Table 1). In a 5 ×2 m plot, each genotype was grown with a 15 cm (between rows) ×10 cm (between plants) spacing. The advised agronomic procedures adopted to raise the crop in good manner. Ten randomly chosen plants from each replication were used to calculate the grain yield per plot (kg) and converted it to kg per hectare.

At a height of 39 meters above mean sea level, the Agricultural Research Station, Paramakudi is situated at 9.5494^0 N latitude, 78.5916^0 E longitude. It was well known as a paddy research sub-center from 1952 to 1958, a state seed farm from 1958 to 1978, a multi-crop experiment sub-station from 1978 to 1981 and then a well-known agricultural research station after 1981. Nearly 9.36 hectares are covered by this station. The northeast monsoon, which begins in September - October, is responsible for 60 % of the station's annual rainfall, which is roughly 840 mm on average. The region where the clay loamy soil has low levels of organic matter, little nitrogen and moderate to high levels of phosphorus and potassium. Rainfall data for all the five cropping seasons is presented in Table 1.

For the grain yields of the tested rice landraces, a pooled analysis of variance (ANOVA) was performed. Every year was treated as a distinct habitat. Using the statistical software for social sciences (SPSS), the primary impacts of genotype, environment and their interaction were identified. The data were pictorially examined to assess adaptation and stable performance using the GGE biplot program when the GE interaction was discovered (6). The GGE concept (6) and the biplot concept (5) are the two pillars of the GGE biplot technique. Previous studies provided a thorough explanation of the GGE biplot's fundamentals (7). The graphs were generated based on, (i) 'what-won-where' pattern (which genotype is best in a site); (ii) ranking of rice landraces based on stable yield; (iii) comparing of production seasons based on representativeness and discriminating ability.

Results and Discussion

Analysis of variance and mean

Analysis of variance revealed that there were substantial differences between genotypes, environments and genotypes and environment interactions. It also revealed that genotypes had a significant impact on the expression of grain yield and those genotypes and environments interacted with one another (Table 2). Additionally, genotypes had the biggest contribution (67.92 %) to the total sum of squares, followed by genotype environment interaction (29.65 %) and environments (2.43 %), indicating that the genetic architecture of the genotypes on the manifestation of the trait compared to the environment and their interaction. This result is consistent with early workers (8, 9).

The genotypes Kallurundaikar (G8) and Poongar (G12) had the maximum (3475 kg/ha) and minimum (2399 kg/ha) grain yield values respectively, when genotypes were averaged across environments (Table 3). Various genotypes displayed variable performance in every scenario. The seasonal average grain yield was determined to be 2888 kg/ha, with a range of 2776 kg/ha for E1 (Rabi 2018-19) to 2960 kg/ha for E3 (Rabi 2020-21). Differential performance of genotypes of rice and other crops in relation to different environments has been estimated by earlier group of scientists (8-14).

The what-won-where view of the GGE biplot

The ability of the what-won-where GGE biplot to display the what-won-where pattern of a GEI is its most noticeable characteristic. To ensure that all additional genotypes are encompassed inside the polygon, a polygon is initially constructed on the genotypes that are farthest distant from the biplot origin. Then perpendicular lines were drawn to each side of the polygon beginning from the origin of biplot (7). Biplot is divided into numerous sectors by these perpendiculars. The environments are divided into two of the four sectors. The macro environment was defined by the environment group within each sector and the genotypes at the polygon's edge (15). Both initial and second principal components (PC1 and PC2) together can explain 95 % of the overall variation, of which 74.8 % was explained by the first principal component (PC1), according to the partitioning of GE interaction by GGE biplot analysis (Table 2). Similarly, the first two principal components of GEI explained 80 % and 98 % of the total variation of the GGE model for yield in Bambara groundnut (*Vigna subterranea* L.) (12, 13).

