

gene mutations (4 missense: p.T93M, p.R352W, p.Y432C, p.E448K; 2 nonsense: p.W151X, p.Q259X; and one splice site: c.831 + 1G > C) were detected. p.T93M was the most frequent (57% of all alleles) mutation. Two of the seven mutations (p.Q259X, c.831 + 1G > C) were defined for the first time in this study.

This study defines the mutation spectrum and genotype phenotype correlation of *DHCR7* gene within the Turkish SLOS patients. As seen in other Mediterranean populations, p.T93M mutation was the most frequent mutation observed in our patients.

(P-55)

Anthropometric Measurements and Complications of Achondroplasia Patients

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Achondroplasia is the most common reason of inherited disproportionate short stature. It is caused by mutations in the *FGFR3* (fibroblast growth factor receptor-3) gene. In this study, we aimed to evaluate the anthropometric measurements and complications in achondroplasia patients.

In this study, using Sanger sequencing or next-generation sequence analysis, *FGFR3* gene mutations were detected in 29 patients (achondroplasia/hypochondroplasia: 15/14) between 2012 and 2016. Nine of the 15 achondroplasia patients and one of the 14 hypochondroplasia patients had been followed by both Pediatric Genetics and Pediatric Endocrinology Subdivisions of Ege University Medical Faculty. Fifty percent of patients were female and 50% were male. Median age was 27 months (min 9-max 96 months). Anthropometric measurements of the patients were found to be in normal ranges using growth curves specific for achondroplasia patients reported by Horton et al. When evaluated according to normal growth curves, mean standard deviations of height, weight, and head circumference were $-4.45 (\pm 1.59)$, $-1.38 (\pm 1.15)$, and $1.99 (\pm 1.20)$, respectively. In one patient, foramen magnum stenosis and cervicospinal junction compression were observed. Another patient had mental retardation and epilepsy.

It has been considered that growth of achondroplasia patients can be maintained in the limits of achondroplasia patients when appropriate follow-up is performed. They should be carefully evaluated for neurological and orthopedic complications.

(P-56)

Mutation Spectrum of *GCK*, *HNF1A*, and *HNF1B* in MODY Patients and 40 Novel Mutations

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MODY (maturity onset diabetes of the young) is a monogenic diabetes mellitus caused by pancreatic beta cell dysfunction. It has been classified into 9 groups according to the underlying molecular etiology. Mutations in the genes encoding the nuclear transcription factor 1 homeobox A (*HNF1A*) and the enzyme glucokinase (*GCK*) are the most common causes of MODY. Additionally, *HNF1B* gene is responsible for 5% of the disease. The aim of this study was to investigate the mutation spectrum of *GCK*, *HNF1A*, and *HNF1B* genes in MODY patients.

Molecular test results of 152 patients carrying mutations in *GCK*, *HNF1A*, or *HNF1B* genes were evaluated. Rate of mutations detected in *GCK*, *HNF1A*, and *HNF1B* genes were 84%, 13%, and 3%, respectively. Fifty-seven different mutations (40 missense, 8 nonsense, 7 frameshift, 1 in-frame deletion, and one splice site) in *GCK*, 15 different mutations (11 missense, 3 frameshift, and one 3' UTR) in *HNF1A* and 4 different mutations (2 missense, one frameshift, and one indel) in *HNF1B* were found. Thirty-three, 5, and 2 mutations were detected as novel mutations in *GCK*, *HNF1A*, and *HNF1B* genes, respectively.

Definition of molecular etiology in MODY patients is important for giving appropriate genetic counseling and disease management. The most commonly affected gene has been found to be *GCK* gene among the MODY patients studied. In the genes *GCK*, *HNF1A*, and *HNF1B*, 40 mutations have been defined for the first time in this study.

(P-57)

MEN 2A Family

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MEN 2 is a rare genetic disorder with autosomal dominant inheritance. Here, we present a family in which MEN2A was detected in the index case and two brothers had detected pheochromocytoma and medullary thyroid cancer.

