

Sequence analysis of spider silk proteins by using bioinformatics: finding relation with evolution and mechanical properties

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Spiders produce silks, which have outstanding mechanical properties, to construct webs for catching prey in nature. Previous researches have been investigated that mechanical properties of spider silks have been diversified while spiders have been diverged to various species. Because main components of spider silks are proteins, it is valuable to find a correlation between silk sequences with mechanical properties and evolutionary steps. However, silk sequences were mostly regarded as a hard information to be analyzed due to its imperfectness and repetitiveness. Therefore, in the present work, bioinformatical tools were newly employed to systemically analyze group of silk sequences from different spider species. Filtered motifs resulted from this analysis were drawn interest because every time new types of spiders had been emerged, novel motifs with three amino acids were appeared. The result could be further used for identification of phylogenic relations among spiders and prediction of mechanical properties of different silks. These serial processes can be a platform technology and applicable for analyzing other group of protein sequences which are thought to be evolutionarily-and-functionally-related.