

INSTRUCTIONS FOR PREPARATION OF ABSTRACTS FOR THE 2025 MEETING

Beginning with the Proceedings for the 24th Rice Technical Working Group meetings, Desktop Publishing software was chosen as a means for expediting the post-meeting publications process. To accomplish this, Microsoft Word (Windows) was identified as the preferred word processing software to be used.

Each electronic file should include:

- 1) title of materials,**
- 2) corresponding RTWG panel, and**
- 3) corresponding author's name, daytime telephone number, e-mail address.**

These criteria apply uniformly to 1) presented paper abstracts, 2) poster abstracts, 3) symposia abstracts, 4) panel recommendations, and 5) list of panel participants. More details with respect to each of these items follow below.

Presented Paper, Poster, and Symposia Abstracts

To be published in the proceedings, presented paper, poster, and symposia abstracts for the RTWG 2025 meeting must be prepared as follows. Please follow these instructions – doing so will expedite the publishing of the proceedings.

1. An electronic file is to be submitted to the respective panel chair no later than December 13, 2024, as stated in the Call for Papers issued by the RTWG 2025 meeting chair and/or panel chairs.
 - a. Use the following file naming system:
(First Initial)(LastName)(Poster/Paper/Symposia)(Panel)
 - b. For example: AFamosoPaperBGG
 - c. Panel Chair abbreviations in file name should follow:
 - i. Student Contest – SC
 - ii. Breeding, Genetics, and Genomics – BGG
 - iii. Economics and Marketing – EM
 - iv. Plant Protection – PP
 - v. Postharvest Quality, Utilization, and Nutrition – PQUN
 - vi. Agronomy and Rice Culture – ARC
 - vii. Weed Control and Growth Regulation – WCGR
2. Use the One-Drive upload link to upload your abstract directly to the panel chair (link available in email notification of proposed paper and/or poster acceptance).
3. Margins: Set 1-inch for side margins; 1-inch top margin; and 1-inch bottom margin. Use a ragged right margin (do not full justify) and do not use hard carriage returns except at the end of paragraphs.
4. Type: Do not use any word processing format codes to indicate boldface, etc. **Use 12-point Times New Roman font.**

5. Heading:
 - a. Panel: Center and type in caps and lower case.
 - b. Title: Center and type in caps and lower case.
 - c. Authors: Center name(s) and type in caps and lower case with last name first, then first and middle initials, with no space between the initials (e.g., **Roberts, T.L.**).
 - d. **DO NOT GIVE AFFILIATION OR LOCATION.** The attendance list will provide each author's affiliation and address.
6. Body: Single space, using a ragged right margin. Do not indent paragraphs. Leave a single blank line between paragraphs.
7. Content is limited to one page.
 - a. Include a statement of rationale for the study.
 - b. Briefly outline methods used.
 - c. Summarize results.
8. **Tables and figures are not allowed.**
9. **Literature citations are not allowed.**
10. **Use the metric system of units.** English units may be shown in parentheses.
11. **When scientific names are used, *italicize* them – do not underline.**

EXAMPLE ABSTRACT:

Breeding, Genetics, and Genomics

Comparison of QTL, GWAS, and Genomic Selection Breeding Approaches for the Quantitative Trait of Grain Length

Angira, B., Cerioli, T., Guerra, R., and Famoso, A.N.

Rice grain shape is a major determinant of rice market value and the end-use. GS3 is a major grain shape gene that controls grain length trait in U.S. rice germplasm. Recently, qGL7.1 grain length gene was mapped to chromosome 7, which explained significant grain length variation in U.S. rice germplasm. Both GS3 and qGL7.1 genes do not segregate within the long-grain or medium-grain U.S. rice germplasm and no other major genes are reported within each grain class. These genes would be useful in long by medium crosses, but it is challenging to make yield gains and achieve the preferred quality for either class from these crosses. Therefore, improvement on grain length within the long grain class would not be possible with marker assisted selection approach on these two major genes.

Grain length in rice is a genetically controlled and highly heritable trait. Thus, an improvement on grain length of long-grain rice can be achieved using other approaches - QTL stacking and genomic selection approaches. We used four bi-parental populations - CL111/RoyJ, CL153/Lakast, CL172/Cypress, and Presidio/Catahoula, developed using elite southern long-grain parents, to map the QTLs for grain length and genomic prediction and two multi-parent populations for the genome-wide association. Our results did not identify any major and consistent QTLs for grain length in the four bi-parental populations. We selected lines having favorable alleles at two QTLs that explained the highest phenotypic variations for one of the populations named MPB and selected 10 lines out of 100 total lines that had favorable alleles for long grain. The average of the selected lines was 7.13 mm. In another approach, we predicted all the lines of the MPB population and selected the top 10 lines for grain length and the average of these lines was 7.24 mm. Similar results were observed in one of the other populations and no significant QTLs were identified in the remaining two bi-parental populations. GWAS in multi-parent did not result in any significant peak for grain length. These results demonstrate that stacking QTLs is less effective in improving grain length within long grain class compared to the genomic selection approach. Moreover, the stacking QTLs approach requires more resources compared to genomic selections.

In case of other questions or in the absence of being able to access the Call for Papers, contact:

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