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Gene deserts bear fruit

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The evidence that 'junk' DNA contains highly conserved sequences that have a regulatory function is mounting: their genetic and (controversial) commercial value had been guessed at as long ago as 1989. In the October 17 *Science*, Marcelo Nobrega and colleagues at the US Department of Energy Joint Genome Institute examined the 'gene deserts' flanking the human DACH gene and report that they contain several important enhancer functions that have been conserved across species in over a billion years of parallel evolution (*Science* 2003, **302**:413).

Nobrega *et al.* compared human DACH flanking sequences with mouse genomic DNA and by combining additional genome comparison information from distantly related vertebrates such as frog, zebrafish, and pufferfish, narrowed the number of conserved sequences from 1098 to 32. Nine of these were cloned upstream of the mouse heat shock protein 68 minimal promoter driving beta-galactosidase expression. These were used to create transgenic mice whose subsequent development revealed enhancer effects of the elements consistent with DACH endogenous gene expression. Genes flanking the DACH orthologues vary with species, but the adjacent gene deserts were found to be maintained.

"The size of genomic regions believed to be functionally linked to a particular gene may need to be expanded to take into account the possibility of essential regulatory sequences acting over near-megabase distances," conclude the authors.

References

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