Events related to asthma exacerbation	Time(s)/year	Pre-treatment (%)	Post-treatment (%)
Worsening of asthma symptoms requiring additional systemic steroid therapy (n = 119)	0	25.21	73.95
	1	18.49	10.92
	2	17.65	4.20
	3	11.76	5.04
	4	26.89	5.88
Hospitalization due to asthma (n = 113)	0	53.98	84.96
	1	18.58	6.19
	2	10.62	3.54
	3	6.19	1.77
	4	10.62	3.54
Emergency room visit due to asthma (n = 101)	0	43.56	78.22
	1	19.80	11.88
	2	8.91	3.96
	3	4.95	1.98
	4	22.77	3.96
Absence from school/work (including housework) due to asthma (n = 55)	0	36.36	78.18
	1	7.27	5.45
	2	10.91	9.09
	3	10.91	7.27
	4	34.55	0

0195 | Prevalence of severe bronchial asthma phenotypes in the middle urals

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Background: to determine the prevalence of severe bronchial asthma in the Middle Urals and to phenotype patients with severe asthma for determination of the need of targeted therapy.
Method: Population studies of bronchial asthma prevalence were conducted in the Middle Urals from 2002 (n = 1057) to 2012 using the standard ECRHS questionnaire. Also registers of patients with asthma were created. In 2018 there was an analysis of outpatient records of patients with asthma (n = 216) living in one of the district of Ekaterinburg. The phenotyping of bronchial asthma was carried out by an allergist-immunologist.
Results: According to population studies the number of patients with bronchial asthma increased in 1.6 times (from 5.7% to 8.9%) over 10 years in the Middle Urals. Regardless of population category, patients with mild asthma and atopic phenotype prevail in the population. Patients with severe asthma in 2002 (n = 1057) accounted for 15.7%. At the same time, 56% of direct and indirect costs for asthma accounted for 15.7% of patients with severe asthma. There were 45.3% of severe asthma, 65.5% of atopic phenotype, 4.4% of eosinophilic phenotype without atopy, 1% of glucocorticoid dependence in the structure of patients with bronchial asthma registered by medical visits in 2018 (n = 216). The patients with atopic severe asthma accounted for 5%. The patients with eosinophilic severe asthma without atopy accounted for 2.3%.
Conclusion: Phenotyping of asthma has important practical significance for planning purchase volume of genetically engineered biologic drugs and improvement of efficiency of targeted therapy in a population of patients with severe asthma.

0227 | Exploiting the EMR as a tool to facilitate asthma reviews

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Background: Making best use of technological solutions to improve patient care is a current priority both from the point of view of patient access but also to improve efficiency. Primary Care computer systems in the UK now offer the facility for patients to fill in questionnaires online. This was a single practice quality improvement initiative to test the feasibility of generating questionnaires from the patient's own electronic medical record (EMR).
Method: Patients over the age of 18 with a diagnosis of asthma who had not had an asthma review since 1st April, and who were registered for online services were identified.
They were sent an SMS (text) message inviting them to complete a short online questionnaire concerning asthma control within their personal electronic medical record. The results of the questionnaires were automatically coded and entered into the EMR. The questions asked were the RCP 3 questions (Have you had difficulty sleeping because of your asthma symptoms (including cough)? Have you had your usual asthma symptoms during the day (cough, wheeze, chest tightness, or breathlessness)? Has your asthma interfered with your usual activities (e.g. housework, work/school, etc)?in the last seven days Y/N) used for the quality outcomes framework (QOF) with the supplemental question: Do you have a personal asthma action plan? (PAAP). Patients who did not respond to the first invitation had a second invitation issued two weeks later.
As a single practice quality improvement scheme, ethics approval was not required.

