Abstract for 2024 ISRFGC

Comparative Genomics & Technology session

**Undercover genes: The hidden impact of introgressions in US rice**

Jeremy D. Edwards1, Trevis D. Huggins1

1USDA ARS Dale Bumpers National Rice Research Center, Stuttgart, AR. 72160

Rice (*Oryza sativa*) is a vital crop in the United States, with long-grain varieties predominantly derived from the *tropical japonica* (TRJ) subpopulation. Breeding programs have historically introduced beneficial genes from other rice subpopulations, including *indica*, to enhance traits such as yield, disease resistance, and stress tolerance. However, alongside these targeted introgressions, inadvertent introgressions of genomic regions have occurred, which may carry unintended consequences for rice breeding. This study aims to identify recombination events flanking introgressions from non-TRJ subpopulations and reveal cryptic introgressions within historical and modern US rice varieties.

Local ancestry inference (LAI), also known as "chromosome painting," was employed to determine the population ancestry of specific chromosome regions within individual’s genomes. In this study, LAI was performed using the software Gnomix. Public raw sequence read data were obtained for a panel of over 5,000 rice accessions, including all available sequenced US rice varieties. Joint variant calling was conducted using a DeepVariant/GLNexus pipeline on the USDA SCINet high-performance computing resources. To train the LAI model, non-admixed individuals from each subpopulation were identified using the software Admixture.

The analysis revealed distinct and persistent patterns of linkage drag surrounding known introgressed gene regions, as well as previously undetected cryptic introgressions across the genomes of US long grain rice varieties. Detecting and characterizing these introgressed regions in US rice varieties is essential for optimizing breeding strategies. This knowledge will help mitigate potential adverse effects of cryptic introgressions and allow breeders to capitalize on beneficial trait associations that may arise from these introgressions.

**Keywords:**

Introgression, local ancestry inference, linkage drag, admixture