

An efficient bioinformatical analysis of tandem repeats in spider silk protein sequences: relations with evolution and mechanical properties

정두엽, 양윤정, 차형준<sup>†</sup>

포항공과대학교

(hjcha@postech.ac.kr<sup>†</sup>)

Spiders produce silks which have outstanding mechanical strength and elasticity. Previous researches have shown that mechanical properties of spider silks have been diverged while spiders have been diverged to various species. Because main components of spider silks are proteins, it is valuable to find a correlation among silk sequences, evolutions, and mechanical properties. However, silk sequences were regarded as a hard information to be analyzed because they are too imperfect and repetitive. To systemically analyze tandem repeats of spider silk sequences, in the present work, several bioinformatical methods were newly applied. The novel idea of this research is to discover sequence motifs harboring evolutionary evidences and extract the most conserved sequence pattern of silk proteins from 10 different spiders. From these results, phylogenetic tree for spider species was constructed and covering portions of sequence motifs were calculated to check the relation with mechanical properties. This research may state that spider species and their silk proteins are co-evolved and can be a platform technology for analyzing other group of protein sequences thought to be evolutionarily-and-functionally-related.