GENETIC DIAGNOSIS OF PATIENTS WITH OVERLAPPING CLINIC RETT-LIKE BY NGS

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Objectives:
It has been studied patients with clinical Rett (RTT) without genetic diagnosis using the *Next Generation Sequencing method (NGS).* This type of diseases requires clinical diagnosis. The finding of a mutation confirms the diagnosis, but not necessarily established it.
NGS methodology facilitates the simultaneous study of causative genes of RTT and others whose mutation produces a similar or overlapping clinic.
The *NGS* has allowed definitively diagnose patients with clinical RTT-like such as Pitt Hopkins syndrome in the same analysis, finding mutations in the *TCF4* gene that cause it.

Material and Methods:
It has been designed a gene panel of 17 genes related to the clinical RTT-like presentation by *HaloPlex Target* technology. *Enrichment System, for Illumina Sequencing.*
Sanger sequencing was used in exons not well covered. If do not find any change, MLPA was done by causative RTT genes (*MECP2, CDKL5* and *FOXG1*).

Results:
We have detected mutations in genes that do not cause RTT pathology, but overlap some features of RTT patients such as Pitt Hopkins syndrome.

Conclusion:
The genetic study by NGS allows to study a larger number of genes associated with RTT simultaneously, significantly reducing response time and the cost of the study. It also allows us to study other related clinical RTT and thus to redirect the clinical diagnosis to another disease genes.
Verification by Sanger of the progenitors of the mutations detected by NGS remains essential for their characterization.

References

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