(93.94%), with 100% specificity. Among food allergens, highest sensitivity was seen in peanut (54.55%), with a specificity of 80.65%.

Consistency analysis for the two systems showed that kappa values for the three inhalants were between 0.727~0.876, with the highest value seen in cat dander as 0.876. They were all better than food allergens which in general fell into < 0.400. Spearman's correlation analysis showed the best correlation was seen in peanut and cat dander, with correlation coefficient as 0.942 and 0.927 respectively. For concordance and discordance analysis, the allergens which showed  $\pm$  1 class difference were Der pteronussinus 91.60%, Der farinae 81.25%, cat dander 98.00%, milk 83.58%, shrimp 59.72% and peanut 76.56%.

Conclusion: The current study shows that the two systems demonstrate good consistency. Compared with ImmunoCAP system, BioIC System is easier to use and has a lower demand for operator training. And greatly reduce the set up and running cost and at the same time, which makes the system particularly suitable for allergy screening in primary care hospitals in China.

## TP1190 | Does specific IgE to grass pollen allergens/total IgE ratio better reflect the presence of clinically relevant allergy than specific IgE itself?

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Background: We investigated whether specific IgE to grass pollen allergens/total serum IgE ratio better reflects the presence of clinically relevant allergy in sensitized patients than specific IgE to grass pollen allergens itself.

Method: Our study group comprised 34 patients with allergic rhinoconjunctivitis and sensitization to grass pollen. All subjects were examined for total serum IgE (BN II ©, Siemens) and specific IgE to timothy allergenic components PhI p 1 and PhI p 5 by using ImmunoCAP ISAC © (Thermo Scientific). The subjects recorded symptoms of allergy and medication use by mobile application AllergyMonitor© during peak grass pollen season 2018 (May to July). Finally, medians of Rhinoconjunctivitis Total Symptom Score (RTSS) and Average Combined Score (ACS) for every subject and statistical evaluation by using chi-square test were calculated. We aimed to reject the null hypothesis stating that the measured laboratory values do not distinguish between clinically insignificant (RTSS ≤ 1; ACS ≤ 0.583 (for RTSS = 1 and Rescue Medication Score = 1)) and significant grass pollen allergy (RTSS > 1; ACS > 0.583).

Results: 30 enrolled subjects were assessed as they completed the records on more than 50% days in peak grass pollen season. Their median of specific IgE PhI p 1 was 8.07 ISU, the median of specific

IgE PhI p 5 was 0 ISU, the median of RTSS was 2, the median of ACS was 0.58. While using cut-off 0.9 ISU for specific IgE PhI p 1 and/or PhI p 5, the null hypothesis could not be rejected both for RTSS (P = 0.45), and for ACS (P = 0.22). However, while using cut-off 0.05 for the ratio of specific IgE PhI p 1/total IgE and/or specific IgE PhI p 5/total IgE, the null hypothesis was rejected for RTSS (P = 0.03), but it could not be rejected for ACS (P = 0.3).

Conclusion: The ratio of specific IgE to main allergenic components of timothy pollen to total serum IgE seems to have better capability of recognizing the presence of relevant grass pollen allergy than specific IgE itself. Possibly, future enlargement of our study group might bring stronger evidence for this assumption.

## TP1191 | Cross-reactive carbohydrate determinant (CCD) inhibition test can help identify false positive for plant allergen-SIgE caused by CCD

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Background: Pollen allergens are important inhaled allergens and can cause respiratory allergic diseases, especially seasonal allergic rhinitis and asthma. Many pollen allergen and seed have the glycoprotein epitope, the specific IgE (sIgE) tests are often affected by cross-reactive carbohydrate determinant (CCD), cause false-positive reactions. This study analyzed the sensitization of pollen allergens in south China and discussed the effect of CCD inhibitor on the results of sIgE test of pollen allergens. Thus, the objective of this study was to investigate the level and feature of serological IgE cross-reactivity between grass pollen and seed in a cohort of respiratory allergic patients in Southern China.

Method: Two hundred and thirteen patients, with a doctor's diagnosis of allergic rhinitis or asthma, IgE towards at least two common inhaled allergens were recruited. Serum samples were analyzed for IgE against tree mix (willow/poplar/elm Tree), common ragweed, mugwort, humulus scandens, peanut, soy, and cross-reactive carbohydrate determinants (CCD) and specific IgE-binding inhibition experiments were performed.

