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Genomics and Proteomics of *Helicobacter pylori* Korean Strain 51

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How can we stop the chain of H. pylori infection with conventional bacteriological methods? Vaccine development and chemotherapy does not appear to be practicable at this moment, and there are limited options available for the eradication of H. pylori. Are there virulent strains in H. pylori? In western countries, H. pylori strains have been divided into 2 types (type 1 or 2). Type 1 strains were isolated from patients with duodenal ulcer and is postulated to be more virulent and more inflammatory to mucosa. In contrast, in Far Eastern countries, there is no association between types and clinical entities. Genomic sequences of strain 26695 and J99 suggested that plasticity zone could be a marker of strain identification. Genomic sequence of strain 51 shows differences in genomic organization as well as variations in nucleotide sequence when compared with those of strain 26695 and J99. Micro- and macrodiversity of genome make strain classification difficult by in vitro DNA technology. Taxonomic principles for strain identification requires genomic sequence of at least 50-100 strains. With this genomic information, high through-put analyses of proteomics will throw the light on the classification for H. pylori strains.

S7-2

Genomics In The Study Of Phytopathogenic Fungus - Magnaporthe grisea

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Magnaporthe grisea, the causal agent of rice blast, is one of the most destructive plant pathogens in rice production. It penetrates the host cuticle directly by way of a specialized infection structure called an appressorium. Genes expressed during appressorium formation were identified by sequencing cDNA clones prepared from conidia forming appressorium. A total of 2325 ESTs corresponding to 1430 unique sequence sets were generated. Differential and subtractive hybridization were used to identify genes showing appressorium stage specific expression. A number of genes were selected as up-regulated. High density cDNA microarrays were employed to examine the expression profile of a large number of genes associated with appressorium formation. Microarrays containing 4582 cDNAs derived from cDNA libraries of the appressorium formation stage and the vegetative stage were used to identify a suite of genes that are differentially expressed during appressorium formation. A 112 kb BAC clone was sequenced and annotated. These results demonstrate that genomics approach is a powerful tool for studying the mechanism of infection process of plant pathogens.