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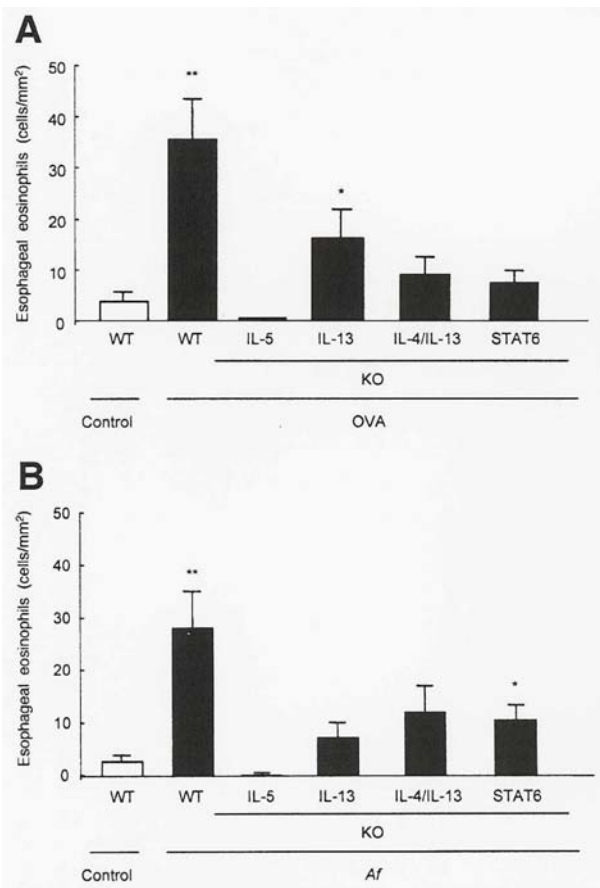
Description of Research:

Dr. Mishra has demonstrated the feasibility of using DNA chips to examine mRNA transcript profiles in esophageal tissue of mouse model of eosinophilic esophagitis (EE). He has tested the hypothesis that microarray analysis of RNA transcripts expressed in the esophagus of experimental EE will provide critical insight into disease characteristics including diagnosis, pathogenesis, and treatment. His analysis indicated a total of 211 genes that were upregulated and 44 downregulated genes by more than 2 fold. This study showed that esophageal tissue from mouse model of EE would have a unique expression profile compared with healthy states. His studies will provide fundamental information concerning the pathogenesis of EE.

Collaborations:

Dr. Mishra has used the **Bioinformatics, Microarray, and Integrative Morphology Cores** in collaboration with Drs. Aronow, Hogan, Rothenberg, and Witte examining the RNA transcripts that are responsible for eosinophilic esophagitis.

Representative Figure:



Esophageal eosinophil levels in Th2 cytokine-deficient mice. Epicutaneously sensitized mice were challenged with (A) control saline or OVA or (B) diluent control or *A. fumigatus*. Mice were wild-type (WT) control or deficient (KO) in IL-5, IL-13, IL-4/IL-13, or STAT6 and analyzed after 29 and 50 days from the initial antigen sensitization for *A. fumigatus* and OVA, respectively. * $P < .05$, ** $P < .01$ compared with wild-type saline group. Data are expressed as mean \pm SEM; $n = 8$ mice per condition. Fig. 4 from *Gastroenterology*, 2005; 129:985-994.