MEN 2A index case;

Index case: A thirty-six-year-old male patient presented with headache, sweating, and palpitations. Urine catecholamines

were significantly higher. A bilateral adrenal mass was detected and bilateral surrenalectomy was performed. Plasma calcitonin level was high. A hypoechoic, coarse calcific thyroid nodule was detected. The patient underwent total thyroidectomy and neck dissection. The parathormone (PTH) level was normal. The RET mutation was positive in the patient. It was decided to screen the family. Second case: A 50-year-old male patient was called for MEN 2A family screening. Bilateral adrenal mass was detected. Bilateral surrenalectomy was performed. Calcitonin level of 267 pg/mL was detected. Hypoactive thyroid nodule aspiration was reported as AUS. Total thyroidectomy and central neck dissection were applied to the patient. Cranial involvement was also observed in the PET/CT scan for metastasis. A mass in the left cerebellum (hemangioblastoma?) was detected in brain MR. Third case: A forty-six-year-old female patient was evaluated; a mass with size of 56x64x50 mm in the left adrenal and normal right adrenal were detected. Metanephrine and normetanephrine were significantly high in the urine. Calcitonin level was significantly high. Firm thyroid nodule was detected. PTH was normal. Left adrenalectomy and total thyroidectomy were planned. The patient refused to be treated.

MEN 2A syndrome is the most common medullary thyroid cancer. Bilateral pheochromocytoma is common. Hyperparathyroidism is observed in 20-30% of patients.

(P-58)

Investigation of Androgen Receptor Gen Mutation Spectrum in the Turkish Patients with Disorder of Sex Development

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Androgen insensitivity syndrome (AIS) is an X-linked recessive condition resulting in a failure of normal masculinization of the external genitalia in chromosomally 46,XY individuals.

This failure of virilization can be either complete androgen insensitivity syndrome (CAIS) or partial androgen insensitivity syndrome (PAIS), depending on the amount of residual receptor function. Mutations in the AR gene on chromosome Xq12 cause AIS. In this study, we aimed to investigate the mutation spectrum in Turkish patients who had AR mutation analysis with suspected gender development disorder and AR insensitivity syndrome.

The AR gene from the DNA material isolated from the peripheral blood of patients was amplified using appropriate primers and sequenced using the new-generation sequence analysis technique on the Mi-Seq device.

In this study, molecular analysis results of 383 individuals who underwent AR genetic analysis in Ege University Medical Genetics Department between 2011 and 2016 were evaluated retrospectively. There were 44 mutations in these cases. Of the 44 cases detected in the mutation, 16 were affected and the karyotype was 46,XY. 28 of them are the 46,XX carrier mothers, carrier relatives, or siblings of the affected cases.

New mutations were detected in our studies between 2011 and 2016-L57Q, T576I, D691Y, P672R, Q739E, p.R544KfsX8, c.1745_1747delTCT, F726S, L881V, R102G, and L863F. Different mutations can be detected in AR gene in Turkish society. In cases with disorder of sex development, AR should be examined.

(P-59)

A Novel HESX1 Mutation in a Case with Panhypopituitarism

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Pituitary gland insufficiency (hypopituitarism) is a clinical condition that results in inadequate production and release of pituitary hormones. The deficiency of one or more pituitary hormones is named partial hypopituitarism and the deficiency of all pituitary hormones is named panhypopituitarism. Hypopituitarism can be attributed to inherited or acquired causes. Our aim was to determine the molecular diagnosis in our panhypopituitarism patient with HESX1 gene sequence analysis.

A 21-year-old woman was referred to our clinic with primary amenorrhea. Her medical history included use of growth hormone, thyroid hormone, and estrogen. Cranial MRI findings were consistent with empty sella syndrome. In the family history of the case, there was no consanguinity between the parents and no similar patient in the family. Based on findings and laboratory results, the diagnosis of panhypopituitarism was considered; HESX1 gene sequence analysis from patient's peripheral blood revealed a heterozygous p.R128K mutation.