Table 1. The details of rice landraces and environment

S.No.	Genotype code	Genotype name	Environment code	Season name	Seasonal rainfall (mm)
1.	G1	Norungan	E1	Rabi 2018-19	277.7
2.	G2	Nootripathu	E2	Rabi 2019-20	417.4
3.	G3	Vellaichithiraikar	E3	Rabi 2020-21	663.0
4.	G4	Sivapuchithiraikar	E4	Rabi 2021-22	920.6
5.	G5	Kuruvaikalanjiyam	E5	Rabi 2022-23	661.0
6.	G6	Kuliyadichan	-	-	-
7.	G7	Mattaikar	-	-	-
8.	G8	Kallurundaikar	-	-	-
9.	G9	Arubadhanguruvai	-	-	-
10.	G10	Chandikar	-	-	-
11.	G11	Kattanur	-	-	-
12.	G12	Poongar	-	-	-
13.	G13	Mysore malli	-	-	-
14.	G14	Kala namak	-	-	-
15.	G15	Kichali samba	-	-	-

Table 2. Pooled ANOVA and partitioning of GEI with GGE model for grain yield of 15 rice landraces over five years/seasons

Source of variation	DF	SS	MS	% explained
Genotypes (G)	14	9315.22	665.37**	67.92
Environments (E)	4	333.84	83.46**	2.43
G × E	56	4066.12	72.61**	29.65
PCA 1	17	30.04	1.76**	74.8
PCA 2	15	7.99	0.53**	19.9
PCA 3	13	1.34	0.10**	3.3
PCA 4	11	0.69	0.06**	1.7
PCA 5	9	0.06	0.01**	0.2

**Significant at P ≤ 0.01; DF = Degrees of freedom SS = Sum of squares MS- Mean sum of squares

Table 3. Mean yield and principal component values of GGE for 15 rice landraces and five environments

Sl. No.	Genotype	E1	E2	E3	E4	E5	Mean	PCA1	PCA2
1.	Norungan	2443	2808	2857	2748	3118	2795	-0.280	-0.232
2.	Nootripathu	2412	2610	2613	2570	3528	2747	-0.535	-0.693
3.	Vellaichithiraikar	2562	2484	2507	2442	2755	2550	-0.780	0.054
4.	Sivapuchithiraikar	3337	3465	3532	3403	3201	3387	1.175	-0.100
5.	Kuruvaikalanjiyam	3548	3461	3551	3394	2536	3298	1.123	0.622
6.	Kuliyadichan	2901	2802	2820	2762	3132	2883	-0.081	-0.206
7.	Mattaikar	3279	3424	3537	3344	2376	3192	0.921	0.745
8.	Kallurundaikar	3247	3531	3592	3468	3535	3475	1.256	-0.383
9.	Arubadhanguruvai	2651	2860	2900	2806	3153	2874	-0.103	-0.230
10.	Chandikar	2780	2480	2454	2461	3355	2706	-0.607	-0.507
11.	Kattanur	2939	3474	3549	3400	3519	3376	1.030	-0.415
12.	Poongar	2308	2454	2513	2393	2329	2399	-1.008	0.445
13.	Mysore malli	2318	2599	2673	2531	2375	2499	-0.772	0.438
14.	Kala namak	2435	2565	2617	2508	2548	2535	-0.743	0.267
15.	Kichali samba	2475	2639	2693	2581	2639	2605	-0.593	0.193
	Mean	2776	2910	2960	2854	2940	2888	-	-
	PCA 1	0.450	0.531	0.547	0.433	0.171	-	-	-
	PCA 2	0.112	0.031	0.093	0.117	-0.982	-	-	-

The best method for identifying winning genotypes and displaying the patterns of GEIs is the polygon view of the GGE biplot (Fig. 1). The placement of all environmental factors in one portion of the biplot ensured that a particular genotype outperformed all other conditions evaluated. On the other hand, if the environmental indicators were placed in a different portion of the biplot, different genotypes acquired different surroundings. Additionally, the genotypes located at the polygon vertex in a biplot section without an environmental indication are genotypes that perform poorly in the entire test environments (16). The 'what-won-where' pattern of the GEI is therefore exposed and this is a key characteristic of the GGE biplot that was recovered by the innermost element of the biplot (17). The genotype that was associated to a polygon's vertex in a region where environmental indicators were found to be snoozed and suggested that this genotype would perform better in that environment. On the other hand, a genotype associated with a polygon vertex where no site indication dropped in the sector showed that this genotype performed badly in all environmental conditions. In comparison to the corner genotypes, the genotypes inserted inside the polygon are less environment-respective (7, 13).

