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The pollen microbiome at the interface of air pollution and allergic sensitization: Genomic and NOx-responsive traits of *Pantoea agglomerans*

Inhalt

Pollinosis is a significant public health burden, with its rising prevalence linked to environmental factors like traffic-related air pollution (e.g. Nitrogen Oxides (NOx)) and climate change. The ability of pollen allergens to induce allergic sensitization depends on the co-delivery of non-allergenic adjuvants like bacterial lipopolysaccharides (LPS) and virulence factors, that promote Th2 polarization over allergy-protective Th1 responses. However, the genetic basis of this process is unknown. While NOx itself acts as an adjuvant by enhancing inflammation, it remains unclear whether frequent NOx exposure additionally enhances the adjuvant activity of pollen-associated bacteria by altering microbial traits related to LPS and virulence. We performed genomic characterization of *P. agglomerans* 11_6 isolated from *Artemisia vulgaris* pollen. Genome analysis detected several virulence factors, incl. proteases, T6SS effectors and hemolysin that might contribute to allergic sensitization. Except for two T6SS effectors and three LPS/EPS biosynthesis genes, virulence factors are highly conserved among *P. agglomerans* from different habitats. Transcriptome analysis of NOx-treated *P. agglomerans* 11_6 showed induction of RpoE-mediated envelope stress response pathways and altered expression of LPS, EPS and biofilm genes. This work provides a first basis for a One Health perspective on the link between air pollution, pollen microbiomes and allergic sensitization in urban environments.

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Junior Scientist Status

Yes, I am a Junior Scientist.

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