

<https://doi.org/10.7124/bc.000B5A>

Y.Y. Hegel-Valentych, M. Khetsuriani, A.M. Shysh

O.O. Bogomoletz Institute of Physiology, NAS of Ukraine
4, Akademika Bohomoltsia Str., Kyiv, Ukraine, 01024
jovalentych@biph.kiev.ua

CONVERGENT STRUCTURAL INTERACTIONS OF LONG NON-CODING RNAs (LNCRNAs) IN VARIOUS RAT MODELS OF CARDIOVASCULAR STRESS: COMMON MECHANISM, DISTINCT BIOLOGICAL TARGETS

Background/Aim. Long non-coding RNAs (lncRNAs) are candidate regulators of cardiac stress responses, yet their sequence-level mechanisms remain undercharacterised. Extending our prior computational analysis of rat cardiac hypoxia [1], we systematically characterised triplex-forming and G-quadruplex-forming lncRNA candidates across four independent rat cardiovascular stress models. **Methods.** 52 differentially expressed lncRNAs ($p_{adj} < 0.05$, $|\log_2 FC| \geq 1-2$; DESeq2) from four GEO RNA-seq datasets – GSE245300 (hypobaric hypoxia [2]), GSE284606 (ischaemic preconditioning [3]), GSE186989 (SU5416/hypoxia PAH + chrysin [4]) and GSE317340 (donation after circulatory death, male/female/OVX [5]) – were analysed using canonical spliced transcript sequences (mRatBN7.2/Ensembl 108), rgt-TDF v1.0.2 (promotertest; -15 – $+20$), RNAfold 2.4.7, and G4Hunter/QGRS quadruplex detection. **Results.** 29 of 52 lncRNA candidates showed significant triplex-forming potential ($p < 0.05$); three appeared in two or more independent datasets, including Nupr111 – upregulated in both PAH right ventricle and donation-after-circulatory-death left ventricle. Seven candidates combined triplex activity with consensus G-quadruplex domains, suggesting dual regulatory capacity. Exploratory comparison of Su/Hx and Su/Hx + chrysin right ventricular transcriptomes revealed no statistically significant differential lncRNA expression after multiple-testing correction ($n = 4$; limited power); however, 32 lncRNAs showed nominal expression changes ($p < 0.05$), including candidates dysregulated in Su/Hx vs Control, suggesting preliminary evidence of lncRNA profile responsiveness to pharmacological modulation of the pathological state. **Conclusions.** RNA-DNA triplex formation is a convergent lncRNA regulatory mechanism across diverse forms of cardiac hypoxia. Cross-dataset candidates with dual triplex/G4 activity – particularly Nupr111 – represent priority targets for functional validation. lncRNA profiles show preliminary responsiveness to pharmacological modulation, warranting larger-cohort studies.

Keywords: lncRNA, RNA-DNA triplex, G-quadruplex, cardiac hypoxia, PAH, ischaemic preconditioning, DCD, Nupr111, chrysin, computational biology.

REFERENCES:

1. Hegel-Valentych YY et al. *Biotechnol 21st Cent: Proc. 20th Conf.* 2026;283.
2. Wang J et al. *Sci Rep.* 2024; **14**:10206.
3. Khan AW et al. *Eur Heart J Open.* 2025; **5**(5):oeaf124.
4. Kobayashi T et al. *Int J Mol Med.* 2022; **49**(5):69.
5. Helmer A et al. *Biol Sex Differ.* 2026.

Received: 08.06.2026; Accepted: 08.09.2026; Published: 29.09.2026

Citation: Hegel-Valentych Y.Y., Khetsuriani M., Shysh A.M. (2026) Convergent structural interactions of long non-coding RNAs (lncRNAs) in various rat models of cardiovascular stress: common mechanism, distinct biological targets. *Biopolymers & Cell*, Special issue(42), 33. <https://doi.org/10.7124/bc.000B5A>

© Publisher PH "Akademperiodyka" of the NAS of Ukraine, 2026. This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted reuse, distribution, and reproduction in any medium, provided the original work is properly cited