

Poster A-2

Gland expression profile derived from ESTs



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Short Abstract: A pattern of expression from different types of glands, generated from ESTs retrieved from public databases has provided an overview onto a variety of gland expression trials amongst several animal groups. This profile is currently being compared to that obtained from venom glands of Brazilian scorpions and snakes.

Long Abstract:

A pattern of expression from different types of glands, generated from ESTs retrieved from public databases has provided an overview onto a variety of gland expression trials amongst several animal groups. A total of 26 different clone libraries accounting for 1,026 up to 35,390 ESTs were analyzed. Seventeen different species, from the fruit fly (*Drosophila melanogaster*) to the common chicken (*Gallus gallus*) were responsible for the input data analyzed. In all, 148,798 ESTs have been acquired and aligned against the KOG database providing a total of 78,223 hits (53% of annotation percentage in average). KOG database coverage stood from 1,8% up to 50,7% of the KOG set, from the 'lone star tick' salivary gland (*Amblyomma americanum*) to the urochordate adult digestive gland (*Ciona intestinalis*), respectively. Moreover, sampling frequencies have been converted as "per 5 thousand" ESTs and sampling values under 1 ESTs/5K have not been considered, which dictated a gland expression profile. Differentially expressed genes were detected by statistical analysis of the R parameter (Steckel et al., 2000). The genes differential expressed in pair to pair comparisons ranged between only 60 (1%) up to just 300 (4%) out of the 4852 KOGs, while most of the genes are evenly expressed. In conclusion, implementation has allowed draw a profile of the transcripts that are specific to each gland. This profile is currently being compared to that obtained by analyzes of ESTs from venom glands of Brazilian scorpions *Tityus serrulatus* and *Mesobuthus gibbosus*, and of the snake *Bothrops insularis*.