ESPE 2015 P3-1255 : Analysis of gene methylation difference and evaluation the effect of growth hormone in Silver Russell syndrome

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OBJECTIVES

To determine novel gene or imprinted gene associated with pathogenicity of SRS through detection genome-wide methylation differences. To observe growth hormone (GH) efficacy in Silver-Russell syndrome (SRS) and the relationship between GH and epigenetic changes.

METHODS

To detect genome-wide methylation site through the Illumina 450K methylation chip in 7 SRS and 5 controls matched age. Other 10 cases of SRS were analyzed GH efficacy.

RESULTS

Imprinted gene OSBP5 has the most significant methylation difference site in case group and normal control group (P = 0.023, β = -0.243). And the gene is located on 11p15-4 5’UTR, it is quite possible pathogenic. Five important genes were found might related with SRS: TGFβ3, GAP43, HSF1, NOTCH4 and MYH14.

10 SRS with GH treatment, the average follow-up period was 13.2 months. The average GH dosages was 0.15 IU/kg.d. Growth velocity (GV) was 9.53 ± 3.918 cm/year, which was higher than normal children’s GV (5cm/year), P=0.005.

5 out of 10 cases did epigenetic detection. One patient was matUPD (7) positive and his GV was 11.13cm/year. Two patients were 11p15 ICR1 hypomethylation and their GV were 8cm/year, 9.141cm/year, respectively. The other two cases were not found in epigenetic changes, whose GV were 14.4cm/year and 9.54 cm/year.

CONCLUSIONS

The imprinted gene OSBP5 is quite possible pathogenicity of SRS. Other 5 important genes, TGFβ3, HSF1, GAP43, NOTCH4, MYH14 may be related to SRS.

We confirmed that the most important epigenetic methylation changes of SRS are located in the 11p15. This group of SRS have good GH efficacy. One case of UPD (7) mat was higher GV than two patients who were 11p15 ICR1 hypomethylation.

References


