Contribution ID: **990** Type: **Poster**

Analysis of possible functional conservation between genes Oxr1 and Ncoa7

Friday, 28 October 2022 14:30 (5 minutes)

Genomics is a rapidly developing research area that studies genome structure, mechanisms of its functioning and genome and genes evolution. One of the key mechanisms of novel gene emergence is gene duplication. These events lead to the emergence of a gene with identical functions that can be lost, can change, or novel functions may be acquired. An example of genes that have evolved following several duplication events are members of the TLDc family. In this work, I investigated the functional conservation of the two most closely related family members - Oxr1 and Ncoa7. These genes possess highly similar domain architecture and have been shown to share some functions and binding partners. Strikingly, Oxr1 knockout in mice leads to a severe phenotype of cerebellar degeneration, ataxia and early death, while Ncoa7 expression disruption is well tolerated and has only been shown to lead to increased urine pH. As Oxr1 and Ncoa7 genes share a high degree of similarity, it is possible that Oxr1 could compensate for the absence of Ncoa7 and protect animals from developing any abnormal phenotype - such a mechanism has previously been shown for other genes. Based on their promoter region sequences, we predict that Oxr1 and Ncoa7 are likely regulated by similar sets of transcription factors and are involved in multiple processes throughout the organism, such as central nervous system development, hematopoiesis and stem cell maintenance.
Keywords: gene duplication, transcriptional regulation

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Session Classification: Online poster session

Track Classification: Life Science