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TITLE OF HIS PRESENTATION

Shared gene regulatory regions link retinoid and vitamin D signaling

RESULTS FOR THE TALENTUM PRIZE 2026 NOMINATION

Genome-wide analyses in differentiated THP-1 cells reveal that RARα and VDR frequently co-occupy genomic regions that regulate genes and function as convergence points for cooperative retinoid and vitamin D signaling

RESEARCH AREA

Cells are capable of dynamically adjusting their functions in response to internal and external signals. One key mechanism enabling these responses is transcriptional regulation, which determines which genes are expressed at a given time in a specific cell type. The research group led by Lajos Széles Ph.D. aims to elucidate specific transcriptional regulatory mechanisms using functional genomic approaches. The resulting datasets are analyzed with bioinformatic methods. The group primarily investigates DNA binding of transcription factors. In previous years, they have studied, among others, nuclear receptors (e.g., VDR, RAR, RXR, and ER) as well as transcription factors activated during antiviral and inflammatory responses (e.g., IRF, STAT, NF-κB, and AP-1 protein families).

TECHNIQUES AVAILABLE IN THE LAB

The group employs various next-generation sequencing methods (ChIP-seq, RNA-seq, and ATAC-seq). These methods are suitable for mapping transcription factor and cofactor binding sites, histone modifications, gene expression changes, and chromatin accessibility. Experimental systems include cell lines as well as ex vivo and primary human and mouse immune cells, such as dendritic cells, macrophages, and other immune cells.

SELECTED PUBLICATIONS

Mianesaz, H., Göczi, L., Nagy, G., Póliska, S., Fadel, L., Bojcsuk, D., Penyige, A., Szirák, K., AlHaman, F., Nagy, L., Vámosi, G., & **Széles, L.** (2025). Genomic regions occupied by both RARα and VDR are involved in the convergence and cooperation of retinoid and vitamin D signaling pathways. **Nucleic Acids Res 53(6):** gkaf230.

Göczi, L., Csumita, M., Horváth, A., Nagy, G., Póliska, S., Pigni, M., Thelemann, C., Dániel, B., Mianesaz, H., Varga, T., Sen, K., Raghav, S. K., Schoggins, J. W., Nagy, L., Acha-Orbea, H., Meissner, F., Reith, W., & **Széles, L.** (2022). A Multi-Omics Approach Reveals Features That Permit Robust and Widespread Regulation of IFN-Inducible Antiviral Effectors. **J Immunol 209(10):** 1930–1941.

Csumita, M., Csermely, A., Horvath, A., Nagy, G., Monori, F., Göczi, L., Orbea, H. A., Reith, W., & **Széles, L.** (2020). Specific enhancer selection by IRF3, IRF5 and IRF9 is determined by ISRE half-sites, 5′ and 3′ flanking bases, collaborating transcription factors and the chromatin environment in a combinatorial fashion. **Nucleic Acids Res 48(2):** 589–604.

Széles, L., Meissner, F., Dunand-Sauthier, I., Thelemann, C., Hersch, M., Singovski, S., Haller, S., Gobet, F., Fuertes Marraco, S. A., Mann, M., Garcin, D., Acha-Orbea, H., & Reith, W. (2015). TLR3-Mediated CD8+ Dendritic Cell Activation Is Coupled with Establishment of a Cell-Intrinsic Antiviral State. **J Immunol 195(3):** 1025–1033.

Nagy, L., Szanto, A., Szatmari, I., & **Széles, L.** (2012). Nuclear hormone receptors enable macrophages and dendritic cells to sense their lipid environment and shape their immune response. **Physiol Rev 92(2):** 739–789.