Search for the 'on' switches may reveal genetic role in development and disease

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A new resource that identifies regions of the human genome that regulate gene expression may help scientists learn about and develop treatments for a number of human diseases, according to researchers at Duke's Institute for Genome Sciences & Policy (IGSP).

"The majority of DNA in our bodies is packaged, or tightly structured," said Gregory Crawford, Ph.D., a researcher in the IGSP and one of the senior investigators on this study. "Our goal was to identify the areas of DNA across the entire genome that are not packaged, because we know those are the regions that are important in regulating gene activity."

The researchers published their findings in the January 25, 2008 issue of the journal Cell. The study was funded by the Duke IGSP and the National Human Genome Research Institute.

They combined two known processes to look at regulatory regions across the whole human genome, Crawford said.

"We used an enzyme called DNase that has been known for decades to preferentially identify unpackaged regions of DNA," he said. "In this study, we identified all unpackaged regions within the entire genome using two extremely efficient methodologies: microarrays and sequencing."

Microarrays are glass slides on which scientists can simultaneously look at millions of short pieces of DNA. New sequencing technologies are

able to determine the genetic code of millions of DNA fragments. Together, these tools generated guides to understanding the location of the unpackaged regions, and the researchers compared the results found using each method and found high levels of agreement.

By combining the two methods, the researchers were able to scan the entire genome efficiently.

“Scientists have used similar methods to look at tiny portions of the genome in the past, but ours is the first technology to really allow researchers to look at the whole genome, so we can see all of the areas where gene regulation occurs,” said Terrence Furey, Ph.D., a researcher in the IGSP and co-senior investigator on this study. “Identifying these sites may help us understand the biological basis for gene regulation expression patterns in different cell types. We'll also compare patterns within and across species, in response to external stimuli and in diseased tissues.”

The researchers said they looked at normal cells for this study because in order to understand anything about disease or the aging processes, it's important to first understand what a normal cell looks like.

“Perhaps in the future, this data resource could help researchers learn to turn a harmful gene off or increase the expression of helpful ones,” Furey said.

Source: Duke University Medical Center