116 Genome-Wide Association Studies of Asthma Indicate Opposite Immunopathogenesis Direction From Autoimmune Diseases

Xingnan Li, *Wake Forest University School of Medicine*
Elizabeth Ampleford, *Wake Forest University School of Medicine*
Timothy Howard, *Wake Forest University School of Medicine*
Dara Torgerson, *University of Chicago*
Huashi Li, *Wake Forest University School of Medicine*
Wendy Moore, *Wake Forest University School of Medicine*
William Busse, *University of Wisconsin*
Mario Castro, *Washington University School of Medicine*
Serpil Erzurum, *The Lerner Research Institute*
Anne Fitzpatrick, *Emory University*

Only first 10 authors above; see publication for full author list.

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range of physiologic and pathological processes including clearance of helminthic infections, and allergy. They are closely associated with recruiting and amplifying T helper 2 (Th2) lymphocyte response in contrast to Th1-asscoiated CAMs. Wide donor-to-donor variability of human primary monocytes and their limited life span in vitro is a current impediment to investigating human AAM biology and their contribution to enhancing Th2-mediated pathologic inflammation found in asthmatic lungs.

Methods: Using the human promonocytic cell line, THP1, we have successfully established a THP1-derived and committed CAM and AAM populations demonstrating typical macrophage-oriented morphological characteristics.

Results: Quantitative PCR and ELISA demonstrated that THP1-AAM cell model express classic pathogen neutralizing dectin receptors such as scavenger type mannose receptor (MRC1) and Th2-associated signature chemokines including CCL13, 17, 18 and 22, and are tolerant to TLR4 challenge by LPS treatment in contrast to THP1-CAM which expressed an LPS enhanced expression of pro-inflammatory mediators such as TNF-a, CXCL10 and -11. Furthermore, THP1-AAM cell model expressed 50- to 100-fold lower expression IFN-alpha 4, IFN-beta, and IFN-lambda1 compared to THP1-CAM. Quantitative PCR array revealed that a select group of interferon regulatory factors (IRFs), antiviral genes such as Mx1, and interferon stimulated genes such as ISG15 are down-regulated only in THP-1 AAM cell model upon differentiation or LPS treatment emphasizing its classic infection tolerant phenotype. In addition, IRF4 was found to be up-regulated only in the THP1-AAM model which may point towards its critical role in orchestrating the macrophage lineage commitment towards an alternatively activated phenotype as well as governing its unique cytokine and chemokines expression profile.

Conclusions: Compared to the donor variability of primary human monocytes, establishing THP1-AAM and CAM cell models will enable a more rapid and efficient investigation of a spectrum of molecular mechanisms governing innate, classic, and alternative phenotypes in macrophage populations and their role in pathologic processes, in particular allergic inflammation of the upper airways.

114

A Highly Sensitive and Specific Universal Mirna Profiling Method

Jia-Wang Wang, PhD,[1] Kunyu Li, BS,[1] Richard F. Lockey, MD,[2] Subhra Mohapatra, PhD,[3] and Shyam Mohapatra, PhD[4]. *[1]Internal Medicine, University of South Florida, Tampa, FL; [2]Division of Allergy & Immunology, University of South Florida and James A. Haley Veterans' Hospital, Tampa, FL; [3]Nanomedicine Research Center and Division of Translational Medicine, Departments of Molecular Medicine and Internal Medicine, University of South Florida and James V Haley Veterans' Hospital, Tampa, FL; [4]USF Nanomedicine Research Center, University of South Florida College of Medicine & VA Hospital, Tampa, FL.*

Background: miRNAs can be used as robust biomarkers for diagnosis, staging, prognosis and the response to therapy in various diseases. Although a wide spectrum of miRNA detection techniques have been developed, none can accurately and sensitively perform genome-wide high-throughput miRNA profiling (Chen C, Ridzon DA, Broomer AJ, Zhou Z, Lee DH, Nguyen JT, Barbisin M, Xu NL, et al 2005. Real-time quantification of microRNAs by stem-loop RT-PCR. *Nucleic Acids Res.* 33:e179). This problem stems from that miRNAs are only ∼22 bases, and multiple species of nucleic acids that contain the mature miRNA sequences are present in the total RNA samples that are usually used for miRNA detection.