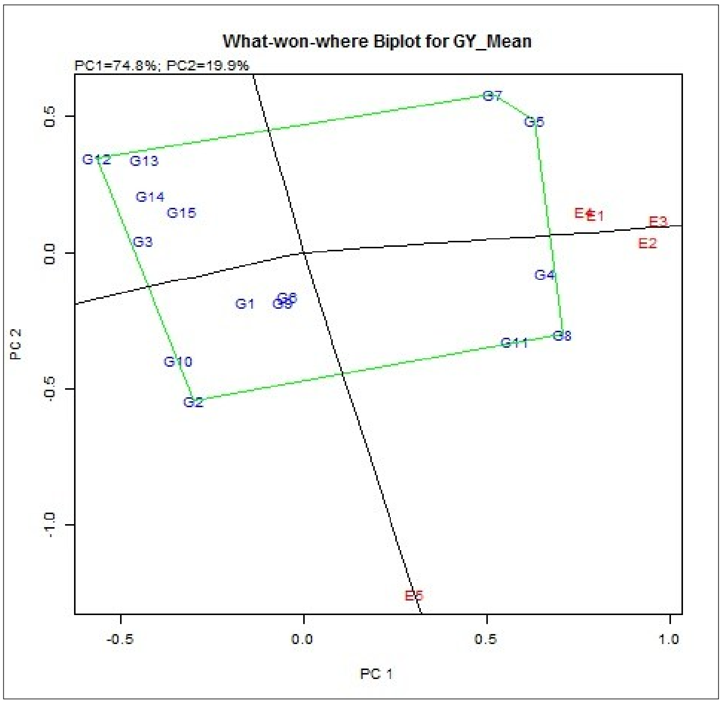

Fig. 1. What-won-where biplot for grain yield of 15 rice landraces in five environments.

In this study, two mega environments exist, one has E2 (Rabi 2019-20) and E5 (Rabi 2022-23) and the other has E1 (Rabi 2018-19), E3 (Rabi 2020-21) and E4 (Rabi 2021-22). So, in environments E2 (Rabi 2019-20) and E5 (Rabi 2022-23), genotype G8 (Kallurundaikar) won, but genotypes G7 (Mattaikar) and G5 (Kuruvaikalanjium) won in environments E1 (Rabi 2018-19), E3 (Rabi 2020-21) and E4 (Rabi 2021-22). This pattern indicated that the target environment might be divided into two mega environments, with different genotypes being chosen for each. Similar result was reported in potato (18), Bambara groundnut (13) and rice (14) for yield.

Average yield and stability performance of rice landraces

The genotype evaluation is an effective strategy for this rainfed ecosystem since all test conditions might be combined into a single mega-environment. The average environment coordination (AEC) was used to assess the genotypes' yield and stability (Fig. 2). According to previous research, the biplot's origin and the mean of all test environments (the little circle on the line) are where the abscissa of AEC is defined (15). The innermost circle and a location somewhat close to the arrow's head in the center of the circle where excellent genotypes were placed (Fig. 2). Compared to the genotypes in the outside circle, the inner circle genotype is far more desired. However, there have been instances where no genotype was located inside the inner circle; as a result, genotypes that are located adjacent to the inner circle are thought to be the best (16). Based on average yields and stability results, 15 rice landraces were ranked (Fig. 2). The AEC abscissa's direction indicated that average yields are higher across all conditions. Thus, among the 15 genotypes, G8 (Kallurundaikar) had the highest yield and G12 (Poongar), the lowest. The line with two arrows that runs parallel to the AEC abscissa and through the biplot origin is the ordinate of AEC. It is used to assess the genotype stability and both arrows indicate less stability.

Therefore, stability of genotype is stronger and the environment has less of an impact on yielding ability when the genotype vector on the AEC abscissa is shorter. The genotypes with higher average yield and more stability are prospective desirable genotypes for breeding. These stable genotypes should have the shortest vector from the AEC abscissa and be located towards the center of the little circle in Fig. 2 of the biplot graph, which represents the average environment. According to this research, the genotypes G8 (Kallurundaikar), G11 (Kattanur) and G4 (Sivapuchithiraikar) had the highest yields across every environment (Fig. 1, 2) and are also known to be stable. Although all environments can be combined into a single mega-environment, the GE interaction appears to have less impact on the yield stability of G8 (Kallurundaikar), G11 (Kattanur) and G4 (Sivapuchithiraikar). Sometimes high yielding genotypes in across environments may be less stable as reported in potato (18). It advocates that the GEI by some means affects the stability of high yielding genotypes even though all testing sites can be clustered into one mega-environment.

