

Complete Genome sequence of *Xanthomonas oryzae* pv. *oryzae*, the pathogen of bacterial blight of rice, and its application strategy

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We report here the complete genome sequence of *Xanthomonas oryzae* pv. *oryzae*, the pathogen of bacterial blight of rice. To determine the nucleotide sequence, whole genome shotgun sequencing was performed using Kxo85 (KACC 10331), the representative of Korean race I. The results showed that the bacterium has a unique genome structure as a pathogen. The total genome size of the strain was 4,941,439 bp, and the genome structure was a single circular chromosome. The number of predicted genes in the genome was 4,637 and an average G+C ratio was 63.7%. The bacterium has 54 tRNA. 245 genes were unique to Xoo genome in comparison with other two xanthomonads. Insertion sequence (IS) was more frequently found in the genome than the other two *Xanthomonas* genomes, which are characteristic features of Xoo genome. Avr genes, which are fundamental to the pathogenesis of the bacterium, were also found in the Xoo genome. Ten copies of *avr/pth* members were scattered randomly in the Xoo genome. The strain Kxo85 of Xoo did not carry any plasmids, while *VirB* operon was not found in the genome. The genome was very rich in genes for putative transposases homologs, accounting for approximately 4.62% of the total genome size. The whole genome sequences of Xoo will be a window in the molecular genetics of the bacterium and the molecular interaction with the host rice plant

The Rice 60K Whole Oligomeric DNA Microarray : Application To The Analysis of Abiotic Stresses In Rice

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Rice 60K Whole Oligomeric DNA Microarray (Rice 60K Microarray) representing the organism's entire genes was developed. We used Rice 60K Microarray to find genes which might play roles in protecting rice against abiotic stress conditions such as high salinity, drought, and cold. Experiments were repeated four times including a dye-swap to adjust the bias due to intrinsic intensity differences between Cy3 and Cy5. Significant spot analysis results in 25,222 spots. Hierarchical clustering was performed for these spots and this analysis revealed at least 4 specific groups: salt and drought specific, salt specific, drought specific, and cold specific groups. Gene expression or its modal changes are accompanied during these stress conditions. To test which transcription factors are involved we extracted 2 kb upstream regions of 45,632 genes from publicly available genome databases. *cis*-elements were analyzed for each abiotic stress specific genes. In addition, signaling pathway might be undergone as plants adjust to these stresses. We collected 4,489 pathway specific components from KEGG databases and tested which one is plausibly perturbed during these conditions. Our data using Rice 60K Microarray showed the massive analysis of gene expression at genome level is achievable with these microarrays.