against influenza in the state of immune response in children with atopic BA.

Object Studied immune status of 39 children with moderate persistent BA in children from 7 to 14 years, which annually for three years were vaccinated influenza subunit vaccine.

Methods Compared the levels of serum markers of activation of apoptosis and immune cells before and one month after vaccination. Results. After the vaccination was demonstrated in the tendency to increase of level of IFNγ and IL12 in the serum. Also demonstrated increased in 1.3 times sCD25 (p < 0.05), in 1.6 times IL8 (p < 0.001), reduction in 1.5 times IL4 (p < 0.001), in 1.3 times TNFα (p < 0.05). In vaccinated children was revealed a tendency to increase sCD25 and the reduction of sCD30, sCD95 (p < 0.05), with the all of the listed indicators were significantly rejected from the reference levels. Reliable dynamics of the content of eotaxin, soluble ligands markers of apoptosis sFASL, TRAIL (Apo-2L), the enzyme Caspase-1/ICE and protein Annexin V have been identified.

Conclusions The data show a pronounced inflammatory process in children with atopic bronchial asthma. At the same time, the observed dynamics of the studied indicators can be interpreted as evidence of an absence of negative impact of vaccination on the various links of the immune response in children with atopic bronchial asthma, including on the processes of activation and apoptosis.

PO-1006 RECIPIENTS WITH IN UTERO INDUCTION OF TOLERANCE UP-REGULATED MHC CLASS I IN THE ENGRAFTED DONOR SKIN

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Background and aims The alterations in MHC class I expression play a crucial step in immune evasion of cancer or virus-infected cells. This study aimed to examine whether tolerized grafts modified MHC class I expression.

Methods FVB/N mice were rendered tolerant of C57BL/6 alloantigens by in utero transplantation of C57BL/6 marrows. Postnatally, engrafted donor skins and leukocytes were examined for their MHC expression by quantitative real-time PCR and flow cytometry.

Results In this murine tolerance model established by in utero marrow transplantation, engrafted donor skins up-regulated their MHC class I related gene transcripts after short-term (1~2 weeks) or long-term (>1 month) engraftment. This biological phenomenon was simultaneously associated with up-regulation of TAP1 gene transcripts, suggesting an important role of TAP1 in the regulation of MHC class I pathway. Notably, the surface MHC class I molecules of H-2Kβ in engrafted donor leukocytes consistently showed over-expression.

Conclusions Induction of allograft tolerance involved biological modifications of donor transplants. The increased expression of MHC class I within engrafted donor skins of tolerant mice might be used as the tolerance biomarkers for identifying a state of graft tolerance, and paved the way to advancing our insights into the mechanisms of allo-tolerance induction.

PO-1007 ASSOCIATION BETWEEN THE CC16 A38G POLYMORPHISM AND CLINICAL PHENOTYPES OF ASTHMA IN MOLDAVIAN CHILDREN

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Background and aims The protein CC16 is secreted in airways by the nonciliated bronchiolar Clara cells and has an important role in inflammation and immune modulation. Our study aimed to investigate the association of the CC16 A38G polymorphism with asthma severity in Moldavian children.

Methods A case-control study was used to detect the genotypes of 38 A/G of CC16 gene of 90 patients with asthma and 90 controls from the Moldavian ethnic group by polymerase chain reaction-restriction fragment length polymorphism. All patients underwent complex clinical and functional examination.

Results No significant differences were observed in the frequencies of polymorphic genotypes in site 38 of CC16 gene between asthmatic children and control subjects (p > 0.05, genotype frequency: AA+AG: 61.1% vs. 58.9%). The frequency of A allele...
was remarkable increased in girls with asthma compared to healthy controls (0.49 ± 0.06% vs. 0.33 ± 0.05%; χ²=3.21; gl=1; p = 0.07). In children with moderate and severe asthma the functionally compromised genotypes AA+AG were identified significantly more frequent comparing to the homozygous normal genotype (GG): 76.9% vs. 23.1% (t=2.3; p < 0.05) and 63.6% vs. 36.4% (t=1.9; p = 0.07), accordingly. The frequency of A allele was significantly increased in severe asthma cases compared with mild ones (0.54 ± 0.1 vs. 0.30 ± 0.06; gl=1; χ²=3.5; p = 0.05).

Conclusions The studied showed an association of the CC16 A38G polymorphism with more complex and severe forms of asthma. The studied gene was selected because of its important role in regulating inflammatory processes, but it is necessary to conduct further studies of extended range of genes in this ethnic group.

Background and aims Acute otitis media (AOM) is the most common infection in childhood, resulting from both anatomic and immunologic specificities of this age group. Recurrent AOM has been defined as one of the warning signs for primary immune deficiencies (PID). In this study we evaluated the strength of recurrent AOM as clinical predictor of PID.

Methods Retrospective study (August 2010–December 2013) which included all patients referred to PID appointment because of recurrent AOM (≥8 AOM episodes/year). Syndromic patients or those presenting with another warning sign for PID were excluded. Clinical, demographic and laboratory results were analyzed and statistical analysis was made using SPSS 20.

Results Seventy-five patients were included (median age 37.8 months; 62.7% male gender), corresponding to 15% of all first appointments. Other comorbidities were present in 20% of the patients and 17% had OHL surgery prior to PID referral. In most patients, the immunologic screening consisted on the evaluation of humoral function, but in selected cases other studies were performed (namely complement and lymphocyte immunophenotyping).

A PID was identified in 12 children (16,0%) and the majority of these patients had other distinctive feature (personal or familiar antecedent of infection or auto-immunity, 66.7%, p < 0.05). Nine children (12,0%) underwent prophylactic cotrimoxazole. The average length of follow-up was 11.2 months.

Conclusion Despite being a very frequent cause of immunologic screening, in this study recurrent AOM was not found to be a good predictor of underlying PID, unless the patients presents other significant personal or family history.

Background and aims Juvenile idiopathic arthritis (JIA) causes significant physical and functional disability. Children miss school due to illness, multiple hospital visits or admissions. Frequent absence from school is consistently reported to adversely affect academic performance. Our aim was to assess the rate of school absenteeism and drop out among Indian patients of JIA.

Methods The study was carried out on 69 children, 32 female, 37 male. The children and their parents were interviewed for details of school attendance, number of days and frequency of absence from school. Medical records were examined for hospital admissions and follow-up visits to supplement the information obtained from families.

Results The median number of school days missed/year were 41 (4–300; IQR- 20,120), representing 21.5% of school days.

Abstract PO-1011 Table 1 School absenteeism - JIA subtypes

<table>
<thead>
<tr>
<th>JIA subtype</th>
<th>Mean ± SD</th>
<th>*p</th>
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<tbody>
<tr>
<td>Polyarticular</td>
<td>61.87 ± 30.34</td>
<td></td>
</tr>
<tr>
<td>Polyarticular RF+ve</td>
<td>46.35 ± 56.28</td>
<td></td>
</tr>
<tr>
<td>Polyarticular RF-ve</td>
<td>75.57 ± 83.39</td>
<td></td>
</tr>
<tr>
<td>Oligoarticular</td>
<td>112.21 ± 75.12</td>
<td></td>
</tr>
<tr>
<td>Still A</td>
<td>51.84 ± 40.27</td>
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</tbody>
</table>

Conclusion Despite being a very frequent cause of immunologic screening, in this study recurrent AOM was not found to be a good predictor of underlying PID, unless the patients presents other significant personal or family history.