emphasizes the importance of vaccination, especially in infants and young children.

Cluster breastfeeding syndrome («cluster feedings», «bunch feedings») is when baby has several feedings close together during a certain period of time, in some cases during the day. The purpose of this study is to examine the frequency and to identify the reasons for the cluster breastfeeding syndrome in lactating women.

Questioning was conducted with 223 lactating women aged 19–44 years.

Questioning including questions regarding the use of the delivery methods and the lactation period. Psychological testing of lactating women was also conducted. The anxiety level was evaluated by Hamilton Anxiety Rating Scale (HAM-A) (score of 14 points is borderline). Lactating women were divided into two groups: without Cluster Breastfeeding syndrome (group I) and with Cluster Breastfeeding syndrome (control group). Statistical analysis was performed using Microsoft Excel 2007, SPSS Statistics v 24.0.0.0. Spearman's correlation coefficient (r) and Pearson's correlation coefficient (rxy) were calculated. Data was compared using chi-square test and P ≤ 0.05 was regarded as statistically significant.

Among the women surveyed, women with one child prevailed (63%). The average duration of the lactation period was 11.1 ± 5 months. The average time the baby was at the breast was 19 ± 4.1 minutes. Syndrome of prolonged, continuous feeding was noted in 5% of cases when the baby was at the chest continuously for a day, with short breaks at night sleep. In this group, in women (90%), labor was performed by Caesarean section. In the group I (cluster breastfeeding syndrome group), the average age of women was 35.8 ± 5.5 years, in the control group 25.0 ±4.6 (p <0.001). In group I, the average score on the Hamilton scale was 28.4 ± 6.5 (level of symptomatic anxiety), in the control group – 12.9 ± 9.7 (p = 0.0003). All baby in the group I have been gaining enough weight and producing sufficient dirty and wet diapers. Correlation analysis revealed a direct strong correlation between the presence of cluster breastfeeding syndrome in a child born by Caesarean section (rxy = 0.97) from mothers who gave birth over the age of 35 and have a level of symptomatic anxiety (r =1).

Cluster breastfeeding syndrome (cluster feedings, bunch feedings) occurs in 5% of cases and is associated with the late birth of the first child, high anxiety of the mother and the birth of a child by Caesarean section.
is known about postnatal CMV (pCMV) infection. Although pCMV infection in term healthy infant is mostly asymptomatic, serious gastrointestinal symptoms (vomiting, diarrhea, abdominal distension, hepatosplenomegaly, blood stools) are described in literature.

We describe two cases of infant hematemesis, focusing on the challenging differential diagnosis between pCMV gastritis and non IgE-mediated Cow’s Milk Protein Allergy (CMPA) enteropathy.

Case 1: a 3-month-old female infant presented with growth impairment, hematemesis and melena. Blood and stool analysis (bacterial, viral and parasites panels) resulted normal. Cow’s milk specific-IgE were negative.

Viral serologies revealed recent CMV infection with positive CMV-DNA Polimerase Chain Reaction (PCR) on urine and blood samples. Congenital CMV infection was ruled out through negative CMV-DNA PCR on the first day of life saliva sample. Esophagogastroduodenoscopy (EGD) revealed petechial elements in antral and duodenal-bulb mucosa; at biopsies normal eosinophils count and negative morphological research of Helicobacter pylori (HP) were found. Intranuclear CMV inclusion bodies were not detected and CMV immunostaining was negative.

Case 2: a 2-month-old male infant presented with dehydration, bloody diarrhea, vomiting and feeding refusal. Blood analysis revealed severe hypalbuminemia, anaemia and hypertransaminasemia. Stool examinations (bacterial, viral and parasites panels) and Mycobacterium Tuberculosis screening were negative. Allergological and immunological investigations resulted normal. CMV-DNA PCR on urine, blood and maternal milk samples were positive. CMV-DNA PCR on Guthrie card was negative. EGD and rettosigmoidoscopy revealed exudative active inflammation in duodenal mucosa. HP research was negative while CMV immunostaining visualized duodenal cells viral inclusions.

Discussion Paediatric hematemesis is mainly caused by foreign bodies ingestion, CMPA, infectious gastritis (Helicobacter pylori, CMV, parasites), drug-induced gastritis (steroids and FANS) and eosinophilic gastropathy. In our cases the differential diagnosis focused on pCMV infection and non IgE-mediated CMPA. Both infants had a partial clinical improvement after starting a cow’s milk protein free diet. However, due to the concomitant pCMV infection and the absence of cow’s milk specific-IgE, a definitive diagnosis could not be established.

In conclusion, paediatric hematemesis differential diagnosis turns out particularly challenging when considering non IgE-mediated CMPA and pCMV gastropathy. In fact, neither the absence of cow’s milk specific-IgE and comparison of gluten-degrading microorganisms (GDM) from feces and saliva of adolescent patients with coeliac disease (CD) and healthy controls (HC). Additionally, we compared genomes of the same bacterial species isolated from samples of feces and saliva obtained from the same individual.

Feces and saliva were obtained from 5 CD patients (2 female, 3 male) on gluten-free diet (GFD) and 5 HC (3 female, 2 male) aged 13-18 years. Samples were inoculated on culturing medium (MCG3) with gluten as a major source of carbon and nitrogen. All colonies with lysis zone were further isolated in pure culture and identified using MALDI Biotyper (Bruker Daltonics). In 4 samples (3 CD, 1 HC), Whole genome sequencing (WGS) was performed on MiSeq platform (Illumina) on all strains that belonged to the same species and were isolated from fecal sample and from saliva in the same individual.

In the CD group 10 GDM strains were isolated (5 were not identified): 2 from feces and 8 from saliva. In contrast to the HC group, where 16 GDM were isolated (1 was not identified): 7 from feces and 10 from saliva, 1 GDM was isolated from both samples (saliva and feces). GDM isolated from CD samples belong to 3 genera of bacteria and 1 yeast (Candida albicans). The latter was also isolated in the HC group along with bacteria from 12 different genera. That indicates higher GDM diversity in HC compared with the CD group.

Three bacterial species were isolated from feces and saliva of the same individual: Veillonella parvula, Lactobacillus paracasei, Lactobacillus rhamnosus. WGS showed identical genomes only in L. rhamnosus. That could indicate transmission between oral cavity and gut.

We found that cultivable GDM are diverse and more often present in feces and saliva of HC than CD, which could be the effect of GFD the CD patients were on. Genomically identical lactobacilli were detected in saliva and in feces of the same individual.

263 HELICOBACTER PYLORI INFECTION IN CHILDREN WITH CELIAC DISEASE

Ekaterina Orlova*, Novkova Valeria, Shapovalova Natalia, Gurina Olga, Demetteva Elena, Klukovna Ksenia. Federal State budgetary Institute of Higher Education «Saint-Petersburg State Pediatric Medical University» of the Ministry of Health of the Russian Federation

Aim: to reveal the effect of H. pylori on course of celiac disease (CD) in children.

Methods 58 children with histologically confirmed CG and newly diagnosed CD were examined. Children were divided into two groups according to presence of H. pylori infection: the first group-12 H.pylori-positive and the second group – 46 H.pylori-negative subjects. All patients underwent histological examination of gastric and duodenal biopsies, histological verification of H. pylori infection and biopsy urease test. Tissue transglutaminase antibodies (tTG IgA, IgG) anti- H+/K+ ATPase and anti-intrinsic antibodies, were measured by ELISA.

Results Mean age of patients was 11.33 ± 0.036 years in group 1 and 10.38±1.43 years in group 2 (p=0.582). Manifestation of CD didn’t differ statistically significantly in groups.