thyroglobulin antibodies during follow up. Genetic analysis revealed: for DUOX 2 gene: 4 polymorphisms, a mutation in compound heterozygosity, a point mutation and a deletion; for TSH receptor gene: 1 point mutation and 2 polymorphisms. The patients with the same mutation showed different phenotypes.
Conclusions: about 30% of patients were euthyroid at the end of follow up and about a half of patients showed a hyperthyrotropinemia, so a high percentage of patients with CH underwent to discontinuation of therapy with LT4. Mutations in DUOX2 gene were the most frequent, however, children carrying the same mutation had a different phenotype, suggesting that other factors are responsible of the clinical characteristics.

PP220 - CLINICAL AND METABOLIC IMPACT OF THREE-TIMES-WEEKLY VERSUS DAILY GROWTH HORMONE (GH) TREATMENT IN NAÏVE GH-DEFICIENT CHILDREN

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OBJECTIVE: Growth hormone treatment (GHT) is commonly administered daily, although the pulsatile GH secretion is unlikely to be achieved and this regimen is often not complied. The auxological effect of three injections per week (TIW) regimen is controversial, while the metabolic effects were never evaluated in children. The objective was to evaluate whether two different regimens of weekly injections could lead to similar auxological and metabolic effects in children with GH deficiency (GHD).
DESIGN: 32 GHD children (25 males, mean age 10.5 ± 2.2 yr) were randomly assigned to receive daily (group A, No 16) or TIW (group B, No 16) GHT for 12 months.
METHODS: Auxological parameters, insulin-like growth factor-I (IGF-I), glucose and insulin during OGTT, glycosylated hemoglobin (HbA1c), lipid profile, the oral disposition index (DIo), the homeostasis model assessment estimate of insulin resistance (Homa-IR), the quantitative insulin sensitivity check index (QUICKI) and the insulin sensitivity index (ISI).
RESULTS: After 12 months, both groups showed a significant and comparable improvement in height ($p<0.001$) and IGF-I ($p<0.001$). As regards the metabolic parameters, in both groups we found a significant increase in fasting insulin ($p<0.001$ and $p=0.026$) and Homa-IR ($p<0.001$ and $p=0.019$), with a concomitant decrease in QUICKI ($p<0.001$ and $p=0.031$). A significant increase in fasting glucose ($p=0.001$) and a decrease in ISI ($p<0.001$) and DIo ($p=0.002$) was only found in group A.
CONCLUSIONS: TIW injections regimen is effective and comparable with the daily regimen in improving auxological parameters and has a more favorable metabolic impact in GHD children

PP221 - MOLECULAR CHARACTERIZATION OF A NEW VARIANT IN THE AAAS GENE CAUSATIVE OF ALLGROVE SYNDROME (AS)

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Allgrove Syndrome (AS) is an autosomal recessive congenital disease, caused by mutations in the AAAS gene, which encodes a protein of 547 amino acids named ALADIN (ALacrima Achalasia aDrenal Insufficiency Neurologic disorder). This protein, whose function is still not completely understood, belongs to the WD-repeat family of regulatory proteins, and is located in the nuclear pore complexes. Here we describe a case of a boy that presented at the age of 14 years because of important weight loss (BMI=14kg/m2) and fatigue. He had been diagnosed with achalasia one year earlier. Past history revealed congenital twisted feet and dysphagia since 4-6 months of age. On clinical examination, cutaneous-mucosal hyperpigmentation, muscle weakness and nasal speech were noted. Endocrine studies confirmed adrenal insufficiency (F=12 mcg/L, ACTH>1250 pg/ml); electromyoneurography demonstrated axonal polyneuropathy and Schirmer test was indicative for alacrima. He was then diagnosed for AS and glucocorticoid therapy was immediately started. The genetic analysis of the AAAS gene showed a novel homozygous intronic variation (IVS11-2 A>G), that was inherited from the two heterozygous unaffected and unrelated parents (both from Sardinia). The molecular characterization of this novel variant, based on the mRNA analysis, demonstrated that it is affecting the splicing site of the exon 11 in AAAS gene causing the retention of 36 intronic base-pairs, the introduction of 9 new aminoacids and the generation of a premature stop codon. This leads to an aberrant early truncated protein, with the lack of the C-terminus domain and an altered expression and localization. Indeed, western blotting analysis was demonstrating a reduced amount of the variant protein compared to wild-type, while the immunohistochemistry analysis evidenced its altered subcellular localization. In conclusion, we have identified a novel IVS in the AAAS gene that generate an aberrant protein causative for the AS.

PP222 - IMPROVING CLINICAL DIAGNOSIS IN SHOX DEFICIENCY: THE IMPORTANCE OF GROWTH VELOCITY

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Background
Haploinsufficiency of short stature homeobox containing gene (SHOX) is one of the main monogenic causes of short stature. The diagnosis of haploinsufficiency of SHOX (SHOXD) in short-statured children is still a challenge because of the highly variable phenotype, especially in prepubertal age, and the low sensitivity of clinical scores.
Aims of this study were 1) to estimate the prevalence of SHOXD in a population of Italian short-statured children, 2) to analyse their phenotype and 3) to evaluate the performance of various clinical scores.
Patients and methods
This was a single-center longitudinal study (January 2009-December 2014) performed at the Division of Pediatrics, University of Piemonte Orientale (Novara, Italy).
Screening for SHOXD was performed in 281 short-statured children aged 2-18 years (mean age 8.6 ± 4.0 years, 50.7% females, 70.8% prepubertal, mean height SDS -2.0 ± 0.5) by direct sequencing and MLPA. Subjects with SHOXD were compared to 117