Methods: A novel RT-qPCR miRNA assay (UQmiR, universally quantitating miRNA) was developed to overcome the difficulty. This assay requires only one RT reaction and one universal set of multiple hydrolysis probes to detect all miRNAs, using one universal RT primer, a common reverse primer, and individual miRNA-specific forward primers. A computer program (MSPPD, miRNA-specific primer and probe designer) was developed for the assay.

Results: The UQmiR has the advantages, but not the disadvantages, of the 2 mostly used miRNA assays. It has the specificity of hydrolysis probe assay and the universal detection of SYBR Green assay. This assay is more sensitive and specific than the commercially available hydrolysis probe assay and SYBR Green assay. Using this method, we have successfully detected 91 out of 96 miRNAs in 0.8 mL of plasma for each miRNA.

Conclusions: This approach affords a highly specific, sensitive, economical and convenient system to profile the expression of all known miRNAs.

115

Caspase-4 Plays a Role in the Activation of the Cryopyrin/NLRP3 Inflammasome

Ruan Cox, Jr,[1] Salman Aljubran, MD,[2] Richard F. Lockey, MD,[3] and Narasaiah Kolliputi, PhD,[1,4]. *[1]Internal Medicine, and; [2]Allergy and Immunology, University of South Florida, Tampa, FL; [3]Division of Allergy & Immunology, University of South Florida and James A. Haley Veterans' Hospital, Tampa, FL; [4]Division of Allergy and Immunology.*

Background: The inflammasome is a multi-protein complex which regulates the activation of caspase-1. This activation results in the cleavage and secretion of the IL-1β super family cytokines, IL-1β, IL-18, and IL-33. NLR family-pyrin domain containing- 3 (NLRP3) is a nucleotide binding domain-leucine rich repeat (NLR) family protein responsible for sensitization and oligomerization of the NLRP3 inflammasome complex. Although various damage and pathogen associated patterns have been implicated as stimuli, the exact mechanism of activation has yet to be elucidated. Capase-5, an inflammatory caspase with similar homology to caspase-1, is a key molecule activation of the NLRP1 inflammasome. Caspase-4, an evolutionary duplicate in humans to murine caspase 12 along with caspase 5, is important in IL-1β processing; its involvement with the NLRP3 inflammasome is unknown. We therefore investigated whether caspase-4 plays a role in the activation of the NLRP3 inflammasome.

Methods: Inflammasomes in THP-1 macrophages were activated using Nigericin (10 μg/mL), a bacterial pore causing toxin and NLRP3 inflammasome activator, in the presence or absence of various concentrations (0.1 μM, 1 μM, and 10 μM) of caspase-4 inhibitor, Z-YVAD-FMK. We analyzed the inflammasome activation, caspase-1 cleavage, and IL-1β release by western blot and ELISA analysis.

Results: Our results indicate that inhibition of caspase-4 leads to a dose dependant decrease in IL-1β secretion. In addition, our results show that caspase-4 contributes to IL-1β and caspase-1 cleavage, both of which are hall marks of inflammasome activation.

Conclusions: These findings suggest that caspase-4 is important to the activation of the NLRP3 inflammasome. In modulating the inflammasome, caspase-4 appears to be a druggable target for treatment of chronic inflammatory pulmonary conditions such as allergy and asthma.

