

Bioinformatic analysis of transcriptional regulation of immune responsive genes in *Anopheles gambiae*. Martínez Barnetche J¹; Hernández Romano J¹; La Madrid H¹; Solano M¹; Salgado H²; Rodríguez MH¹.

Instituto Nacional de Salud Pública, Cuernavaca, Mexico¹.

Centro de Ciencias Genómicas. Universidad Nacional Autónoma de México. Cuernavaca, México².

The *Anopheles gambiae* and *Drosophila melanogaster* genomes in conjunction with published data of transcriptional profiling in response to immune challenge in both species was used to identify relevant DNA sequence patterns and motifs associated with transcriptional regulation (DeGregorio et al, 2001; www.fruitfly.org/expression/immunity; Provided by G. Dimopoulos). For both species, we selected a group of up-regulated and unmodified genes as control. Up to 2.5 kb upstream of the putative transcription initiation site was of each gene was retrieved using EnsMart at <http://www.ensembl.org>. Search for patterns and motifs was based on 2 general strategies: 1) Search for known motifs corresponding to response elements of transcription factors known to be involved in insect immune regulation such as REL/NFκB, GATA and STAT families by means of published positional weight matrices. 2) *ab initio* search of statistically overrepresented motifs with different tools publicly available in the web. Given that transcriptional regulation is tightly related to chromatin structure, nucleosome forming potential was analyzed with RECON (Levitsky, et al. 2001) and correlated on a positional basis with found motifs by either two strategies. So far, distinctive findings in putative 5' regions of immune challenge up-regulated genes are:

- Enrichment of putative NFκB binding sites, highlighting the central role of REL/NFκB TF in the regulation of the immune response in insects
- In contrast to what is found in *Drosophila*, only few *An. gambiae* upstream regions contained NFκB/GATA paired motifs, suggesting different TF interactions.
- Significant enrichment of the ATAA tetrads compared to unmodified and whole genome 5' regions in *Anopheles* and *Drosophila*.
- Significantly higher overall nucleosomal formation potential. Moreover, the positions of ATAA tetrad correlate with regions of high nucleosomal potential in *Anopheles* and *Drosophila*. This correlation may be related to the delimitation of transcriptional territories.

Further research is focused on the experimental validation of such findings, extending the analysis with other algorithms and to include in the analysis the down-regulated gene sets.

imbarnet@insp.mx