Representativeness and discriminating ability of production seasons

Research indicates that the cosine of the angle between two vectors roughly represents the correlation between two test sites; a sharp angle indicates a positive correlation, whereas a flat angle denotes a negative correlation (7). To determine the relationships among the test environments, the environmental vectors producing angles between them or each environment point with the biplot's origin point connected by the lines, were

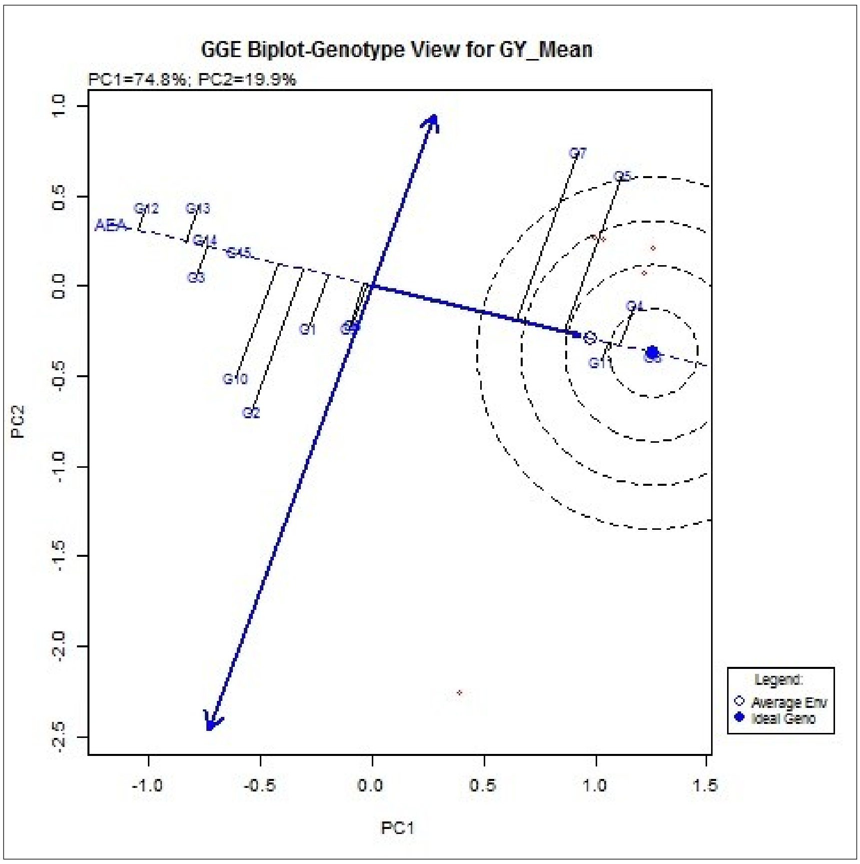

Fig. 2. GGE biplot genotype view with AEA axis for grain yield of 15 rice landraces in five environments.

used (Fig. 3). Due to acute angles in their vectors, all five test environments exhibit positive correlation, indicating that they are all extremely similar in terms of their ability to distinguish between genotypes in terms of yield performance. Additionally, the relatively narrow angle between the vectors of E1 and E4 suggests that trial data from both E1 (Rabi 2018-19) and E4 (Rabi 2021-22) could be highly comparable. As a result, one of them might be deleted without substantially reducing the knowledge about the genotypes for the subsequent trials. Similar finding was reported while evaluating rice genotypes in six locations (14).

Previous studies reported that the average environment coordinate (AEC), also known as the average environment axis (AEA) and the environment vector, have a correlation coefficient between them that is roughly equal to the cosine of the angle between them (19). The test environment is better when the angle between the AEC abscissa and the test environment vector is less. The direction of the AEC abscissa line is indicated by an arrow and the average value of the test environment is indicated by a small concentric circle, with the discriminating ability being inferred from the length of the test environment vector. Each environment vector's length provides an indication of how effective it is at identifying different genotypes in the environment (16).

In this study, the optimal test environment is shown by the center of the AEA's concentric circles (Fig. 3). The longest vector of all environments, E5, serves as the distance between the ideal test environment and the biplot origin (Rabi 2021-22). As a result, the E5 site (Rabi 2021-22) might not be used to choose superior genotypes but it might be helpful to eliminate unstable genotypes. One of the best environments for this study's evaluation of superior genotypes adapted to the entire rainfed region is the site of E2 (Rabi 2019-20), which is closest to the center of the concentric rings. As well one superior environment was identified while analyzing 95 Bambara groundnut accessions in two testing sites in two consecutive years (12).

