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Bioinformatics application in identification of cross-reactive allergenic risk of novel food proteins

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When evaluating the potential cross reactivity of a novel protein with known allergens, amino acid sequences are often compared using bioinformatic approaches. A high quality curated database containing allergen sequences is a fundamental requirement for executing sequence comparisons. Existing sequence comparisons have been based on sequence similarity, identical short-mer amino acid matches, motif identification, machine-learning models, and 3-D structure prediction. Tools based on these approaches are publically available and have been investigated for their sensitivity and selectivity. Although fraught with poor specificity and other technical issues, the FAO/WHO/Codex Alimentarius method is the standard for regulatory submissions to government agencies. This approach involves searching for >35% identity over 80 amino acids or more by local alignment algorithms such as FASTA or BLAST. However, the literature has clearly demonstrated that use of amino acid similarity in combination with a statistical measure of power, like E-values, can be equally sensitive but with greater specificity (fewer false-positives). A one-to-one FASA comparison with a biologically relevant E-value as a criterion is such an approach, and this method additionally avoids some of the technical shortfalls of an amino acid identity-based algorithm. In the future, modern genome sequencing techniques offer the promise of increasingly powerful bioinformatic analysis of food proteins for allergenic risk.

Biography

Ping Song has completed his PhD in 1994 from Texas Tech University. He is a global regulatory team leader for seeds/traits in Dow Agro Sciences LLC, a R&D driven agricultural company. He has published two book chapters and more than 25 papers in peer-reviewed journals.

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