Results: Among the patients sensitized to multiple allergens, 83 patients (39.0%) were plant allergen sensitization (slgE positive for any of the above six allergens was defined as plant allergen sensitization, PAS), and 57.8% of PAS patients were positive to CCD-slgE. PAS subjects were more often sensitized to CCD, known to be cross-reactive between grass and seeds.

CCD inhibited binding to all pollen and seed allergen by 73% to 100% (Table 1). The highest inhibition rate was obtained for Humulus scandens, followed by mugwort and peanut (both 85.2%), common

	CCD pre-inhibited n (%)	CCD inhibited n (%)	Turned rate(%)
Mugwort	27 (81.8)	4 (12.1)	85.2
Common ragweed	27 (81.8)	5 (15.1)	81.5
Tree mix	26 (78.8)	7 (21.2)	73.0
Soy	25 (75.8)	5 (15.2)	80.0
Peanut	27 (81.8)	4 (12.1)	85.2
Humulus scandens	15 (45.5)	0 (0.0)	100.0

ragweed (81.5%), soy(80.0%) and tree mix (73.0%). It was surprised to find that all sIgE against to pollen and seeds from 23 PAS patients were turned to negative after CCD inhibition.

Conclusion: CCD was positive in the serum of most plant allergenslgE positive patients in South China. More than 73% plant allergenslgE were eliminated into negative after CCD inhibition experiment, suggesting majority the plant allergic patients in southern China, particularly the slgE against peanut, soybean and pollen allergens, were false-positive caused by the CCD interference. CCD inhibition test should be used in clinical diagnosis, which can help to avoid misdiagnosis of plant allergens.

## TP1192 | Identification of unique grass species peptides, in a thirteen grass species aqueous extract sample by LC-MS/MS

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Background: LC-MS/MS is a powerful tool used in proteomics for the identification of proteins by comparing known characteristic peptides against a database. Grass main allergen proteins can have amino acid sequences which are 89% similar and thus provide similar peptides on tryptic digestion. Not all grass main allergens have been thoroughly sequenced or characterised in databases, which makes specific identification only by database searches impossible. Data and methodology is presented for the selection of characteristic peptides to identify thirteen grass species in an aqueous extract for grass, including those with limited or no database sequences.

Method: Method 1, individual and mixed grass species aqueous extract samples were prepared with a standardised tryptic digestion. The resulting complex peptide maps were screened against an in-house grass species specific database created from SwissProt. Database hits were then screened manually for false positives and individuality, to identify unique grass species peptides.

Method 2, Samples of thirteen grass species aqueous extracts were prepared with a standardised tryptic digestion. The resulting complex peptide maps were screened manually against the identified unique peptides in method one to identify unique peptides across

the thirteen grass species. These were then used to confirm the presence of grass species in blinded samples containing up to thirteen different grass species.

Results: Method 1, multiple unique peptides for grass species were identified for seven of the thirteen grass species (Holcus lanatus, Poa pratensis, Secale cereal, Festuca pratensis, Lolium perenne, Dactylis glomerata and Phleum pratense) via database and manual screening. The six grass species for which unique peptides were not identified (Cynosurus cristatus, Alopecurus pratensis, Arrhenatherum elatius, Anthoxanthum odoratum, Bromus inermis and Agrostis capillaris) are not sufficiently characterised in databases.

Method 2, multiple unique peptides for grass species were identified for the remaining six species (Cynosurus cristatus, Alopecurus pratensis, Arrhenatherum elatius, Anthoxanthum odoratum, Bromus inermis and Agrostis capillaris) not identified above. Thirteen grass species were identified using the unique peptides in blinded samples.

**Conclusion:** In depth screening of peptide maps by LC-MS/MS can be used to identify thirteen grass species in a complex mix via unique peptides.

## TP1193 | Characterization of a panel of profilin allergens for a structure-based IgE-epitope mapping

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Background: Panallergens frequently cause respiratory allergy and oral allergy syndrome. Profilins are important panallergens because of their highly conserved structure and ubiquitous presence in allergy sources. Therefore, determination of the structure and biophysical characterization are important tasks to complement IgE-binding studies and enable structure based epitope prediction. In this project six recombinantly produced profilins will be used for structural characterization and experimental determination of cross-reactivity between important respiratory and food allergens. The examined profilins are the food allergen Cuc m 2 (melon – Cucumis melo) and Cit s 2 (orange – Citrus sinensis), the pollen allergen Ole e 2 (olive tree – Olea europaea), Fra e 2 from