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致病菌III型分泌系统分子伴侣序列保守性分析及新伴侣的预测

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很多革兰氏阴性致病菌使用III型分泌系统将毒力因子直接注射到宿主细胞质中，其中某些效应蛋白（即毒素）需要专一的III型分泌系统分子伴侣才能有效分泌。以往的研究认为：这些分子伴侣间几乎没有相同的氨基酸序列，也很少同源。但是，我们用生物信息学手段对45个III型分泌系统分子伴侣的氨基酸序列进行分析，发现这些分子伴侣之间存在着广泛的远缘同源关系，广泛存在的已知的2个III型分泌系统分子伴侣模体和新发现的3个可能的III型分泌系统分子伴侣模体组合揭示了序列中存在广泛保守的位点，并基于此分析预测出27个新的可能的III型分泌系统分子伴侣。

Conservative analysis of type III secretion system chaperone protein sequence and prediction of new chaperone

Abstract: Many Gram negative pathogen utilize type III secretion system (TTSS) to inject toxins into the cytosol of eukaryotic cell. Some effector proteins (toxins) are secreted by their cognate chaperones through the TTSS. Previous studies indicated that there is little amino-acid sequence similarity among these chaperones. However, by bioinformatics methods, we find that many chaperones have more than one homologous chaperones, and two known motifs and three newly identified motifs exist widely in these chaperones which indicate that there must exist some conservative sites in TTSS chaperones protein sequences. Base on above, we predicted 27 new possible TTSS chaperones.

关键词

III型分泌系统(type III secretion system); 分子伴侣(chaperone); 毒力因子(toxin)