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[Previous Issue](#) | [Next Issue](#)

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Abstracts

Pages: 23-423 | First Published: 15 November 2021

[First Page](#) | [Full text](#) | [PDF](#) | [Request permissions](#)

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Abstract

Pages: 424-582 | First Published: 15 November 2021

[First Page](#) | [Full text](#) | [PDF](#) | [Request permissions](#)

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Abstracts

Pages: 583-637 | First Published: 15 November 2021

[First Page](#) | [Full text](#) | [PDF](#) | [Request permissions](#)

ABSTRACTS LB TPS

 [Free Access](#)

Abstracts

Pages: 638-661 | First Published: 15 November 2021

[First Page](#) | [Full text](#) | [PDF](#) | [Request permissions](#)

AUTHOR INDEX

 [Free Access](#)

Author Index

Pages: 662-693 | First Published: 15 November 2021

[First Page](#) | [Full text](#) | [PDF](#) | [Request permissions](#)



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875 | Environmental DNA analyses reveal links between abundance and composition of airborne grass pollen and population scale respiratory health.

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Background: Grass (Poaceae) pollen is the most important outdoor aeroallergen, exacerbating a range of respiratory conditions, including allergic asthma and rhinitis. Understanding the relationships between respiratory diseases and airborne grass pollen with view to improving forecasting has broad public health and socioeconomic relevance. Yet, the relative contributions of the >11,000 (worldwide) grass species to respiratory health outcomes have been unresolved, as grass pollen cannot be readily discriminated to species level using standard microscopy. However, emerging opportunities focusing on environmental DNA analyses, combined with spatio-temporally resolved epidemiological data offer novel population level insights into linkages between taxonomically resolved pollen data and disease.

Method: We used novel environmental DNA (eDNA) sampling and combinations of quantitative PCR (qPCR) and metabarcoding, to measure the composition and relative abundances of airborne pollen from common grass species, during two grass pollen seasons (2016 and 2017), across the UK. Using a series of generalised additive models (GAMs), we explore the relationship between the incidences of species level airborne pollen and severe asthma exacerbations and prescribing rates of drugs for respiratory allergies.

Results: We quantitatively demonstrate discrete spatiotemporal patterns in airborne grass pollen assemblages. Our results indicate that a subset of grass species may have disproportionate influence on these population-scale respiratory health responses during peak grass pollen concentrations.

Conclusion: The work demonstrates the potential for sensitive and detailed biomonitoring of harmful aeroallergens in order to investigate and mitigate their impacts on human health.

716 | Betula: tree with stable pollen season promoting pollen-food syndrome

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Background: Betula is a tree species in the Eastern Europe, which is a key factor of seasonal allergy. The latest data suggest that birch pollen sensitization promotes cross-reactivity to related food allergens. The aim of our study was to analyse Betula pollen season over the decade and sensitization to its pollen in Ukraine.

Method: Pollen collection from 2009 to 2020 used volumetric methods employing a Burkard trap placed at a height of 25 meters above the ground on the roof of a Vinnitsa Medical University, Ukraine. Samples taken from February until November were analyzed by mean of three horizontal transects in years 2009-2011 and by mean of twelve vertical transects at a bi-hourly mode in years 2012-2019 under the light microscope with x400 magnification. Trends for changing of season parameters were calculated using the excel program. Sensitization was assessed by 8016 ALEX tests performed in different regions of Ukraine in 2017-2019 in patients from 1 to 78 years old.

Results: All tree species analyzed including Corylus, Alnus, Carpinus, Fraxinus, Quercus, but except Betula demonstrated expressed tendency to early season start and early seen peak and variability of other indices including either shortened or prolonged pollen season, and changing pollen index with the most variability seen for early-flowering Alnus and Corylus. However, only Betula demonstrated tendency to later start and all other indices like peak day, peak value, pollen index were stable over the study period. Just a little tendency to season shortage was observed. Analysis of sensitization to Betula allergens was not so surprising. Despite it was recorded in all regions of Ukraine, the highest rates were seen in the Western and Northern regions of our country, which are located in forest zone. Up to 62 % of people with Betula sensitization in the Forest zone were also sensitive to the Mal d allergens expressing pollen-food syndrome.

Conclusion: Despite it is widely reported that climate change affects plant pollination all over the world; it does not affects much Betula specie, namely, in Ukraine. Its season looks very stable and unchanged over the last decades. The highest sensitisation rates to Betula pollen are seen in Forest zone with up to 62% of patients sensitive to apple allergens.

718 | Symptoms year round: up to 40 % of pollinosis' sufferers in Ukraine are sensitive to allergens of all pollen groups

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Background: Pollen forecast is important tool for control of seasonal allergy symptoms. It is considered that pollen data can be interesting to up to 30% of European population sensitive to pollen and molds. In practice, people use pollen forecast just at the time when they experience the symptoms. However, among those can be a group of patients, polysensitized to different outdoor airborne allergens.

These people experience the symptoms throughout all vegetation season and are potential pollen data users during entire year.

