Summary

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- A total of 133 field strains of *M. oryzae* have been isolated from three host plant species – rice, finger millet and foxtail millet – across fifteen different geographic regions in India.
- All the field strains were grouped based on molecular markers (transposable elements, AVR genes and mating type), phenotypic characteristics (colony morphologies, sporulation ability, cross-infectivity on different hosts) and their geographic location and host of origin.
- Fifteen representative field strains of blast fungus from aforementioned three hosts were sequenced for whole genome using Illumina NGS platform.
- Genome-wide SNPs in the fifteen genomes nicely correlated with their specificity towards host of origin, rather than the geographic locations.
- Lineage-specific genes, identified based on orthologous gene families, mostly constituted of those with distinct effector-like and/or virulence related functions.
- Analysis based on identification of homologs of 46 known blast protein effector genes showed the variation in terms of their presence/absence among different host-specific lineages.
- With an average of 59 BGCs per genome, we were able to predict a total of 4224 SM-producing BGCs from 68 *M. oryzae* genomes belonging to six different host-specific lineages. This suggests their potential in producing diverse, yet uncharacterized, SMs with likely roles in various biological processes.
- Similarity network analysis on all the BGCs led us to the identification of three lineage-specific BGCs. One of them, BGC-O1, which is specific to *Oryza* lineage, was found to be the only functional BGC. The other BGCs carry mutations and/or truncation in their core biosynthetic genes, leading to pseudogenization.
- BGC-O1 was found to be expressed specifically during pathogenesis, especially during host penetration and colonization by the blast fungus.
- BGC-O1 is located in the sub-telomeric region on the chromosome 2 of the reference strain 70-15 and translocated to a mini-chromosome in another strain FR13 of *M. oryzae*.

- The genomic regions covering the BGC-O1 and its flanking sequences were highly syntenic in strains from the *Oryza* lineage; whereas only the upstream flanking region of this locus was found conserved in all the other lineages.
- The closest ortholog of rPKS (MGG_08236), belonging to BGC-O1, was found in taxonomically distant fungal pathogen *Colletotrichum eremochloae*. Retention of BGC-O1 in only a certain species is most likely driven by the selection pressure from their respective hosts.