

Title (en)
CONSTRUCTION OF A COMPARATIVE DATABASE AND IDENTIFICATION OF VIRULENCE FACTORS THROUGH COMPARISON OF
POLYMORPHIC REGIONS IN CLINICAL ISOLATES OF INFECTIOUS ORGANISMS

Title (de)
KONSTRUKTION EINER VERGLEICHENDEN DATENBANK UND IDENTIFIZIERUNG VON VIRULENZFAKTOREN DURCH VERGLEICHEN
POLYMORPHER BEREICHE IN KLINISCHEN ISOLATEN INFEKTIÖSER ORGANISMEN

Title (fr)
CONSTRUCTION D'UNE BASE DE DONNÉES COMPARATIVE ET IDENTIFICATION DE FACTEURS DE VIRULENCE PAR COMPARAISON
DES RÉGIONS POLYMORPHES D'ISOLATS CLINIQUES D'ORGANISMES INFECTIEUX

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Application
EP 04744233 A 20040712

Priority
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Abstract (en)
[origin: WO2006008575A2] The present invention is directed to novel nucleotide sequences to be used for diagnosis, identification of the strain, typing of the strain and giving orientation to its potential degree of virulence, infectivity and/or latency for all infectious diseases more particularly tuberculosis. The present invention also includes method for the identification and selection of polymorphisms associated with the virulence' and /or infectivity in infectious diseases more particularly in tuberculosis by a comparative genomic analysis of the sequences of different clinical isolates/ strains of infectious organisms. The regions of polymorphisms, can also act as potential drug targets and vaccine targets. More particularly, the invention also relates to identifying virulence factors of M. tuberculosis strains and other infectious organisms to be included in a diagnostic DNA chip allowing identification of the strain, typing of the strain and finally giving orientation to its potential degree of virulence. Although the present invention has been illustrated with specific reference to the polymorphic region in the Mycobacterium tuberculosis, the said invention is not to be understood and construed as being limited to Tuberculosis but is applicable to all infectious diseases.

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