Background. Congenital multiple pituitary hormone deficiency (MPHD) may result from defects of transcription factors that govern the early pituitary development. The most prevalent are two mutation of PROP1 gene: the 296delGA and 150delA.

Methods:

• Seventy five Lithuanian MPHD patients were tested for PROP1 defects by Sanger sequencing.

• Perinatal/postnatal growth data, hormonal profiles and pituitary size were analyzed.

Results:

DNA analyses results of PROP1 mutation

- 50% familial cases (ten sibling pairs and two sibling triples).
- The highest rate of PROP1 mutations among MPHD patients from populations studied so far (17.5 per million).
- The mutation carriers were found to share a common ancestor with the 296delGA mutation having arisen about 187.9 generations ago (range 156.8-229.5 generations).

Conclusions:

1. The population-based cohort of patients with PROP1 gene mutation is the largest described so far.
2. High prevalence of PROP1 defects in Lithuania is due to a founder effect of 296delGA mutation.
3. The 296delGA mutation of Lithuanian patients originating earlier than in another European countries patients (187.9 vs. 112 generations ago).

Birth1 year2 years3 years4 years5 yearsGH start
-8 -6 -4 -2 0 2

Length/Height (SDS)

Genotypes:

50 patients – homozygote of 296delGA
1 patient – heterozygote of 296delGA/R71H
1 patient – heterozygote of 296delGA/150delA

References: