

Complete genome sequence based evolutionary analysis of bacterial two-component systems

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Bacteria sense their environmental condition by two-component systems, and alter their metabolic behavior to adapt new environment. Two-component systems consist of histidine kinase (HK) and response regulator (RR) components. The HK autophosphorylates a conserved histidine residue in response to an environmental stimulus. The phosphate is transferred to a conserved aspartic acid residue in the RR, and then transcription of appropriate genes is activated.

Behalf of complete genome sequence projects of living organisms, whole genome based evolutionary analysis, which can give more global and integrative insight than single gene based evolution analysis, became possible.^{1,2)} In this study, two-component systems of 79 bacteria was collected and evolutionary relationship between two-component systems was evaluated.

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