PublisherInfo				
PublisherName	:	BioMed Central		
PublisherLocation		London		
PublisherImprintName	:	BioMed Central		

Counting vertebrate microRNAs

ArticleInfo		
ArticleID	:	4718
ArticleDOI	:	10.1186/gb-spotlight-20030310-01
ArticleCitationID	:	spotlight-20030310-01
ArticleSequenceNumber	:	70
ArticleCategory	:	Research news
ArticleFirstPage	:	1
ArticleLastPage	:	2
ArticleHistory	:	RegistrationDate: 2003–3–10OnlineDate: 2003–3–10
ArticleCopyright	:	BioMed Central Ltd2003
ArticleGrants	:	
ArticleContext	:	130594411

Jonathan B Weitzman Email: jonathanweitzman@hotmail.com

MicroRNAs (miRNAs) are short non-coding RNAs that play a role in the control of gene expression. In the March 7 Science, Lee Lim and colleagues at the Massachusetts Institute of Technology report attempts to predict the total number of miRNAs in the human genome (*Science* 2003, **299**:1540). They used a computational program called MiRscan to identify miRNA genes in vertebrate genomes by evaluating conserved stem loop structures. Around 15,000 potential stem loop structures were found in the human genome. MiRscan found a set of 188 human loci with high scores. This set includes 81 (74%) out of 109 known human miRNAs. Lim *et al.* extrapolate to predict that the upper limit for the number of human miRNAs is 255 genes. Which implies that there are only another 40 or so miRNA genes yet to be found. When all these have been tracked down, the challenge will be to work out the precise functions of this large gene family.

References

- 1. An abundant class of tiny RNAs with probable regulatory roles in Caenorhabditis elegans.
- 2. Science, [http://www.sciencemag.org]
- 3. Massachusetts Institute of Technology , [http://www.mit.edu]

This PDF file was created after publication.