

## Breaking News on Laboratory Equipment

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# DNA flexibility reveals clues about gene expression

By David Robson

05/02/2008- **A new technique that analyses the structural characteristics, and not the sequence, of DNA has revealed previously unknown areas of the human genetic code responsible for gene expression.**

Promoters are an important component of the genome that play a crucial role in determining when a gene will be expressed to produce an effect in the body. By finding where promoters for a gene occur in the genetic code, scientists will be able to investigate which proteins bind to these sites to promote or inhibit gene expression, and how this process can be controlled artificially.

*"A gene is important not only for what it does, but where and when it does it,"* David Torrents, a member of the team from the Institute for Research in Biomedicine in Barcelona, Spain, told LabTechnologist.com.

Previous genetics research had focused on analysing the sequence of nucleotides found in the genetic code to find common patterns that may signal the presence of a particular type of gene. However, according to Torrents, the code of promoters varies too much from region to region to be able to find any meaningful signals in this way.

*"This technique produced a lot of false positives,"* he said.

Instead, the researchers tried to find common similarities in the physical characteristics of the structure of the DNA molecule at promoter regions. The team built large computational simulations of DNA molecules based on their chemical composition to model the physical structure throughout the genome.

The research, published in the last issue of *Genome Biology*, shows that, at promoter regions, the DNA exhibited a common characteristic in the flexibility of the molecule which could be used to track down further promoters in the human genome.

*"Normally DNA is very well packed in the nucleus of the cell,"* explained Torrents. *"But when a gene is expressed, it must be unpacked and the double helix must be opened to allow the proteins to access the gene. The promoter regions must be flexible so the proteins can unwrap and unpack these regions."*

The simulations modelled the genome to atomic detail, analysing the structure of three billion nucleotides. It was a Herculean computational task that required the processing powers of the MareNostrum supercomputer at the Barcelona Supercomputing Centre.

Torrents claims that, while this technique had been applied before to study the genome of bacteria, this is the first time it has been used for a more complicated organism. *"The structure of DNA has usually been ignored as it is difficult to analyse. Our research is very important as it's the starting point for a new way of looking at the genome,"* he said.

Once more promoter regions have been identified successfully, geneticists will know which areas of the genome to target in future research. Many cancers are caused by the poor regulation of the expression of genes that control cell growth, and it is hoped that by localising the promoters for these genes scientists will be able to find therapies to control this poor regulation.

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