

F318 A Cluster of Genes Involved in Arginine Biosynthesis from *Corynebacterium glutamicum*

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A cluster of arginine biosynthetic genes has been cloned and sequenced from fragments of *Corynebacterium glutamicum* DNA isolated by complementing a *Escherichia coli* mutants. Clones complementing defects in *argC*, *argJ*, *argB*, *argD*, *argF*, *argG*, and *argH* of *E. coli* were isolated. The gene order has been established as *argCJBDFGH* by linkage and sequencing analysis. Nucleotide sequences of 9.2-kb region allowed the identification of eight ORFs which showed significant homology with the *arg* genes of *Mycobacterium tuberculosis*. The *argR* has also been located in the upstream region of *argG*. Transcriptional analysis by Northern hybridization experiment reveal that three transcripts corresponding to *arg C-J*, to *argB-D-F-R*, and to *argG-H* were identified. To gain deeper insight into the regulation of arginine overexpression, we have cloned and characterized the genes involved in the arginine biosynthetic pathway of *C. glutamicum*.

F319 Molecular Cloning of the *hisB* and *hisC* Genes from *Corynebacterium glutamicum*

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The *hisB* and *hisC* genes, encoding for Imidazolglycerol-phosphate dehydratase and histidin-phosphate aminotransferase were isolated from *Corynebacterium glutamicum* gene library by complementation of an *Escherichia coli* histidin auxorophic mutants. The codinig region of *hisB* and *hisC* genes are 205 and 366 amino acids in length with a predicted size of about 23 and 40 kDa, respectively. Computer analysis also revealed that the amino acid sequence of the *hisB* and *hisC* gene had a high simlarity to *hisB* and *hisC* of *Mycobacterium leprae* and *Mycobacterium tuberculosis* about 61% and 59%, respectively.