

Novel *MECP2* mutations in Czech patients with Rett syndrome

Daniela Zahorakova¹, Alice Baxova², Vladimir Gregor³, Martina Langová³, Martin Magner¹, Zumrova Alena⁴, Pavel Martasek¹

¹Department of Pediatrics and Adolescent Medicine, 1st Faculty of Medicine, Charles University in Prague and General University Hospital, Czech Republic; ²Institute of Biology and Clinical Genetics, 1st Faculty of Medicine, Charles University in Prague and General University Hospital, Czech Republic; ³Department of Medical Genetics, Thomayer Hospital, Prague, Czech Republic; ⁴Department of Paediatric Neurology, 2nd Faculty of Medicine, Charles University in Prague and Motol University Hospital, Czech Republic.

Background: Rett syndrome (RTT) is a progressive X-linked dominant neurodevelopmental disorder primarily caused by *de novo* mutations in the methyl-CpG binding protein 2 gene (*MECP2*). MeCP2 is a multifunctional protein involved in transcription regulation, chromatin architecture, and other biologically relevant phenomena. We report an update on mutation analysis of the *MECP2* gene in Czech patients with Rett syndrome and intellectual disability with Rett-like features and describe 3 novel pathogenic mutations.

Subjects and Methods: The *MECP2* gene was analyzed in 350 patients using high-resolution melting analysis and Sanger sequencing. Large deletions and duplications were analyzed by multiplex ligation-dependent probe amplification (MRC-Holland).

Observations: Pathogenic mutations were identified in 76 patients (75 girls, 1 boy): 55 had classic RTT, 8 had atypical RTT, 11 had intellectual disability with Rett features or possible Rett syndrome, 1 had autism, and 1 boy had *MECP2* duplication syndrome. We identified 3 novel mutations:

c.155_1189del1035;909_932inv;insC, c.573delC, and c.1163_1200del38. A boy with *MECP2*-duplication syndrome inherited the mutation from his asymptomatic mother. The duplication involved genes *MECP2*, *SLC6A8*, *IRAK1*, *IDH3G*, and *L1CAM*.

Conclusions: We confirmed high frequency of *MECP2* mutations in classic RTT (80%) and identified 3 novel pathogenic mutations. Confirmation of molecular defect enabled genetic counseling in affected families.

Supported by grants NT 13120-4/2012, UNCE 204011/2012, MZCR RVO-VFN64165/2012.