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Barking up the right tree

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The value of comparative genome analysis is becoming increasingly apparent in the derivation of gene structure and regulation data for use in developing treatments for human diseases - both inherited and acquired - and for understanding phylogeny and the mechanisms of evolution. Whole genome sequencing with multiple genome coverage is expensive, and the decision to sequence a specific organism involves questions of quantity versus quality of genome sequencing in the first world and questions of cost in the developing world. In the September 26 Science, Ewen Kirkness and colleagues at the Institute for Genomic Research assess the data obtained from sample sequencing of the dog genome that may provide answers to encourage inhabitants of both worlds (*Science,* 301:1898-1903, September 26, 2003).

Kirkness et al. assembled 6.22 million sequence reads from the DNA of a standard poodle, and contigs and singletons were ordered with the scaffolder Bambus to yield 1.5x sequence coverage. Randomness and fidelity of assembly were assessed using bacterial artificial chromosomes and revealed 77% coverage, with 31% of the sequence identified as being repetitive.

"One of the most important discoveries is that even though the dog genome was surveyed at relatively low coverage (1.5x), it annotates slightly more human transcripts (29,563) and genes (18,473) than does the more complete 8x mouse sequence (29,529 transcripts, 18,311 genes)," write Stephen O'Brien and William Murphy at the National Cancer Institute in an accompanying article in the same issue.

Comparison with human and mouse genomes revealed a faster rate of mutation in the latter, and the prior divergence of dog to mouse and human. More than 4% of noncoding intergenic regions were observed to be conserved among the three species.

"Because one would predict that functional [intergenic conserved sequence blocks]... would be constrained like gene exons, their decay in mouse (twice the rate of that in human or dog) suggests that a fair portion may be constrained by non-functional forces," continue O'Brien and Murphy.

"Our work with 1.5x sequence coverage of the dog genome has highlighted some of the insights, potential applications, and limitations that derive from survey sequencing... We have shown that 1.5x coverage of a genome provides a valuable, cost-effective resource for both organism-specific biology and comparative genomes," conclude Kirkness et al.

References

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