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Life after ESTs

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Expressed sequence tags (ESTs) have given researchers a quick if dirty look at the coding potential of the human genome. But now in the November *Nature Genetics*, Penn *et al.* use microarray experiments to conclude that the human genome project will uncover many genes not previously discovered by EST sequencing (*Nat Genet* 2000, **26**:315-318). They scan 350 Mb of finished and draft human sequence using three different gene-finding algorithms. Open reading frames (ORFs) predicted by at least two of the programs were amplified and spotted onto glass slides. Of these 9498 ORFs, 31% are completely novel and 29% are similar, but not identical, to sequences in public databases. Approximately one half of the ORFs are expressed in at least some of the ten tissues and cell types queried by the microarray. Some of these apparently novel exons may be extreme ends of genes that have already been captured as ESTs, but many of the genes will probably have only be found by genomic sequencing.

References

1. Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence.
2. *Nature Genetics*, [<http://www.nature.com/ng/>]