Comparative genome structure, secondary metabolite, and effector coding capacity across Cochliobolus pathogens.

ABSTRACT

The genomes of five Cochliobolus heterostrophus strains, two Cochliobolus sativus strains, three additional Cochliobolus species (Cochliobolus victoriae, Cochliobolus carbonum, Cochliobolus miyabeanus), and closely related Setosphaeria turcica were sequenced at the Joint Genome Institute (JGI). The datasets were used to identify SNPs between strains and species, unique genomic regions, core secondary metabolism genes, and small secreted protein (SSP) candidate effector encoding genes with a view towards pinpointing structural elements and gene content associated with specificity of these closely related fungi to different cereal hosts. Whole-genome alignment shows that three to five percent of each genome differs between strains of the same species, while a quarter of each genome differs between species. On average, SNP counts among field isolates of the same C. heterostrophus species are more than 25× higher than those between inbred lines and 50× lower than SNPs between Cochliobolus species. The suites of nonribosomal peptide synthetase (NRPS), polyketide synthase (PKS), and SSP-encoding genes are astoundingly diverse among species but remarkably conserved among isolates of the same species, whether inbred or field strains, except for defining examples that map to unique genomic regions. Functional analysis of several strain-unique PKSs and NRPSs reveal a strong correlation with a role in virulence.

Keyword: Cochliobols heterostrophus; Genome; Fungal; Peptide Synthases; Cochliobolus miyabeanus; Cochliobolus victoriea; Cochliobolus carbonum