

CB-05

Genomics of industrial filamentous fungi, *Aspergillus oryzae* and *Aspergillus awamori*

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Aspergillus oryzae has been widely used in Japanese fermentation industries, Japanese alcohol beverage, soy sauce and so on for longer than a thousand of years. High potential of secretory production of proteins has led *A. oryzae* to extensive use in modern biotechnology. Comparison of *A. oryzae* genome with those of other *Aspergillus* species of smaller genome size revealed existence of non-syntenic blocks (NSBs) specific to the *A. oryzae* genome. The NSBs possess the *A. oryzae*-specific genes, which are the genes expanded in the *A. oryzae* genome (extra homologs) and secondary metabolism genes. Transcriptional expression levels of the NSB-genes were significantly lower than those on syntenic blocks (SBs). The genes on NSBs and SBs were globally down- and up-regulated, respectively, at heat shock. In contrast, the genes on NSBs appeared globally up-regulated in solid-state cultivation (SSC), which is widely used in the Japanese fermentation industries. As the extra homologs include the genes encoding secretory hydrolytic enzymes, up-regulation of the NSB-genes might enhance degrading efficiency of raw materials. The expansion of metabolic pathway genes and production of metabolites by *A. oryzae* will also be discussed.

Aspergillus awamori is another industrial filamentous fungus, widely used for brewing Japanese traditional spirits, Awamori, in Okinawa prefecture. *A. awamori* is genetically very close to *Aspergillus niger* and close to *Aspergillus oryzae*. Like *A. niger*, *A. awamori* vigorously produces citric acid, lowering pH of the product. We have sequenced *A. awamori* NBRC 4314 (RIB 2604). Comparison between the genomes of *A. awamori* and *A. oryzae* showed higher diversity of genes located on the non-syntenic blocks of the *A. oryzae* genome. We are currently sequencing various strains of *A. awamori* by SOLiD. Analysis of the relationship between genetical and phenotypical differences among the strains should provide important information for gene function.

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Distribution of mutations distinguishing the most prevalent disease-causing *Candida albicans* genotype from other genotypes

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Candida albicans is a major opportunistic pathogen of humans. Previous work has demonstrated the existence of a general-purpose genotype (GPG; equivalent to clade 1 as defined by multi locus sequence typing data) that is more frequent than other genotypes as an agent of human disease and commensal colonization, may be more virulent and may differ from the remainder of the species in terms of reproductive strategies. We undertook a genomic screen, which indicated that a large number of mutations differentiate GPG strains from other strains and that such mutations are scattered throughout the genome. However GPG-specific mutations are non-synonymous more frequently than expected by chance, and are not randomly distributed across functional and structural gene categories. Our analysis has identified three categories of genes in which GPG-specific mutations are overrepresented, namely genes for which expression changes during the yeast-hyphal transition, genes for which expression changes as a result of exposure to antifungal agents and repeat-containing ORFs. Although we have no direct evidence that the individual polymorphisms identified confer selective advantages to GPG strains, the results support our contention that the high prevalence of GPG strains is not merely due to genetic drift but that GPG strains have reached a high prevalence because they possess a multitude of fitness-enhancing traits. They also indicate that the distribution of genes marked by GPG-specific mutations across functional and structural categories could identify physiological traits that are of particular importance to the success of GPG strains in their interactions with the human host.