Results: Total patient population 9747
Total with asthma > 18yo: 620

Patients diagnosed with asthma over 18 with an online registration: 207

Patients diagnosed with asthma over 18 with online registration and no review since 1st April 2019: 109

Invitations issued: 109

Responses 23 (21 analysed) 3, first invitation; 20, second invitation

Controlled 12 4 without PAAP

Partly controlled 7 All with PAAP

Uncontrolled 2 All with PAAP

Conclusion: Limitations the response rate was only 25%. A second invitation yielded a significant increase in responses. Over 80% of patients had a PAAP and 70% were controlled. Implications: Non-responders, partially controlled, uncontrolled and those without PAAP will be identified for face to face review. Patients who are well controlled do not have to attend a face to face review, freeing up their time and clinician time.

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0264 | Polymorphism of IL13, IL31 and IL33 genes in the pathogenesis of moderate-to-severe asthma in Siberian children

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Background: Multifunctional cytokines, such as IL-13, IL-31, and IL-33, play an important role in asthma pathogenesis. Several single nucleotide polymorphisms of these cytokines are associated with asthma susceptibility in specific populations; however, further replicative studies in other ethnic groups are mandatory, especially with respect to asthma severity.

Method: 203 children with moderate-to-severe asthma (European population of East Siberia) were divided into two groups: uncontrolled asthma (n = 132) and controlled asthma (n = 71). The diagnosis, severity and level of control over the course of the disease were established in accordance with GINA-2018. Control group was represented by healthy individuals (n = 135). All examined individuals have given consent for the research and publish of the results. DNA was extracted from the blood using salting out method. Genotyping of the polymorphisms of candidate-genes of asthma with different level of the diseases control (IL13 (rs1800925), IL31 (rs7977932) and IL33 (rs7044343)) was carried out by RT-PCR. The comparison of the allele prevalence between the groups was carried out by the Chi-square test.

Results: The research resulted in obtaining the data on cytokine polymorphism distribution in the patients with asthma in the Europeans origin (Eastern Siberia, Russia): rare allele variants were represented by T*IL13, G*IL31 and C*IL33 allele, which goes in conformity with world databases. The frequency of the CT genotype in patients with controlled asthma was significantly higher in comparison with control (46.2%/36.6%, OR 1.51 [1.03-2.19], P = .033). We also obtained statistically significant differences in the frequency of the TT genotype between the population sample (6.7%) and the group with uncontrolled asthma (15.5%, OR 1.65 [1.06-2.56], P = .027).

Conclusion: We have shown genetic markers of the risks of asthma development: both CT and TT IL13 genotypes associated with asthma. Li J. et al. (2014) previously shown that the homozygous variant of the allele T* IL13 (rs1800925) is associated with increased production of IL-13 and respiratory tract hyperresponsiveness, which occurs in severe asthma. The obtained in present study results have contributed to the data on the role of polymorphisms of IL-13 into the development of asthma in children as exemplified by a European population of East Siberia, Russia.

0268 | Interweaving between genetic and epigenetic studies on asthma

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Background: The etiology and underlying mechanisms that contribute to asthma pathogenesis is not well known. Both genome-wide and epigenome-wide association studies have identified genes associated with asthma risk. It is unknown to what extent genes identified in these two types of studies overlap.

Method: Based on existing literature and database, we extracted overlapping genes identified in genetic and epigenetic asthma studies. Through analyses of variance (ANOVA), we assessed whether DNA methylation at CpGs on the overlapping genes were associated with neighboring SNPs within 1M base pairs among the asthma-related genes.

Results: In total, 1671 genes from genetic studies and 233 genes from epigenetic studies were shown to be associated with the risk of asthma, of which 27 overlapping genes were observed. Of the 27 genes, 433 CpGs and 483 neighboring SNPs were included in the assessment of methQTL. We tested the associations of DNAm at each of the 433 CpG sites with its neighboring SNPs, and identified statistically significant associations in five genes and 21 unique methQTLs, after adjusting multiple testing by controlling false discovery rate of 0.05.

Conclusion: The rather limited overlap in identified genes between genetic and epigenetic studies on asthma highlights the significance and needs to examine joint genetic and epigenetic effects on asthma risk to discover novel and informative biomarkers.