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Re-write the textbooks: transcription is bidirectional

A genome wide study of transcription in yeast redefines the concept of promoters

Heidelberg/Hinxton, 25 January 2009 - Genes that contain instructions for making proteins make up less than 2% of the human genome. Yet, for unknown reasons, most of our genome is transcribed into RNA. The same is true for many other organisms that are easier to study than humans. Researchers in the groups of Lars Steinmetz at the European Molecular Biology Laboratory (EMBL) in Heidelberg, Germany, and Wolfgang Huber at the European Bioinformatics Institute (EMBL-EBI) in Hinxton, UK, have now unravelled how yeast generates its transcripts and have come a step closer to understanding their function. The study, published online in *Nature*, redefines the concept of promoters (the start sites of transcription) contradicting the established notion that they support transcription in one direction only. The results are also representative of transcription in humans. Investigating all transcripts produced in a yeast cell, the scientists found that most regions of the yeast genome produce several transcripts starting at the same promoter. These transcripts are interleaved and overlapping on the DNA. In con-

trast to what was previously thought, the vast majority of promoters seem to initiate transcription in both directions.

Not all of the produced transcripts are stable, many are degraded rapidly making it difficult to observe what they do. While some of the RNA molecules might be 'transcriptional noise' without function, other transcripts control the expression of genes and production of proteins. The act of transcription itself is also likely to play an important role in regulation of gene expression. Transcribing one stretch of DNA might either help or in other cases interfere with the transcription of a gene close by. Moreover, transcripts without a current purpose can serve as 'raw material for evolution' and acquire new functions over time.

The results shed light on the complex organisation of the yeast genome and the insights gained extend to transcription in humans. A better understanding of transcription mechanisms could find application in new technologies to tune gene regulation in the future. ●

Source Article

Xu, Z., Wei, W., Gagneur, J., Perocchi, F., Clauder-Münster, S., Camblong, J., Guffanti, E., Stutz, F., Huber, W. & Steinmetz, L.M. Bidirectional promoters generate pervasive transcription in yeast, *Nature*, 25 January 2009

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The European Bioinformatics Institute (EBI) is part of the European Molecular Biology Laboratory (EMBL) and is located on the Wellcome Trust Genome Campus in Hinxton near Cambridge (UK). The EBI grew out of EMBL's pioneering work in providing public biological databases to the research community. It hosts some of the world's most important collections of biological data, including DNA sequences (EMBL-Bank), protein sequences (UniProt), animal genomes (Ensembl), three-dimensional structures (the Macromolecular Structure Database), data from microarray experiments (ArrayExpress), protein-protein interactions (IntAct) and pathway information (Reactome). The EBI hosts several research groups and its scientists continually develop new tools for the biocomputing community.

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