Conclusion

The findings conclusively show that genotypes and the combination of genotypes with environments have a major impact on grain yield expression. The genotypes G8 (Kallurundaikar), G11 (Kattanur) and G4 (Sivapuchithiraikar) were identified as stable in the GGE Biplot genotype view and were located close to the average environment. Additionally, E2 (Rabi 2019-20) is regarded as the most stable environment overall. More parallels between E1 (Rabi 2018-19) and E4 (Rabi 2021-22) were shown. In order to conserve resources, one of them might be removed without substantially losing knowledge about the genotypes. What-won-where bi-plot clearly showed that genotypes G5 (Kuruvaikalanjium) and G7 (Mattaikar) fared well in E1 (Rabi 2018-19), E3 (Rabi 2020-21) and E4 (Rabi 2021-22) whereas genotype G8 (Kallurundaikar) performed better at E2 (Rabi 2019-20) and E5 (Rabi 2022-23). The GGE biplot turns out to be a very helpful tool for compiling and analyzing the results of multi-environmental rainfed rice trials and for examining how genotype and environment interact.

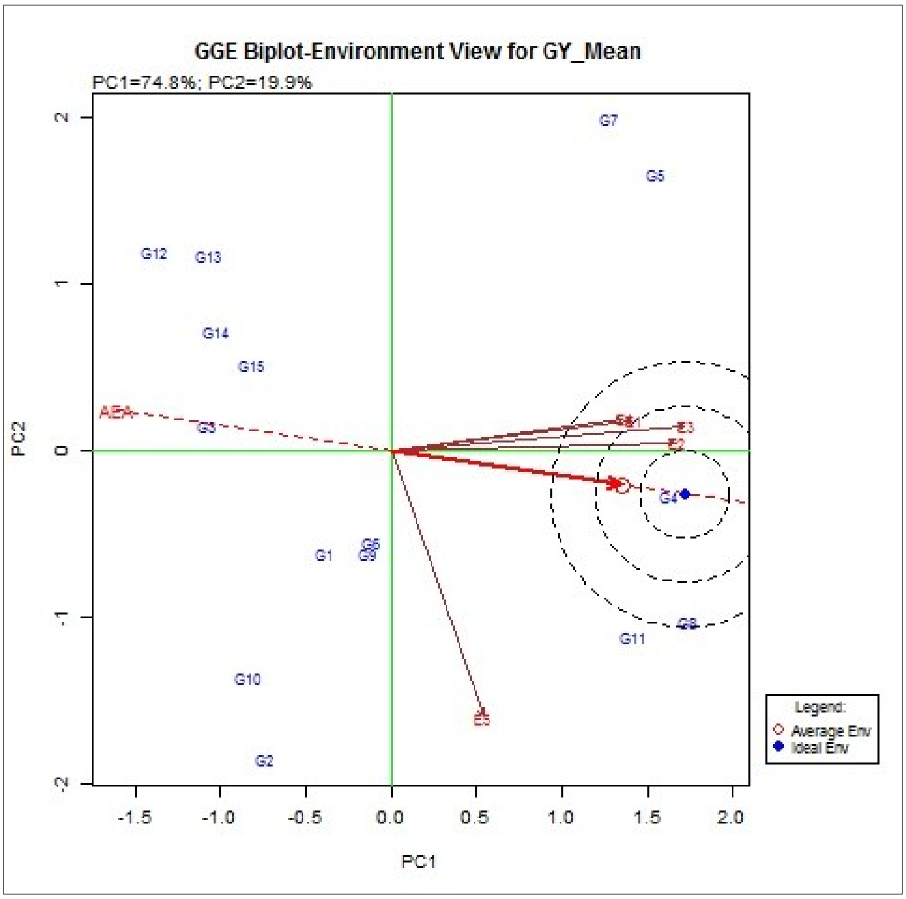

Fig. 3. GGE biplot environment view with AEA axis for grain yield of 15 rice landraces in five environments.

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Authors' contributions

SM conducted the experiments and wrote the original draft. KT and MG supervised the research trial. AS, MG and KT validated all data. JR and MP reviewed the content, whileMJ and AV edited the manuscript. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interests to declare.

Ethical issues: None

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