

Diversity and Evolution of Fimbriae Gene Clusters

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Motivation

Fimbriae mediated adhesion to biotic surfaces is the first step in initiation of many bacterial infections. Therefore, the study of fimbriae has many biomedical applications. However, one major limitation to this goal is the extensive diversity of fimbriae. Though, a large number of studies have been conducted to understand the fimbriae, majority of these studies were done using only a handful type of fimbriae, mainly from the bacteria strains belonging to the family Enterobacteriaceae. The genes encoding for fimbriae have been found in diverse taxonomic groups. Fimbrial structures have tremendous diversity in morphology, function and receptor specificity. Thus, in order to understand the fimbriae and to use them for medical applications, there is a strong need to characterize systematically the diversity in fimbriae.

Results

Genes encoding for fimbriae are found as clusters on bacterial genome. We studied the diversity in fimbriae in terms of content and order of genes involved in fimbrial assembly. Using various computational tools, we have identified, characterized and annotated 2573 fimbrial genes in genomic and plasmid DNA sequences of 1471 bacterial strains. Of these 972 genes were ushers, 1246 genes were chaperones, 355 adhesins/subunits. Considering length as only criterion for distinction between subunits and adhesins we found 175 adhesins and 180 subunits. The fimbrial genes were found primarily in strains belonging to Alpha, Beta, Gamma and Delta subdivisions of phylum proteobacteria and phylum Deinococcus-Thermus. Bacterial strains belonging to the Gamma and Beta subdivisions contained maximum number of fimbrial genes. Many strains from these two taxonomic groups contain multiple fimbrial gene-clusters.

More than 90% of the bacterial strains containing fimbrial genes interact with human or other eukaryotic hosts. All the organisms containing fimbrial genes were mesophiles. The collected data was stored in a series of MySQL tables. A web interface, for searching the information in the database was developed using PERL/CGI and Joomla Content Management System. The database can be searched using text based queries.

Keywords: Fimbriae gene cluster, Fimbriae database, Fimbriae diversity