116

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Xingnan Li, PhD, MS,[1] Elizabeth Ampleford, PhD,[1] Timothy Howard, PhD,[1] Dara Torgerson, PhD,[2] Huashi Li, MS,[1] Wendy Moore, MD,[1] William Busse, MD,[3] Mario Castro, MD, MPH,[4] Serpil Erzurum, MD,[5] Anne Fitzpatrick, PhD,[6] Benjamin Gaston, MD,[7] Elliot Israel, MD,[8] Nizar Jarjour, MD,[9] W. Gerald Teague, MD,[7] Sally Wenzel, MD,[10] Gregory Hawkins, PhD,[1] Carole Ober, PhD,[2] Dan Nicolae, PhD,[2] Eugene R. Bleecker, MD,[1] and Deborah Meyers, PhD[1]. *[1]Center for Genomics and Personalized Medicine Research, Wake Forest University School of Medicine, Winston Salem, NC; [2]Department of Human Genetics, University of Chicago, Chicago, IL; [3]Department of Medicine, University of Wisconsin, Madison, WI; [4]Division of Pulmonary and Critical Care Medicine,*

Washington University School of Medicine, St. Louis, MO; [5]The Lerner Research Institute, Cleveland, OH; [6]Department of Pediatrics, Emory University School of Medicine, Atlanta, GA; [7]Department of Pediatrics, University of Virginia Health Systems, Charlottesville, VA; [8]Brigham & Women's Hospital, Harvard University, Boston, MA; [9]Departments of Medicine and Public Health Sciences, University of Wisconsin Hospitals and Clinics, Madison, WI; [10]Medicine, University of Pittsburgh, Pittsburgh, PA.

Background: Genome-wide association studies (GWAS) of asthma and asthma-related traits, including our previous TENOR study[1], have consistently identified *ORMDL3-GSDMB, IL33, IL1RL1-IL18R1, RAD50-IL13, TSLP-WDR36,* and *HLA-DR/DQ* regions.[2]

Methods: In this study, GWAS of asthma was performed in non-Hispanic white population from STAMPEED study (813 cases and 1564 controls). Our GWAS results were compared with the published GWAS of asthma and autoimmune diseases (AD).

Results: Multiple SNPs in *TNFAIP3* interacting protein 1 (*TNIP1*) on chromosome 5q32-q33.1 were associated with asthma in STAMPEED: rs1422673 ($P = 3.44 \times 10^{-7}$) and rs10036748 ($P = 1.41 \times 10^{-6}$). rs1422673 was weakly associated with asthma in the published GABRIEL study ($P = 0.018$ for meta-analysis)[2] but not in the TENOR study ($P = 0.18$ but same trend).[1] *TNIP1* may interact with *TNFAIP3* and inhibit *TNFα*-induced *NFκB* inflammation pathway. Joint analyses were performed on 6 SNPs in *GSDMB* (rs2872507), *IL33* (rs3939286), *IL1RL1* (rs13431828), *IL13* (rs20541), *TSLP* (rs1837253), and *HLA-DRA* (rs2395185) in STAMPEED and TENOR populations, but only limited variance can be explained (percentage of deviance = 1.5–1.9%; the area under the receiver operating characteristic curve (AUC) = 0.58–0.59). Minor allele T of rs20541 in *IL13* is the risk allele for asthma but the protective allele for psoriasis. Minor allele A of rs2872507 in *GSDMB* is the protective allele for asthma but the risk allele for rheumatoid arthritis, Crohn's disease and ulcerative colitis. T allele of rs10036748 in *TNIP1* is the minor protective allele for asthma, but the minor or major risk allele for systemic lupus erythematosus in non-Hispanic white or Chinese population, respectively.

Conclusions: Our study provides genetic evidence that asthma and AD have opposite immunopathogenesis directions.

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117

Allergy is an Epithelial Barrier Disease

Risto Renkonen, MD. *Transplantation Laboratory & Infection Biology Research Program, University of Helsinki & Helsinki University Central Hospital, Helsinki, Finland.*

Background: The purpose of this study is to explore the role of epithelium in acute allergic diseases.

Methods: Birch pollen allergic patients and healthy control subjects were recruited. In vivo nasal pollen challenges were performed and nasal epithelial specimens were collected. A systems biology approach using a wealth of methods, including several microscopy techniques (light, confocal, immuno transmission electron [TEM]), transcriptomics (chips and massive parallel sequencing), mass spectrometry, immunohistology, in silico analyses were used.

