Rice is a major world food crop with USA being the third largest exporter of rice, and Arkansas accounting for more than 40% of U.S. rice production. Rice production in Arkansas is dependent on water reservoirs for stable irrigation. Rice productivity is dependent on water availability, with rice using 2-3 times more water than other food crops. The objectives of the research were: 1) screening and dissection of drought resistance mechanisms in diverse rice genotypes and a recombinant inbred line (RIL) population; 2) identify molecular markers for drought resistance (DR) traits in the segregating population. The rice genotypes exhibited differential drought resistance mechanisms categorized as drought tolerance, drought avoidance, and drought escape on the basis of morphological and physiological differences (ABA response). The documented morphological, physiological, and grain yield parameters differed significantly between the genotypes ($P \leq 0.01$) and treatments ($P \leq 0.01$) with a strong genotype x treatment interaction (($P \leq 0.01$). A RIL population derived from the varieties Kaybonnet (DR) and ZHE733 (sensitive), termed K/Z RILs, was chosen for molecular genetic analysis of drought resistance traits. The RIL population was screened using controlled drought stress treatment at the reproductive stage in the field, and the effect of stress quantified by the number of filled grains per panicle. Based on the DR scores, a genetic screen was done using bulked segregant analysis (BSA), where sets of 10 DR and sensitive RIL plants were used for screening of SSR markers to find polymorphisms linked to the yield-related traits under drought. From this BSA screen, 6 polymorphic markers were identified: RM9 (Chr 1), RM109 (Chr 2), RM236 (Chr 2), RM114 (Chr 3), RM131 (Chr 4) & RM139 (Chr 11). Our results provide valuable information for dissecting the genetic basis of drought resistance mechanisms and provide a valuable resource for breeding US rice cultivars for a water saving agricultural system.

PO0855: Rice

Regulatory Network Mediated By the Rice Decussate Gene (DEC) Under Drought Stress

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Identification and characterization of regulatory genes are important for understanding the complex genetic complex network that defines phenotypic expression potential under a given environmental condition. The *Decussate* (*DEC*) gene was initially discovered as a regulator of leaf phyllotaxy. Our recent studies showed that one of the *DEC* genes in rice is part of *qDTY12.1*, a QTL with major effects in yield maintenance under drought. DEC- *qDTY12.1* expression is important for the maintenance of flowering time under drought. The parents (IR64, Way Rarem) and the backcross introgression lines (BILs) in IR64 displaying high (HPB) and low (LPB) yield penalty under drought were used in this study. BILs carrying the Way Rarem allele showed robust *DEC* expression at the booting stage when the flower organs develop. Expression was further enhanced under drought stress. However, LPB had much higher expression compared to its siblings. A putative interacting gene (*OsC3H56*) was found to be upregulated during the booting stage and under drought only in the LPB. Sequence analysis showed that the BILs and Way Rarem showed the same *DEC* allele, indicating proper introgression of *qDTY12.1.* However, *OsC3H56* sequences differ between the genotypes examined. Promoter analysis of the different *DEC* alleles showed unique stress-inducible cis-elements in the Way Rarem allele. Collectively, these results suggest that *DEC* expression is important for maintained yield under drought. However, to be fully functional, *DEC* needs its interacting partners, one of which is possibly *OsC3H56*. The authors will present progress in characterizing the *DEC* partners in the regulatory network.

PE0856: Rice

Marker-Assisted Backcrossing for Introgression of the Saltol Locus Conferring Salt Stress Tolerance in Rice

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Soil salinization represents a threat for rice cultivation. The H2020 project NEURICE (New Commercial EUropean Rice) aimed at identifying and introducing genetic variation for salt tolerance in European rice germplasm, mainly by exploiting the positive effect of the *Saltol* QTL in maintaining the Na/K homeostasis. The *Saltol* QTL from the *indica* rice donor IR64-Saltol (located on chromosome 1) was introgressed into two *japonica* Italian varieties, Onice and Vialone Nano following a marker-assisted backcross (MABC) scheme, through three backcrosses and two selfing to achieve the BC3F4 generation. During the backcrosses, the scheme was coupled to an embryo rescue technique to fasten the process. At each backcross cycle, the *foreground* and *background* selections relied on SNP-based KASP markers. The BC3F1 selected lines showed a 91-98 and 93-98 recovery percentage for Onice and Vialone Nano backcrosses, respectively. BC3F2 lines were genotyped to identify homozygous lines at *Saltol* locus and the best BC3F3 lines (10 in Vialone Nano and 12 in Onice) were subjected to genotyping by sequencing (GBS) to allow a more precise screening of the recurrent parent genome. Finally, the best BC3F4 lines were subjected to field phenotyping in salinized fields on delta Po river, to *in vivo* assess their salt tolerance.

PO0857: Rice

Positive and Negative Complementation Effects Determine Transgressive Salt Stress Tolerance in Recombinant Inbreds of Rice

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The new plant breeding paradigm has a grand challenge of creating novel adaptive phenotypes that have not been achieved before, in order to contribute an innovative solution to food security in the 21st century. Methods for creating optimal varieties for different environmental conditions needs to be re-envisioned. In this study, extremely salt-tolerant and salt-sensitive recombinants of rice were identified from an F_8 recombinant inbred population derived from a cross between salt-sensitive *indica* (cv. IR29) and salt-tolerant *aus* (cv. Pokkali) parents. A minority of recombinants showed tolerance that are beyond the phenotypic ranges of the parents. The mega-sensitive recombinant FL499 was unique in comparison to the rest of its siblings based on a battery of physiological traits involved in maintaining ionic homeostasis. On the other hand, the mega-tolerant recombinant FL510 was more of a hybrid between the two parents. We inferred that complementation occurred between parental beneficial alleles, creating a stronger phenotype hence reduction of physiological drags. Hyperspectral image analysis showed minimal change between stress and control in FL510, thus providing a mechanistic basis for its acquired salt tolerance potential. This is reflected in the overall transcriptome configuration, which showed very gradual changes compared to the rest of the population. Metabolome profiles also showed significant similarity to IR29 profile, further indicating that despite its inherent sensitivity, IR29 does have important contributions to the expression of superior tolerance potential. These results indicate that genome shuffling led to various combinations of beneficial and detrimental alleles in transgressive individuals.

PE0858: Rice

QTL Mapping for Resistance to Scirpophaga Incertulas Using indica Rice Recombinant Inbred Lines

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Abstract: *Scirpophaga incertulas* is one of the most destructive pest of rice and mainly drill and eat rice stems, resulting in reduced yield. There are few resistant species against the widespread Chilo suppressalis and Scirpophaga incertulas in germplasm resources .We found that the indica rice A232 is moderately resistant to *Chilo suppressalis* and *Scirpophaga incertulas*. Our research was to clone the resistance genes (QTLs) of A232 to the rice *Scirpophaga incertulas*. We constructed a recombinant inbred line(F12) using A232 and Gang46B (susceptible indica rice varieties to *Scirpophaga incertulas*). We evaluated the level of resistance to *Scirpophaga incertulas* for 265 recombinant inbred lines under natural rice fields condition in Hainan province by measuring the dead-heart index (DHI) in 2012 and 2013. Among A232 and Gang46B, a total of 833309 SNPS were detected, including 644062 SNP markers with a depth of at least 4X that were applicable to RIL. A High density linkage map from this