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Late Breaking Abstract - Seasonal variation in nasal epithelium gene expression

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Introduction: Environmental seasonal changes such as exposures to allergens, temperature, and humidity may impact gene expression in various human tissues. We aim to investigate seasonal gene expression variation in the upper airways, as this is the barrier tissue exposed to these environmental factors.

Methods: Differential gene expression analysis was performed between samples collected by nasal brushing in spring-summer (01.03 to 31.08, 201 samples) and autumn-winter (the rest of the year, 217 samples) from asthmatic and healthy participants included in the ATLANTIS study. Mann-Whitney U test of Gene Set Variation Analysis (GSVA) scores was used to assess seasonal gene signatures among different groups of participants. One-tailed Gene Set Enrichment Analysis (GSEA) was used to replicate the results in an independent cohort (PIAMA).

Results: We identified 949 higher and 1069 lower expressed genes in the spring-summer compared to autumn-winter ($FDR < 0.05$). GSVA scores of season-associated genes showed similar changes in participants with and without asthma or allergy, suggesting that seasonal gene expression variation is independent of these factors. Season-associated genes were significantly enriched in the PIAMA cohort (GSEA p-value = 3.95×10^{-40} and 5.81×10^{-32} for higher and lower expressed genes, respectively). Finally, when comparing patients with asthma to healthy controls, including season as a confounding variable in the model significantly increased the number of differentially expressed genes from 126 to 264, $FDR < 0.05$.

Conclusions: Seasonal changes can contribute to variability in upper airway gene expression, and season-adjusted analysis should be considered to reveal asthma-associated expression changes.