

PP-361 [Apitherapy]

Proteomic study of the Bioactive molecules of bee venom of *Apis cerana* and *Apis mellifera* and its health implications

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The word “proteome” represents the complete protein pool of an organism encoded by the genome. Proteomics helps in understanding the alteration in protein expression during different stages of life cycle or under stress condition. It helps in understanding the structure and function of different proteins as well as protein-protein interactions. Bee venom contains many proteins such as melittin (major protein), enzymes such as phospholipaseA2, hyaluronidase and other various proteins that has many medicinal efficacies. These proteins vary in their concentration and composition between different *Apis* species and with respect to season, so it is analyzed with the help of proteomics. Amino acid variation in the proteins can also make profound changes in the action of proteins. This is done by Two-Dimensional Gel Electrophoresis technique. Proteins are first separated based on their individual charges in 1D. The gel is then turned 90 degrees from its initial position to separate proteins based on the difference in their size. This separation occurs in 2 dimensions hence the name 2D. The spots obtained in 2D electrophoresis are excised and further subjected to mass spectrometric analysis of each protein present in the mixture. Once the sequence of the proteins is obtained, it can be used for drug development by screening for suitable targets using online tools. It can also be used for finding out the genetic background of the proteins; the switching mechanism of genes involved which will be helpful in rDNA studies.