The improved annotated genome of loblolly pine (*Pinus taeda* L.) may allow fine-mapping of important Mendelian traits such as disease resistance. *Cronartium quercuum* f. sp. *fusiforme* (CQF) causes fusiform rust disease on pine, a major disease threat to the timber industry in the southern US. Genetic major gene for gene resistance is the primary approach to control losses. A high priority for breeders and forest managers is to identify candidate resistance genes in pine and avirulence genes in CQF. We conducted bulk segregant analysis of next-generation sequence data from both host and pathogen. In pine, half-sibling progeny from a resistant mother were phenotyped as either resistant or susceptible to CQF. These progeny were sequenced with a custom sequence-capture method targeting a genomic region linked to resistance alleles by prior work. In CQF, analysis of whole-genome sequence of rust grown on resistant or susceptible seedlings identified a 200 kbp region containing several likely effector proteins. In pine, we will test any identified candidate R genes for interaction with the candidate avirulence genes identified in CQF. By identifying candidates for an interacting avirulence and resistance gene pair in this conifer-rust pathosystem, we will discover markers that will guide breeding and deployment of resistant pine and enable us to identify additional interacting gene pairs that are known to exist but have yet to be molecularly discovered in this pathosystem.

First report of non-2NS resistance to wheat head blast

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Wheat blast, caused by the fungus *Magnaporthe oryzae Triticum* (MoT), is a devastating emerging disease affecting S. America and S. Asia. Despite 30-yrs of intensive effort, the 2NS translocation from *Aegilops ventricosa* contains the only source of useful head blast resistance identified to date. Our goal was to identify non-2NS resistance to MoT. At least 1000 elite cultivars, breeding line materials, and wild accessions were tested at 2 biosafety level-3 laboratories in the US and under controlled and field conditions in Bolivia. In controlled conditions, heads were inoculated after full emergence and individually rated for percentage of diseased spikelets. Under field conditions, susceptible spreaders were inoculated at tillering to guarantee sufficient inoculum. Disease incidence and severity were evaluated as the average rating for each meter-row plot. The diagnostic marker Ventriup-LN2 was used to test for the presence of the 2NS translocation. Among the germplasm tested, four non-2NS CIMMYT lines (i.e., CM22, CM36, CM58, and CM61) averaged 6.5, 17.5, 6.7, and 0% of disease severity under controlled conditions. Under field conditions, averages of two locations (2017 growing season) were 3, 18.5, 0, and 12%. Meanwhile, susceptible checks averaged 91% (controlled-environment) and 34% (field). Additional experiments are being conducted to validate our results. New resistance sources from this study can be incorporated into wheat head blast breeding programs.

Broad-spectrum resistance and susceptibility to bacterial blight and bacterial leaf streak of rice

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Quantitative trait loci (QTL) that confer broad-spectrum resistance (BSR) have been elusive targets of crop breeding programs. Bacterial leaf streak (BLS) and bacterial blight (BB), caused by *Xanthomonas oryzae* pv. *oryzicola* (*Xoc*) and *Xanthomonas oryzae* pv. *oryzae* (*Xoo*), respectively, are responsible for major losses in rice production in Asia and Africa. Controlling these two diseases is particularly important in Sub-Saharan Africa, where no sources of BSR are available in currently deployed varieties. Our goal is to identify novel, broad-spectrum resistance sources to control BLS and BB in rice, using a Multi-parent Advanced Generation Inter-Cross (MAGIC) population, derived from eight elite indica cultivars. MAGIC populations have an increased level of recombination and provide higher precision and resolution to detect QTL. The MAGIC parents and lines were genotyped and phenotyped in both greenhouse and field conditions by screening with diverse strains of *Xoc* and *Xoo*. Using genome-wide association and interval mapping analysis, we identified 37 strain-specific QTL, and 14 QTL effective against multiple *X. oryzae* strains. From these, three QTL are pathovar-specific and 11 confer resistance to both pathovars. By detecting phenotypic effects of causal alleles, we have identified resources that will facilitate a better understanding of how the involved genes contribute to resistance or susceptibility. Because the MAGIC founders are elite varieties, the BSR QTL identified can be rapidly incorporated into breeding programs to achieve more durable resistance to BLS and BB.

Genome-wide association mapping of resistance to *Fusarium proliferatum* in soybean

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Fusarium root rot is an important constraint to soybean (*Glycine max* L.) production in the United States. In 2014, yield losses due to Fusarium root rot in the United States were 116,000 tonnes (58.4 million dollars). In South Dakota, 10 species of *Fusarium* were identified causing root rot of soybean, and among a collection of 59 *Fusarium* isolates representing the 10 species, *Fusarium proliferatum* isolate FUS026 was determined to be the most aggressive on a susceptible soybean cultivar. In this study, 146 plant introductions from 21 countries and from maturity groups 0 (90) and I (56) in the USDA Soybean Germplasm Collection, were inoculated with isolate FUS026 at planting using the inoculum layer method. At 14 days after inoculation, lesion length caused by *F. proliferatum* on the soybean roots were measured. One hundred and twenty genotypes in this collection were significantly less susceptible ($P < 0.05$) to isolate FUS026 when compared to the susceptible soybean cultivar, which indicated that these 120 genotypes could be used as potential parental lines to develop soybean varieties with resistance to *F. proliferatum*. A genome-wide association mapping analysis was performed with a total of 34,604 single nucleotide polymorphic (SNP) markers. Thirty five significant markers-trait associations ($-\log_{10} (P) > 3.0$) were identified across five chromosomes (1, 8, 9, 10 and 13). The discovery of these loci through association mapping is a significant step to identify sources of resistance to *F. proliferatum*.

Dissecting interactions of rice major and minor blast resistance genes with yield related components

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A large recombinant inbred line (RIL) mapping population consisting of 800 individuals was developed to investigate functional interactions of blast *R* genes, *Pi-ta* with *Pi-b*, other minor blast resistance QTL, and yield related components with US long grain tropical japonica rice varieties Cybonnet (CYBT) and Saber (SB). CYBT is known to contain *Pi-ta* (avirulent on blast races, IB1, IB17, and IB49 and virulent on IE1K) and *Pi-km* (virulent on IB1, IB17, IB49, and IE1k) and SB has *Pi-b* (avirulent on IB1, IB49, IE1k and partial avirulent on IB49). The entire population was evaluated with *Pi-ta* and *Pi-b* using gene specific PCR, and with their differential blast isolates/races under greenhouse conditions. A subset of this population (243

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