IMPRINTING

Transcriptomics delivers

A study using transcriptomics has provided new insights into the extent and complexity of genomic imprinting.

Babak and colleagues reciprocally crossed two wild-type mouse strains, extracted total RNA from embryos, made strand-specific cDNAs and carried out high-throughput sequencing. By comparison with the mouse reference genome the authors detected over 160,000 expressed SNPs, a subset of which showed parent-of-origin bias. Combining information from multiple SNPs per transcript provided a sensitive means to identify potentially imprinted transcripts.

Unlike other methods, this approach does not rely on poly(A) priming for cDNA synthesis, and so is not limited to detecting polyadenylated transcripts. It also avoids several limitations of microarray methods, notably the need for prior knowledge of SNP and transcript sequence, and the uncertainty associated with probe cross-hybridization.

An important insight from this study is that our understanding of imprinted loci is incomplete. At several known imprinted loci the authors identified additional imprinted non-coding RNAs, and found evidence of more extensive transcription of known imprinted non-coding RNAs than was previously recognized. This study also reveals new imprinted protein-coding transcripts, both near to previously identified imprinted genes and at other positions in the genome.

Increasing the number of sequencing reads, assessing additional developmental stages and tissues, and surveying other species using this approach promises to add further detail to our currently limited understanding of the functions and mechanisms of genomic imprinting.

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ORIGINAL RESEARCH PAPER Babak, T. *et al.* Global survey of genomic imprinting by transcriptome sequencing. *Current Biol.* **18**, 1735–1741 (2008)