Results: Episodes of abdominal pain are common. Intensity, duration, and localization of episodes are variable. Enlargement of the liver and spleen occurs particularly among affected infants and children. The enlargement of these organs may vary, often in parallel with the fat content of the diet. The risk is the same for boys and girls.

Conclusions: Familial lipoprotein lipase deficiency is an inherited condition that disrupts the normal breakdown of fats in the body. It is characterized by absence of lipoprotein lipase activity and a massive accumulation of chylomicrons in plasma and a corresponding increase of plasma triglyceride concentration. Higher levels of plasma LPL activity are associated with decreased TG and increased HDL cholesterol levels in children.

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RARE GENETIC ANOMALIES IN A CASE WITH GROWTH RETARDATION

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Background and aims: To emphasize the genetic background of a child with growth failure.

Methods: The authors have evaluated a 7 year-old boy in context of failure to thrive. The family history: no related parents. The clinical exam: normal proportioned body, height -3.73 SD, weight -2.078 SD, microcephaly, face dimorphism (down-slanted palpebral fissures), 2nd and 5th fingers clinodactily for both hands, mental retardation, hypoprosopia and aggressive behavior. Achondroplasia and familial short stature were excluded based on clinical criteria.

Results: The blood tests revealed negative serology for celiac disease. The sweat test was normal. Endocrinological evaluation: normal thyroid gland function, low levels for growth hormone and IGF-1 (baseline and after clonidine and insulin stimulation tests). Regarding imagistic investigations: delayed skeletal maturation and cerebral IRM without brain or sella anomalies. Short stature associated with mental disabilities have justified genetic tests (karyotype) identifying double translocation between 1 and 13 chromosomes and between 5 and 11 chromosomes [46,XY, t(1:13) (p31.2; q32), t(5;11) (q14;q25)]. Due to normal parents' karyotypes

we consider this genetic anomalies as "de novo". The growth hormone therapy was followed by improvement of growth velocity.

Conclusions: The authors present a child with short stature secondary to growth hormone deficiency associated with very rare and "de novo" genetic anomalies. There is a chance that one of the four breakpoints disrupts a major gene on 1p31.2 or 13q32 or 5q14 or 11q25. Another possibility is a submicroscopic deletion on one of these four loci, justifying further cytogenetic investigations.

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NEWBORN FEMALE INFANT WITH HAEMOPHILIA A PHENOTYPE ASSOCIATED WITH NOVEL GENOTYPE

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Background: The differential diagnoses for reduced Factor VIII activity/level in a female infant include Turner's syndrome and Normandy (type 2N) variant of Von Willebrand's Disease (VWD).

Case: We present a female infant with low factor VIII activity/levels and raised APPT. She presents in a pedigree comprising both Haemophilia A and VWD.

Genetics: CGH array confirmed XX constitution and DNA testing excluded Normandy variant.

Mutation screening of the F8 gene showed the infant to be heterozygous for a c.2128G>A substitution. This novel base change predicts the replacement of the native Glycine residue at codon 710 with an Arginine residue; p.Gly710Arg. Although this variant has not previously been described, in-silico analysis supports its potential for pathogenicity as Haemophilia A. Two additional variants (c.3780C>G and c.1010-27G>A) were detected on the alternate allele. These polymorphic variants occur in linkage, and have been reported to be associated with reduced Factor VIII levels. Atypical Lyonisation was confirmed by X-inactivation analysis of peripheral blood.

Mother and maternal grandmother were heterozygous for the F8 variant. It is possible that the two additional variants were either de novo mutations or inherited from the father.

Conclusions: The clinical phenotype noted may represent a compound heterozygous state associated with atypical lyonization and characterised by a novel mutation in the F8 gene accompanied by two additional mutations also associated with low factor VIII levels on the alternate allele.

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CRITICAL ILLNESS IN PRETERM INFANTS IS ASSOCIATED WITH DIFFERENTIAL EXPRESSION OF STRESS-ACTIVATED PROTEIN KINASE SIGNALLING AND DRUG METABOLIZING CYP450 GENES

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Background: Preterm infants often suffer from critical conditions involving stress that requires advanced treatment including increased oxygen supply. We aimed to examine the influence of critical illness at the molecular level represented by gene expressions.

Methods: 20 premature infants in a level III NICU at Oslo University Hospital, Rikshospitalet, were studied. Inclusion criteria was critical illness defined by conditions requiring surgical procedures and severe drop in oxygen saturation, SaO₂ (< 60%), following more than 80% oxygen supply. For peripheral blood preparation we used RiboPure™-Blood, GLOBINclear™-Human protocol, and NugeneOvation RNA-Amplification system. Gene expressions were assessed using GeneChip Human Genome-U133 Plus2.0-arrays from Affymetrix. Ethical approval was granted by the Regional Committees for Medical and Health Research Ethics in Norway.

Results: A total of 107 peripheral blood samples were assessed. Thirteen samples at the time of critical illness from 7 infants showed significant

differential expression for 6000 genes. Further investigation identified higher expression levels in a group of genes related to oxidative stress and stress activated protein kinase (SAPK) signalling pathway. We also found significant differential expression of CYP450 genes involved in drug metabolism, including CYP1A2, CYP2D6, and CYP3A4. Interestingly, CYP1A2 was standing out with more than a 6 fold increased level.

Conclusion: This is the first study on simultaneously expressed genes in preterm babies. Our results highlight the significance of critical illness, pathophysiological mechanisms following stress and their effect on gene expression levels. Thus, molecular biomarkers are important to understand the impact of stress on gene expression, including CYP450 genes, in preterm infants.

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EXPRESSION OF CYTOCHROME P450 METABOLIZING ENZYMES IN PRETERM INFANTS DEPENDS ON AGE, BUT NOT GENDER

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Background: The neonatal period is a critical time for premature born infants. Variability in drug response may be due to differences in expression of the metabolizing CYP450 genes. Comprehensive studies of CYP450 gene expression at clinical relevant time points are lacking. We aimed to compare the gene expression levels of all CYP450 genes simultaneously in relation to gestational age (GA) and gender.

Materials: Peripheral blood at subsequent time points was withdrawn from premature born infants between GA 25.2-37.0, in a level III NICU at Oslo University Hospital, Rikshospitalet. We used the RiboPure™-Blood-, GLOBINclear™-Human protocol, NugeneOvation RNA Amplification system, and GeneChip Human Genome U133 Plus 2.0 arrays from Affymetrix to analyse global gene