Sixth European Conference of Apidology

EurBee 6

Murcia (Spain) 9 - 11 September 2014
sulphite-reducing *Clostridium* spores and *Salmonella*. Total aerobic mesophilic counts ranged from $6.8 \times 10^3 \pm 8.8 \times 10$ to $3.0 \times 10^4 \pm 4.8 \times 10^2$ CFU g$^{-1}$; psychrotrophic counts ranged from $1.0 \times 10^2$ to $3.5 \times 10^2 \pm 7.5 \times 10$ CFU g$^{-1}$; while the values for yeasts and molds were between $1.6 \times 10 \pm 0.5 \times 10^2$ and $2.0 \times 10^4 \pm 4.1 \times 10^2$ CFU g$^{-1}$. All the samples were absent regarding sulphite-reducing *Clostridium* spores and *Salmonella*. Microbial contamination of this product can occur through primary sources such as flower pollen, nectar, environment and bees or secondary sources, during collection and processing by beekeepers. According to the literature available, the bacterial and yeasts and molds counts identified were usual for that product, but it is important to consider that these microorganisms can cause spoilage and diminish shelf life, so quality control programs should be implemented. Lastly, the absent of sulphite-reducing *Clostridium* spores and *Salmonella* was important to ensure the consumer health.  

Acknowledgments: FAPESP.

Proteom based comparison of venom extraction methods for *Bombus* sp.

Nezahat Pınar Baıkan, Duygu Özçel Dencıralp, Ahmet Murat Aytekin  
Hacettepe University, Faculty of Science, Department of Biology, Beytepe, Ankara, Turkey  
E-mail: pinarbaıkan@gmail.com

The aim of the study is to compare the protein profiles of *Bombus* (*Bombus*) *terrestris* venom by using two different extraction methods; disruption of venom sac and manual milking. Protein concentrations were determined from each group, followed by two-dimensional gel electrophoresis and peptide mass fingerprinting analysis by using matrix-assisted laser desorption ionization/ time of flight mass spectrometry.

A total of 111 protein spots were observed on each gel in PDQuest analysis. These spots were then subjected to student’s t-test both in PDQuest and SPSS. According to our results, there were no statistically significant difference in protein spots between the two extraction groups. The proteins that are identified from *B. terrestris* venom obtained by using two different methods are: Pseudohemocyanin-1 (Fragment), L-2-hydroxyglutarate dehydrogenase mitochondrial, actin-2 muscle-specific, arginine kinase, S-methyl-5'-thioadenosine phosphorylase, phospholipase D LySinTor-alphaClaI (Fragment), Serine-threonine-protein phosphatase PP1-beta, venom protease, venom allergen 5,02 (fragment) and potassium channel blocker alpha-KTx 26.1.

Results of the present study suggest that protein profiles of venom samples obtained from disruption of venom sac and manual milking are similar. Importantly, the results show the potential of disrupting the venom sac and that it can also be favoured as a venom extraction method for bumble bees.