The main tree groups of outdoor airborne allergens include tree, grass and weed pollen. The aim of our study was to establish how many seasonal allergy sufferers are sensitive to the pollen of every group and are potential users of pollen forecast during all pollen season.

Method: To check the polysensitization of Ukrainian population we used data of 1076 Alex tests performed in Ukraine in years 2017–2019 for children and adults aged from 1 to 78 years. We calculated number of individuals, sensitized to all pollen groups then.

Results: Study showed, that 415 or 38,6 % of all tested individuals were polysensitized to the pollen of tree, grass and weeds at the same time. This makes this group of people potentially experiencing pollinosis' symptoms during entire pollen season.

What is more, such individuals, sensitive to all pollen groups, were seen among children of 4, 5 (1 person for each), 7, 8 (2 persons of each), 10 (1 person), 15 (2 patients), 16 (1 person) and 17 (1 patient) years old.

Conclusion: Medical doctor' control and Allergen-specific immunotherapy can be essential for people, suffering from pollinosis' during entire pollen season. Pollen data provided for these individuals also may help to reduce the severity of seasonal allergy symptoms.

17 | The comparative analysis of molecular profile of patients with allergic diseases in different regions of Ukraine

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Background: The prevalence of allergic diseases is increasing worldwide every year. The causes include ecological and climate changes, regional features of lifestyle and nutrition, migration of population. The conducting of molecular allergic diagnostics and assessment of molecular profile of allergic patients provide the opportunity for personalized approach to specific allergen immunotherapy.

The **aim** was to investigate the features of molecular profile of patients with allergic diseases in West Ukraine and to compare them with prevalence of specific IgE by ALEX in whole Ukraine.

Method: An investigation group included 263 patients with allergic pathology (West Ukraine) aged 25,2±9,5; 52,0% females and 48,0% males. The data of component examination of 1500 patients were analyzed. The investigation groups were comparable with age and gender. The specific IgE investigation by ALEX were performed.

Results: The increased level of tIgE were detected in 63,4 % residents of West Ukraine; 68,7 % - whole Ukraine. The patients with polysensitization were (62,5 % / 65,4 %) respectively. The most common sources of inhalation allergens in West Ukraine were cereals, house dust mites, spring trees, and, respectively, protein groups – Expansin, NPC 2, PR-10. Among components in West Ukraine in comparison with whole Ukraine Phl p1 (63,65 % / 40,3 %), Lol

p1 (60,1% / 40,4 %), Der p1 (42,15% / 47,43 %) were prevailed. In whole Ukraine the most common allergens were weeds: Amb a1 (9,85%/44,97%); Amb a4 (4,5%/14%); trees – Bet v1 (30,25% / 43,6%); cat Fel d1 (27,8%/50,2%).

Conclusion: Allergen "leaders" in West Ukraine were grasses (Phl p1, Lol p1), HDM (Der p1), in whole Ukraine – weeds (Amb a1, Amb a4), trees (Bet v1), cats (Fel d1).

545 | Mast cells are locally activated and express functional MRGPRX2 in biopsies from symptomatic eosinophilic gastritis and duodenitis patients

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Background: Eosinophilic gastritis (EG) and/or duodenitis (EoD) are associated with the pathologic accumulation and activation of eosinophils (Eos) and mast cells (MCs) in the stomach and/or duodenum. The MC-specific neuropeptide receptor, MRGPRX2 has been shown to mediate inflammation and pain through IgE-independent mechanisms of MC activation. MRGPRX2-mediated MC activation has been implicated in multiple gastrointestinal (GI) diseases, including irritable bowel syndrome and inflammatory bowel disease. However, the role of MRGPRX2-mediated MC activation has not been explored as a potential driver of symptoms and inflammation in EG/EoD.

Method: Gastric and duodenal biopsies were obtained from symptomatic EG/EoD patients meeting pre-defined symptom severity and histologic criteria as assessed by a validated symptom questionnaire and asymptomatic, non-diseased subjects. Flow cytometry and bulk RNA-sequencing were used to phenotype MCs and Eos in GI tissue biopsies. Levels of inflammatory mediators were measured after incubating whole GI tissue biopsies ex vivo to assess local MC, eosinophil, and MRGPRX2 activation.

Results: Eos and MCs in gastric and duodenal biopsies obtained from patients with EG/EoD showed significantly elevated expression of activation markers compared to gastroduodenal Eos and MCs in control subjects (Figure 1). GI tissue mast cells from EG/EoD patients also displayed increased surface expression of MRGPRX2, but only nominally elevated IgE (Figure 1). Transcriptomic profiling of sorted EG/EoD MCs further demonstrated global MC activation. Consistent with local activation of MCs and Eos, supernatants from ex vivo cultured GI biopsies from EG/EoD patients contained increased levels of MC- and Eos-specific mediators and inflammatory cytokines compared to control GI biopsies, including IL-5, CCL11, and CCL26. Ex vivo stimulation with known MRGPRX2 ligands significantly induced further MC activation from GI biopsies of EG/EoD patients. Moreover, supernatants from human MCs activated with