

Focus	Generation of genome sequence diversity information for wild relatives of rice
PI	Nori Kurata Genetic Resource Center, National Institute of Genetics
Period	FY2014
Overview	<p>The NBRP rice resource project has been making progress on the issue of “Construction of rice resource foundation for harnessing the diversity of the genus <i>Oryza</i>”. In the program we have prepared about 1700 accessions of wild relatives of rice from 9 genome types and 23 species covering almost all of the wild species in the genus <i>Oryza</i>, originally collected from all over the world. Among them, we selected 280 accessions as a core collection and have investigated their various trait characters. We have accumulated genome information for an additional 350 wild AA genome accessions at about 10% genome sequence coverage. An international consortium for comparative genomics of rice is now performing genome-wide sequencing on wild diploid species such as those possessing AA, BB, CC, EE, FF and GG genomes. As part of that consortium, we, the National Institute of Genetics group, were assigned to construct CC genome sequences and have been making progress on doing so for one of the species.</p> <p>As part of the proposed program, we plan to construct precise pseudo-molecules for the remaining two CC genome species. In addition, we plan to read the sequences of about 300 representative accessions for all genome types at x10 depth and aiming to achieve more than 50% coverage of each genome. This high quality data would serve as an indicator for a molecular basis of genome diversity for each accession and species. This information will be released to researchers worldwide to form a foundation for diversity and evolutionary studies of <i>Oryza</i>. We believe that this information together with our biological resources will contribute to future progress in the research community.</p> <div data-bbox="456 1003 1214 1733" data-label="Image"> <p>The image is a composite of four panels illustrating rice diversity and genomics. The top-left panel shows a row of rice seeds of various colors (red, brown, black) next to a ruler. The middle-left panel shows a close-up of a rice panicle with green grains. The middle-right panel shows a whole rice plant in a blue pot. The bottom panel is a complex genomic map with multiple tracks of colored bars representing different genomic features or data points across a chromosome.</p> </div>
Progress	OryzaGenome