

Abstract

Understanding plant-pathogen interactions is crucial for effective management of diseases on crop plants. The blast fungal pathogen *Magnaporthe oryzae* poses a significant threat to global food security by infecting agro-economically important cereal crops worldwide. Although *M. oryzae* is a single species, subdivided into multiple host-specific genetic lineages, a new strain on a different host species can emerge and cause devastating outbreaks. Population studies pertaining to genetic composition, virulence variability and molecular signatures of *M. oryzae* would help understand the molecular mechanism underlying host specialization. Many studies thus far have focused on protein effector molecules at the plant-pathogen interface; however, the role of chemical effectors in pathogenesis and/or host specialization has hardly been explored. In the current study, 133 field strains of *M. oryzae* strains were isolated from infected rice, finger millet and foxtail millet host plants collected across fifteen different geographic locations of India. Based on the molecular and phenotypic characteristics, fifteen representative blast fungus strains were sequenced using the Illumina NGS platform. Genome-wide SNPs analysis and investigation of homologs of known blast effectors indicated that the genetic diversity in different host-specific strains was likely more associated with the host selection pressure rather than the geo-climatic conditions. We mined a total of 68 *M. oryzae* genomes, including the 15 Indian field isolates and publicly available genomes, belonging to six host-specific lineages, to identify biosynthetic gene clusters (BGCs), possibly producing chemical effectors (secondary metabolites - SMs) associated with host specificity. Interestingly, while most of the BGCs were present in all the *M. oryzae* lineages, one BGC (BGC-O1) was found specifically in the *Oryza* lineage. Importantly, the genes constituting the *Oryza* specific BGC-O1, which is present in the sub-telomeric region of chromosome 2, were expressed specifically during host penetration and colonization. We propose that this *Oryza* lineage-specific BGC is likely associated with a metabolite effector involved in specialization of *M. oryzae* to rice host. Our research findings highlight the need to explore and characterize more such chemical effectors involved in host-pathogen interactions, which in turn will shed light on the metabolic strategies used by the blast fungal pathogen to adapt to a new cereal host.