miR-107 Is Associated with House Dust Mite Sensitization in Asthmatics

M. Yang¹, U. Srivastava¹, A. Kho², J. C. Celedon³, A. Tiwari⁴, A. Wang⁵, S. T. Weiss⁴, M. Mcgeachie⁴, K. Tantisira¹; ¹Pediatrics, University of California San Diego, San Diego, CA, United States, ²Computational Health Informatics, Boston Children's Hospital, Boston, MA, United States, ³Pediatrics, University of Pittsburgh, Pittsburgh, PA, United States, ⁴Channing Division of Network Medicine, Brigham and Women hospital, Boston, MA, United States, ⁵Channing Division of Network Medicine, Brigham and Women's Hospital, Boston, MA, United States.

Corresponding author's email: msyangmd@gmail.com

RATIONALE MicroRNAs are important in regulating allergic inflammation. However, it is not known whether microRNAs also play a role in sensitization to certain allergens in asthmatics. The purpose of this study was to identify microRNAs involved in house dust mite (HDM) sensitization and to examine their effects on asthma and asthma-related outcomes. METHODS Serum samples from 1,126 children with asthma who participated in the Genetics of Asthma in Costa Rica Study (GACRS) were profiled for 304 microRNAs. Subjects were divided into HDM-positive and HDMnegative groups according to the results of skin prick tests to HDM. We identified microRNAs that were differentially expressed (DE) between the two groups using the DESeg2 package in R (version 4.1.2). Gene ontology (GO) enrichment analysis for target genes of the DE microRNAs was performed using the enrichr package. Asthma-related outcomes such as lung function and asthma control were also compared between the two groups. Validation was performed in the Childhood Asthma Management Program (CAMP), in which expression data of 258 microRNAs of 491 children were available. We replicated DE miRNAs and GO enrichment analyses in this cohort. RESULTS There were 906 (80.5%) and 220 (19.5%) subjects in the GACRS HDM-positive and HDM-negative groups. A total of 17 microRNAs were DE (p > 0.05) between the two groups. Among them, miR-642a-3p, let-7c-5p, and miR-107 showed the strongest association with HDM sensitization. The 17 microRNAs were enriched for the cadherin binding pathway. HDM sensitization was associated with decreased percent predicted forced expiratory volume in 1 sec (FEV₁) (98.2 % in HDM-positive vs. 102.0 % in HDM-negative groups, p = 0.002) and percent predicted FEV₁/forced vital capacity (FVC) ratio (94.1 % in HDM-positive vs. 96.7 % in HDMnegative groups, p < 0.001), as well as increased bronchodilator responsiveness (6.2 % in HDMpositive vs. 3.2 % in HDM-negative groups, p < 0.001). Moreover, HDM sensitization was associated with higher peripheral blood eosinophil count (621.7 cells/µl in HDM-positive vs. 258.9 cells/µl in HDM-negative groups, p < 0.001) and serum total lgE level (862.9 IU/ml in HDM-positive vs. 211.9 IU/ml in HDM-negative groups, p < 0.001). In CAMP, there were 39 DE microRNAs and increased expression of miR-107 was replicated in this cohort. These 39 microRNAs were also enriched for the cadherin binding pathway. CONCLUSION In children with asthma, miR-107 is associated with HDM sensitization, a predictor of worse asthma outcomes.

This abstract is funded by: NIH(R01 HL162570 and R01 HL 127332)

Am J Respir Crit Care Med 2022;205:A5711 Internet address: www.atsjournals.org