Mapping Yield Related Traits in a Suite of Six *Oryza rufipogon* Species Complex Chromosome Segment Substitution Line Libraries in *Indica* and *Japonica* Rice Backgrounds

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The two varietal groups of cultivated rice (*Oryza sativa*) are *indica* and *japonica.* The rice ancestral species are *O. rufipogon* and *O. nivara*, collectively identified as the *Oryza rufipogon* species complex (*ORSC*) and are an underutilized resource for rice improvement. To make the *ORSC* genepool more accessible, three genotypically and phenotypically diverse *ORSC* accessions were selected as donors, OrA (W1944) from China, OrB (IRGC106148) from Loas and OrC (IRGC105567) from Indonesia, to develop chromosome segment substitution line (CSSL) libraries from crosses with IR64, an IRRI *indica* long grain and Cybonnet, a U.S. *tropical japonica* long grain. This study was conducted to characterize the libraries for yield-related traits and demonstrate how substitution mapping is used to discover the underlying genes. IR64 and 219 single IR64 CSSL plants from the three IR64 libraries were grown in the greenhouse and characterized for six agronomic, two panicle architecture and five seed traits. Cybonnet and 212 Cybonnet CSSLs from the three libraries were evaluated in replicated field studies for six agronomic, six panicle architecture and eight seed traits. Across the Cybonnet libraries, 62 CSSLs were significantly different from Cybonnet for one or more traits. To ascertain the chromosome region and underlying candidate gene(s) causing these differences, substitution mapping was performed with previously reported genotypes and results compared to substitution mapping with the IR64 libraries. Mapping will be illustrated using the CSSLs which had delayed heading under long days and revealed five genes, *OsMADS50*, *RFT1*, *HD3A*, *SE1* and *GHD7*, associated with rice flowering time pathways.