# Modern-looking lampreys 'older' than thought

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It had been assumed up until Lthe late twentieth century that cyclostomes, living jawless vertebrates that include the lamprey and hagfish, evolved from armoured jawless vertebrates that supposedly lived from the Ordovician to the Devonian periods, 490 to 358 Ma within the evolutionary/ uniformitarian timescale.1 Furthermore, lamprevs and hagfish were supposed to have diverged from a common ancestor sometime in the early Mesozoic about 250 Ma ago.<sup>2</sup> Then lampreys and hagfish were

discovered in 'older' rocks from the Carboniferous period. Just recently a lamprey was discovered from the late Devonian period, considered 360 Ma.<sup>3</sup> This discovery pushes back the oldest dates for lampreys by about 35 Ma. The most amazing aspect of the new fossil is that it looks *surprisingly modern*, indicating little or no change in lampreys for 360 Ma! Janvier is astonished:

'This shows that lamprey morphology has been astonishingly stable for 360 Myr, and proves that lampreys and hagfishes had already diverged by late Devonian times, earlier than previously thought.'<sup>2</sup>

Furthermore, DNA and RNA sequence data supposedly shows that lampreys and hagfish are 'sister groups', while morphological and physiological aspects tell researchers that they evolved from different groups.<sup>2</sup> Their evolution now is thought to have occurred *before* the armored jawless vertebrates.<sup>4</sup> So, there is much confusion over the supposed evolution of cyclostomes.

Photo courtesy www.wikipedia.org



Mouth of a River Lamprey.

Not only does the new discovery push back the supposed evolution of both lampreys and hagfish, but it also shows *little change* in all that time. Maybe, the fossil record is trying to tell us that hagfish, lampreys and various armoured, extinct fish are independent creations.

#### References

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- 2. Janvier, ref. 1, p. 923.
- Gess, R.W., Coates, M.I. and Rubidge, B.S., A lamprey from the Devonian period of South Africa, *Nature* 443:981–984, 2006.
- 4. Janvier, ref. 1, p. 924.

## Myriad mechanisms of gene regulation

### Alex Williams

The recent ENCODE pilot study report on the human genome showed astonishing complexity in the *structure* of the information stored on, in and around the DNA molecule.<sup>1</sup> Now come two new studies that show astonishing complexity in the *function* of the information copying and usage systems in cells.

### **Ingenious transcripts**

The first step in *using* the complex information stored on the DNA molecule is to *transcribe* (copy) it onto a messenger RNA molecule (mRNA). Transcription is carried out by a molecular machine called RNA polymerase (RNAP) which attaches to the DNA strand at the START end of a gene and works its way, nucleotide by nucleotide, to the STOP end, producing an exact complimentary copy of each nucleotide at each step in the chain. More than one RNAP can work on a particular gene at any one time, and a recent study by an international team working on the mechanics of transcription found that in a culture of human cells there were, on average, two RNAPs per gene.<sup>2</sup>

The rate of transcription often needs to vary—for example, in response to environmental stress or a fight-or-flight threat situation—and one might think that the best way to increase the rate would be to increase either the number of copying machines working on the gene, or to increase the speed at which the machines progress along the DNA. Surprisingly, cells use neither of these options.

In a normal metabolic state, RNAP copying seems stunningly inefficient. Only about 1 in 90 transcripts produce mature messenger RNA; the majority are aborted. Furthermore, the measured step-by-step transcription rate goes about twice as fast as previously measured for whole transcript