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# The origin and functional evolution of long non-coding RNAs

## Results in Brief

### Function and evolution of long non-coding RNAs

Long non-coding RNAs (lncRNA) represent numerous non-protein coding transcripts longer than 200 nucleotides. European scientists studied the function and evolution of lncRNA to understand its significance for mammalian species.



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lncRNAs are a heterogeneous class of RNA implicated in many biological processes including the inactivation of sex chromosomes, imprinting and the regulation of gene expression. At present, lncRNAs are the least studied class of genomic transcripts. The EU-funded EVOLNCRNAS (The origin and functional evolution of long non-coding RNAs) fellowship investigated critical aspects of the biology of lncRNAs.

Researchers focused on the study of lncRNA expression throughout mammalian development. They created a large-scale transcriptomics resource covering the development of major mammalian lineages. The aim was to understand lncRNA creation as well as identify their function and contribution to genome evolution.

Expression development profiles covered males and females of seven mammalian species including humans, rats, and chicken for nine major organs (brain,

cerebellum, liver, heart, kidney, ovary, testis, placenta and decidua). Sampling started as soon as the organs primordiums could be identified and continued all the way through adulthood at different developmental timepoints. This dataset provided a unique gene expression profile throughout mammalian development.

These libraries helped researchers identify the sets of lncRNAs that are expressed throughout development and those that are developmentally regulated, comparing them to such regulators as transcription factors. Comparison of lncRNA expression with protein-coding genes whose functions are known led to the prediction of those lncRNA functions that are involved in development.

Importantly, researchers identified lncRNAs that together with protein-coding genes underlie phenotypic differences between mammalian species. This study within a developmental framework revealed the potential functions of a large fraction of genes as important regulators and contributors to mammalian phenotypes.

Additionally, project members studied lncRNA expression in the developing placentas of six mammalian species and a set of 30 human placentas. Study outcomes are expected to aid in correlating lncRNA expression with different placenta morphologies and pregnancy outcomes.

## Keywords

[Long non-coding RNA](#)

[EVOLNCRNAS](#)

[mammalian development](#)

[transcriptomics](#)

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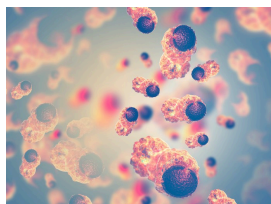
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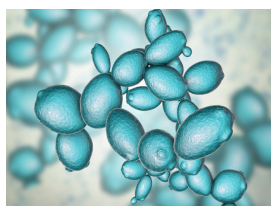
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### Project Information

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Project closed

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#### **EU contribution**

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