The phenotype connected to *POU1F1* mutations is characterized by profound GH and PRL deficiencies, variable degrees of TSH deficiency, severe proportional short stature, atypical facies, and feeding difficulties in infancy. Patients harboring mutations within *PROP1* gene present with GH, PRL, and TSH deficiencies in addition to variable defects in luteinizing hormone/follicle-stimulating hormone and adrenocorticotropic hormone secretion. *PROP1* mutations are the most common known genetic cause of CPHD cases.

Here, we present 3 cases with *POU1F1* mutation and 1 case with *PROP1* mutation, who were molecularly diagnosed in Medical Genetics Department of Ege University.

The three cases (1 female, 2 males) carrying *POU1F1* mutations all had short stature. One male case with a novel mutation, p.K216T, also presented with micropenis in addition to short stature. The other mutations detected in *POU1F1* gene were S50A, R265W; S50A being novel. The case with *PROP1* mutation also had short stature and micropenis. Molecular analysis revealed a frameshift p.L102CfsX8 mutation in the *PROP1* gene. Biochemical testing showed PRL and GH deficiencies in all cases. Two cases with *POU1F1* defect and the case with *PROP1* defect also had central hypothyroidism.

It is considered that in patients with growth retardation together with combined pituitary hormone deficiency, *POU1F1* and *PROP1* gene mutations should be investigated. In this study, two novel *POU1F1* mutations were detected for the first time.

(P-53)

FGFR2 Gene Mutations in Patients with Syndromic or Isolated Craniosynostosis

Emine İpek Ceylan[1], Aslı Ece Solmaz[1], Hüseyin Onay[1], Ayça Aykut[1], Asude Durmaz[1], Gözde Yeşil[2], Filiz Hazan[3], Aslıhan Kiraz[4], Beyhan Tüysüz[5], Meltem Cerrah Güneş[6]

[1]*Ege University Faculty of Medicine, Department of Medical Genetics, İzmir, Turkey*

[2]*Bezmialem Vakıf University Faculty of Medicine, Department of Medical Genetics, İstanbul, Turkey*

[3]*Dr. Behçet Uz Children's Hospital, Clinic of Medical Genetics, İzmir, Turkey*

[4]*Kayseri Training and Research Hospital, Clinic of Medical Genetics, Kayseri, Turkey*

[5]*İstanbul University Cerrahpaşa Faculty of Medicine, Department of Pediatric Genetics, İstanbul, Turkey*

[6]*Erciyes University Faculty of Medicine, Department of Medical Genetics, Kayseri, Turkey*

Craniosynostosis, premature closure of one or more cranial sutures, may occur in both non-syndromic and syndromic forms. Birth prevalence of craniosynostosis is 1/ 2,100–1/2,500. *FGFR2*, *FGFR3*, *FGFR1*, *TWIST1*, and *EFNB1* genes play a role in the syndromic craniosynostosis presenting with craniofacial abnormalities, including hypertelorism, proptosis, and midfacial hypoplasia. Limb, cardiac, central nervous system, and tracheal malformations have also been described. Mutations in the *FGFR2* gene located on 10q26 that encode fibroblast growth factor receptor 2 is responsible for a part of the syndromic craniosynostosis. The aim of this study was to determine *FGFR2* gene mutations in 85 craniosynostosis cases including Apert, Pfeiffer, and Crouzon syndromes, and isolated craniosynostosis patients who were referred to molecular genetics laboratory of Medical Genetics Department, Ege University between 2010 and 2016.

Sequence analysis was performed on 2 exons (exons 7-8) of the *FGFR2* gene in 85 cases referred for pre-diagnosis of craniosynostosis between 2010 and 2016. Sanger sequencing analysis method was used for sequence analysis.

Mutations were detected in twenty of the cases (23%). The frequency of *FGFR2* mutation in this study was 20% S252W and P253R (4 cases), 15% Y382C (3 cases), 10% Y308C (2 cases) and 5% A314S, A266P, P253A, W290C, W290R, S351C, S252P (1 case).

In syndromic and isolated craniosynostosis patients, the analysis of exons 7 and 8, which is one of the mutational hot spot of *FGFR2* gene, allows diagnosis in 23% of patients. It has been concluded that performing complete *FGFR2* gene analysis will provide larger numbers of molecular diagnosis.

(P-54)

The Mutation Spectrum of *DHCR7* Gene and Two Novel Mutations

Esra Işık[1], Hüseyin Onay[2], Bilçağ Akgün[1], Tahir Atik[1], Ayça Aykut[2], Asude Durmaz[2], Munis Dündar[3], Yaşar Bekir Kurtbay[4], Ercan Mıhçı[5], Ferda Özkınay[1]

[1]*Ege University Faculty of Medicine, Division of Pediatric Genetics, İzmir, Turkey*

[2]*Ege University Faculty of Medicine, Division of Medical Genetics, İzmir, Turkey*

[3]*Erciyes University Faculty of Medicine, Department of Genetics, Kayseri,*

[4]*Tepecik Training and Research Hospital, Genetic Diagnostic Center, İzmir, Turkey*

[5]*Akdeniz University Faculty of Medicine, Division of Pediatric Genetics, Antalya, Turkey*

Smith-Lemli-Opitz syndrome (SLOS) is a rare autosomal recessive syndrome. It is one of the 46,XY disorders of sexual development. Molecular defects in *DHCR7* gene are responsible for this syndrome. In this study, the mutation spectrum of *DHCR7* gene in SLOS patients has been evaluated.

Thirteen patients from 11 families carrying mutations in the *DHCR7* gene were included in this study. Seven different *DHCR7*

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

Esra Işık[1], Şükran Darcan[2], Ayşenur Kavasoğlu[3], Tahir Atik[1], Hüseyin Onay[3], Damla Gökşen Şimşek[2], Asude Durmaz[3], Ayça Aykut[3], Özgür Çoğulu[1], Ferda Özkınay[1]

[1]Ege University Faculty of Medicine, Division of Pediatric Genetics, İzmir, Turkey

[2]Ege University Faculty of Medicine, Division of Pediatric Endocrinology, İzmir, Turkey

[3]Ege University Faculty of Medicine, Department of Medical Genetics, İzmir, Turkey

Achondroplasia is the most common reason of inherited disproportionate short statue. 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 (± 1.59), -1.38 (± 1.15), and 1.99 (± 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

Ferda Özkınay, Esra Işık, Damla Gökşen Şimsek, Ayça Aykut, Emin Karaca, Samim Özen, Hilmi Bolat, Tahir Atik, Hüseyin Onay

Ege University Faculty of Medicine, Division of Pediatric Genetics, İzmir, Turkey

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 GCKL, *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-tree, 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

Zafer Pekkolay, Hikmet Soylu, Belma Özlem Tural Balsak, Mehmet Güven, Alpaslan Kemal Tuzcu

Dicle University Faculty of Medicine, Department of Adult Endocrinology, Diyarbakır, Turkey

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