Effects of rs3744262, rs3744263 and DNA Methylation on Symptoms in Participants with Allergic Rhinitis During Grass Pollen Exposure in the Environmental Exposure Unit (EEU)

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Abstract

• Allergic rhinitis is a symptomatic allergic nasal disorder involving upper-airway inflammation, rhinorrhea, sneezing, congestion, and aggravation of comborbid asthma. Allergic rhinitis affects 10% - 25% of the population worldwide [1].
• While some genetic associations have been established, genomic DNA sequence changes to the genetic code [4]. DNA methylation occurs when DNA environment interactions. Epigenetics refers to genomic modifications, such as DNA methylation at position 1 vs. A) TNSS and B) TSSS (Figure 5).

Conclusions
In this study we found that both DNA methylation and SNPs in EFNB3 affect allergic rhinitis symptoms. However, the effects appear to occur at different time points, baseline and post-pollen-exposure, respectively. DNA methylation was associated with nasal airflow after allergen exposure. Effects of genotype on DNA methylation were noted, but did not occur at CGP sites that were associated with symptoms, suggesting that in the case of this gene, genotype and epigenetics exert independent effects.

References

Figure 1: A) Addition of a methyl group to cytosine. B) In general, unmethylated DNA and acetylated histones promote looseness of the DNA strand, allowing transcription to take place.

Figure 2: Location of SNP and CpG sites in the ephrin-B3 gene. Objective: To characterize the effects of genotype and epigenetics on allergic rhinitis symptoms and nasal air flow upon allergen exposure.

Figure 3: A) Diagram, and B) photograph of the Environmental Exposure Unit (EEU), showing the placement of the pollen distribution system directional fans, Rotorod® pollen samplers, ventilation and participant seating.

Figure 4: A) Effect of rs3744262 and B) rs3744263 on DNA methylation at position 1 vs. A) TNSS and B) TSSS. C) Spearman correlation of DNA methylation at position 2 vs. PNIF at baseline (p<0.05) and p<0.01, respectively) (Figure 5A and B). Increased DNA methylation at position 2 was associated with PNIF at 27H (Figure 5C).

Figure 5: Spearman correlations of DNA methylation at position 1 vs. A) TNSS and B) TSSS. C) Spearman correlation of DNA methylation at position 2 vs. PNIF.

Figure 6: A) Effect of rs3744262 and B) rs3744263 on DNA methylation at baseline (p<0.05 and p<0.01, respectively) (Figure 5A and B). Increased DNA methylation at position 2 was associated with PNIF at 27H (Figure 5C).