Sequencing method yields fuller picture

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University of Southern California biologists have developed a method for sequencing both chromosomes of an organism.

Their study appears in a recent issue of *Genome Research*.

The statistical method is significant because when researchers announce they have sequenced an organism's genome, they really mean that they have created a mosaic of two chromosomes, said USC computational biologist Lei Li.

"A mosaic means it's not real," Li said.

Lead author and former graduate student Jong Hyun Kim, advised by Li and USC University Professor Michael Waterman, was able to infer a complete sequence of the chromosomes of Ciona intestinalis, a marine invertebrate, from existing sequencing data.

Kim's method exploited the high rate of genetic mutations in the organism. Other organisms with high genetic variability, such as certain fish, also may be suitable.

Because the human genome has a relatively low mutation rate, the method cannot be applied to people.

However, Kim said, the method might be useful in sequencing parts of the human genome that display high variability.

As a by-product of their analysis, the researchers added to growing evidence that so-called junk DNA may have a function after all.

Recent studies have shown that junk DNA expresses proteins which may regulate gene function, and that sections of junk DNA have been highly conserved during evolution, suggesting that they play an important role.

The Genome Research study confirms that many short sections of junk DNA are highly conserved, Li and Kim said.

Source: University of Southern California

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