Results: Already 1 minute after the birch pollen perturbation Bet v 1 was found both on cell surfaces as well as within villae, in cytoplasm, in intracellular vesicles, and also in nuclei of epithelial cells in allergic patients, but not in the healthy individuals. Anti-Bet v 1 stainings in conjunctival biopsies supported a very rapid traffic through the epithelium in allergic patients, but not in healthy subjects. A striking specificity is observed when birch pollen allergic subjects were also challenged with timothy grass pollen and no entry of this pollen allergen Phl p 1 into epithelial cells was detected. While the specific transport mechanism for birch pollen remains unsolved the first hints of the role of caveolae in this have been obtained. In the double immunoTEM analyses caveolin 2, but not caveolin 1 or 3, was present on the conjunctival epithelial surface in the same clusters as Bet v 1. Transcriptomics indicated that the health epithelium displayed a strong immune response against pollen allergens while this response was absent in the epithelium of allergic patients.

Conclusions: Active transport of allergens through the epithelium might be incorporated to the pathogenesis of allergy. It is possible that the healthy epithelium displays a strong immune response against pollen allergens and thus escapes from becoming allergic. If allergy turns out to be, at least in part, a result of epithelial hyposensitivity, it could have major consequences in the strategies of prevention and treatment of these diseases. Towards this end, a national allergy program has been launched in Finland, which changes the basic idea of trying to avoid allergens to the concept of natural exposure and tolerance.

MECHANISMS OF ASTHMA

118

EGCG Downregulates Mucin Gene Expression Through the Mapk Signaling Pathway in Asthma

Yong-Dae Kim, Sang Baik Ye, Chang Hoon Bae, and Si-Youn Song. *Yeungnam University College of Medicine, Daegu, South Korea.*

Background: Mucus plays an important role in protecting human airway from external environments. Highly glycosylated mucin proteins are the major components of mucus, responsible for its viscoelastic properties. Excessive mucus is major manifestation of inflammatory respiratory diseases. Epigallocatechin-3-gallate (EGCG) is major component of green tea extract and known to provide numerous functions, such as anti-oxidant effect, anti-tumor effect, anti-diabetic effect and anti-inflammatory effect. But precise mechanisms are still unclear.

Methods: Using NCI-H292 human airway epithelial cells, we measured phorbol 12-myrisate 13-acetate (PMA)-induced MUC5B mRNA expression with the treatment of indicated doses of EGCG. We also measured PMA-induced MUC5B protein secretion with the treatment of indicated doses of EGCG using ELISA technique in NCI-H292 cells. To test the brief signaling pathways, we performed activation study of mitogen-activated protein kinase (MAPK) pathways, which is well-known to signaling the PMA-induced mucin gene over-expression, using Western blot technique in NCI-H292 cells. And then we performed in vivo study using ovalbumin-induced asthmatic mice model and control mice group. In ovalbumin-sensitized asthmatic mice model, EGCG was treated with indicated dose. And then ovalbumin was challenged and we sacrificed the mice. Tissue samples from the mice were stained with PAS (periodic acid-Schiff) for mucin distribution in bronchioles of each group. Immunocytochemical stain was performed using MUC5B specific antibody. MUC5B mRNA and protein level was measured using extracted lung tissues.

Results: PMA-induced MUC5B mRNA and protein level was significantly decreased after treatment of EGCG at all doses in NCI-H292 cells. PMA-induced phosphorylation of p38 MAPK was significantly decreased after treatment of EGCG at all doses in NCI-H292 cells. Results from in vivo studies showed that decreased bronchiolar mucin distribution in the group of pretreated with EGCG in asthmatic mice. MUC5B mRNA and protein levels were significantly decreased in the group of pretreated with EGCG in asthmatic mice.

Conclusions: PMA-induced MUC5B mRNA and protein over-expression in both NCI-H292 cells and extracted tissues from asthmatic mice were significantly decreased with the treatment of EGCG. We demonstrated that