

Spinal intradural lipoma

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A [spinal lipoma](#) in the intradural compartment is a rare condition, accounting for < 1% of all [spinal cord tumors](#). [Spinal cord lipomas](#) are frequently associated with [dysraphism](#) and occur in the [thoracic spine](#).

Isolated nondysraphic cervical lipomas are a rare entity.

see [spinal cord lipoma](#).

Tao et al., explore the abnormality of chromosomes of patients with lipoma tethered cord syndrome and the probable association between Copy Number Variations (CNV) and lipoma tethered cord syndrome. Methods: By using the Agilent SurePrint G3 Human CGH 8×60K Microarray Kit, we performed genome-wide screening for CNV on 11 patients with lipoma tethered cord syndrome adopted by the Neurosurgery Department of Chinese PLA General Hospital and their healthy parents from March 2015 to May 2015. We analyze CNVs got by the kit against the gene databases. Unrelated confirmed polymorphisms contained in Database of Genomic Variants (DGV) were discarded. Database of Chromosomal Imbalance and Phenotype in Humans using Ensemble Resources (DECIPHER) helps us with similarity inquiry, and UCSC Genome Browser helps in identification of non-polymorphic CNV. Biological process, cellular component and molecular function enrichment of these genes were conducted to confirm the association between the CNV and lipoma tethered cord syndrome. Results: 17 CNV were discovered by aCGH in 11 patients. Chr8: 39258894-39386158 and Chr15: 20481702-22509254 showed a high frequency of 5/11. Angelman syndrome and Prader-Wolli syndrome were found to be associated with the CNV of Chr15. Gene function enrichment analysis revealed that ADAM5P and ADAM3A contained in CNV obtained from patients with lipoma tethered cord syndrome was also associated with orofacial clefts. Conclusions: CNV in Chr8 and Chr15 of patients with lipoma tethered cord syndrome had a higher frequency than that of common human. It revealed that there is probable association between these two pieces of CNV and lipoma tethered cord syndrome. To explorer related genes or CNV, focusing on certain type of NTDs may increase the research efficiency and get more accurate results ¹⁾.

¹⁾

Tao BZ, Yu XG, Cheng C, Zong R, Zhao ZY, Wang LK, Shang AJ. [Copy number variants analysis in whole-genome of patients with lipoma tethered cord syndrome]. *Zhonghua Yi Xue Za Zhi*. 2017 Jan 3;97(1):12-16. doi: 10.3760/cma.j.issn.0376-2491.2017.01.004. Chinese. PubMed PMID: 28056283.

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