

Marc E. Rothenberg, MD, PhD

Professor and Director of Allergy and Immunology
Department of Pediatrics; Division of Allergy and Immunology

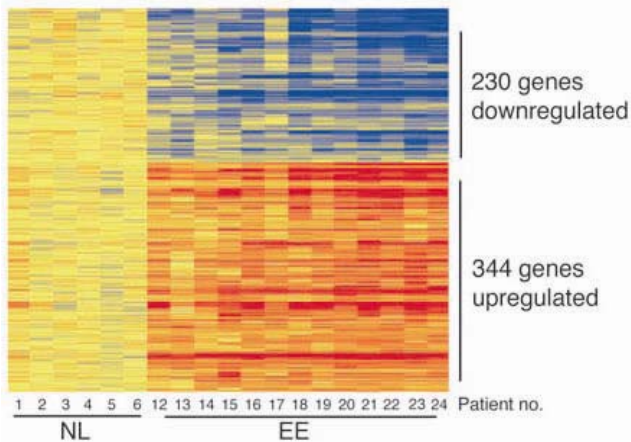
Description of Research:

Dr. Rothenberg's investigates the mechanisms of allergic responses especially in mucosal tissues with a primary focus on the gastrointestinal tract. The goal of the research is to develop the best treatment strategy for allergic disorders (especially eosinophilic gastrointestinal disorders (EGIDs)) based on mechanism-driven research. He uses multiple approaches involving analysis of the cellular and molecular processes *in vitro* and *in vivo*, often utilizing genetically engineered mice. In addition, several novel models of antigen-driven allergic gastrointestinal disorders have been developed and these provide the experimental framework for identifying mechanisms of disease. Furthermore, translational research involving several aspects of patient-based research including innovative drug intervention clinical trials, genome wide expression profiling of intestinal tissue, and genetic analysis using candidate gene approaches are underway. For example, early results with humanized anti-IL-5 therapy in patients with EGIDS have revealed a promising role for this new biological modifier, prompting an ongoing placebo-controlled clinical trial.

Collaborations:

He has collaborated with Dr. Aronow using the **Microarray and Bioinformatics Cores** to define genes that constitute an "allergy genome" and new pathways involved in disease pathogenesis. He also used the **Integrative Morphology Core** in collaboration with Dr. Cohen to study gastrointestinal inflammation, and with Drs. Hogan, Mishra, Morrow, and Wang to study the epidemiology of EGIDs and other allergic disorders.

Representative Figure:



Microarray analysis of the transcripts expressed in esophageal biopsies. RNA from each patient was subjected to chip analysis using Affymetrix Human Genome U133 Plus 2.0 GeneChips. The normal (NL) group is composed of 6 individuals numbers (1–6), the chronic esophagitis (CE) group is represented by 5 patients (numbers 7–11), and 13 patients (numbers 12–24) are in the eosinophilic esophagitis (EE) group. The 574 genes differentially expressed ($P < 0.01$) in the EE group compared with normal healthy patients have been ordered (standard correlation); upregulated genes are represented in red and downregulated genes in blue. The magnitude of the gene changes is proportional to the darkness of the color. Each column represents a separate individual and each line a gene. Fig. 1A from *J Clin Invest*, 2006; 116:536-547.