

The availability of high through-put sequencing technology has improved our ability to detect and characterize pathogens without *a priori* knowledge. However, the abundances of host and environmental nucleic acids can impact the success of accurately identifying low abundant viral nucleic acids. ViroCap is a sequence capture panel which consists of probes designed to enrich sequences representing viral species that infect vertebrates which sequence information is available. ViroCap was designed to capture sequences from viruses representing 190 genera, and has been previously tested on 32 viruses representing 19 genera that affect humans. Here, we further tested ViroCap against a panel of blinded cell culture amplified viruses and clinical/field samples containing another 26 viral species representing 19 genera and 12 families that affects livestock, wildlife and humans. All viral species were accurately identified and a few unexpected viruses were detected. Full or near full genomes were obtained for most tested viral species and enrichment was observed when compared with pre-captured material. These results indicate ViroCap is a useful tool for improving the sensitivity of NGS for identification and sequencing of a broad spectrum of viruses that affect vertebrates.

PO1027: Rice

Development of Herbicide Tolerant Basmati Rice Lines through Marker Assisted Backcross Breeding

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Pusa Basmati 1121 (PB1121) is the landmark Basmati rice variety developed at ICAR-IARI, New Delhi, earns foreign exchange of US\$ 3.41 billion annually. The decrease in water availability coupled with labour scarcity has necessitated the shift in rice cultivation from transplanted rice to direct-seeded rice (DSR). Weed management is the major constraint in DSR which has a direct impact on productivity. Therefore, there is a need to develop herbicide tolerant (HT) rice varieties. We used marker assisted backcross breeding (MABB) to transfer the mutant allele of Acetohydroxy acid synthase (*AHAS*) gene, which confers tolerance to imidazolinonones group of herbicide from donor parent Robin into the genetic background of an elite Basmati rice variety, PB1121. Foreground selection was carried out using gene linked SSR marker RM6844 and background selection using 112 SSR markers polymorphic between PB1121 and Robin. Phenotypic selection for agronomic, grain and cooking quality traits was carried out in each of the generations to accelerate the recovery of recurrent parent phenome. In BC₄F₄ generation, 12 near isogenic lines (NILs) with recurrent parent genome recovery ranging from 98.66 to 99.55% were isolated and evaluated under sprayed and unsprayed conditions. These NILs were either at par or superior to PB1121 under controlled conditions; and possessed no significant effect on yield, grain and cooking quality parameters under sprayed conditions. HT-PB1121 is expected to be the prime technology for rapid adoption of DSR in the Basmati growing areas.

PE1028: Other Plant Species

A Gene Expression Atlas of *Vellozia nivea*, a Desiccation-Tolerant Species from the Brazilian Campos Rupestres

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Velloziaceae are an angiosperm family that contains the most desiccation-tolerant species (approximately 200 out of 270 species). More than 80% of the *Velloziaceae* species occur in South America, where the greatest morphological diversity is also found. The genus *Vellozia* comprises both desiccation-tolerant and non-desiccation-tolerant species, offering an excellent model for studying the evolution of desiccation- and drought-tolerance traits on plant genomes. To date, only limited genomic or transcript sequences are available for *Velloziaceae* species. Here we present a *Vellozia nivea* gene expression atlas across different plant organs and tissues, including flower, developing seeds, root, leaf, stem and seedling. *Vellozia nivea* is a desiccation-tolerant species, endemic to the Brazilian *campos rupestres* (rupestrian grasslands) and highly adapted to their extreme conditions. A total of 180.67 Gb of raw data were generated, and of these, 152.79 Gb were subjected to downstream analysis after quality control (QC). *Vellozia nivea de novo* transcriptome assembly was performed with the Trinity bioinformatics tool, resulting in 684.615 contigs. After filtering contaminated sequence contigs from bacteria and fungi and removal of contigs with less than 10 sequence reads associated with the initial assembly, the transcriptome resulted in 195.512 remaining sequences. A GO enrichment analysis was performed on tissue-specific transcripts. The *Vellozia nivea* transcriptome should be a useful resource for genome annotation and gene function discovery studies.

PO1029: Other Plant Species

Gingerroot: A Novel DNA Transposon Encoding Integrase-Related Transposase in Plants and Animals

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Transposable elements represent the largest components of many eukaryotic genomes and different genomes harbor different combinations of elements. Here, we discovered a novel DNA transposon in the genome of the clubmoss *Selaginella lepidophylla*. Further searching for related sequences to the conserved DDE region uncovered the presence of this superfamily of elements in fish, coral, sea anemone, and other animal species. However, this element appears restricted to Bryophytes and Lycophytes in plants. This transposon, named *GingerRoot*, is associated with a 6 bp (base pair) target site duplication, and 100–150 bp terminal inverted repeats. Analysis of transposase sequences identified the DDE motif, a catalytic domain, which shows similarity to the integrase of *Gypsy*-like long terminal repeat retrotransposons, the most abundant component in plant genomes. A total of 77 intact and several hundred truncated copies of *GingerRoot* elements were identified in *S. lepidophylla*. Like *Gypsy* retrotransposons, *GingerRoots* show a lack of insertion preference near genes, which contrasts to the compact genome size of about 100Mb. Nevertheless, a considerable portion of *GingerRoot* elements was found to carry gene fragments, suggesting the capacity of duplicating gene sequences is unlikely attributed to the proximity to genes. Elements carrying gene fragments appear to be less methylated, more diverged, and more distal to genes than those without gene fragments, indicating they are preferentially retained in gene-poor regions. This study has identified a broadly dispersed, novel DNA transposon, and the first plant DNA transposon with an integrase-related transposase, suggesting the possibility of *de novo* formation of *Gypsy*-like elements in plants.

PE1030: Methods: Sequencing

"Seqoccin" : A Long Read Project to Find Optimal Technologic Combinations for Genome Assembly and Their Variability, Epigenetic Marks Detection and Metagenomic Analysis

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