Mode and tempo of promoter evolution as observed in the Paramecium aurelia species complex

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Associate Editor:

Abstract

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Key words: *cis*-regulatory regions, gene duplicates, paralogous genes, Paramecium, promoter evolution, TSS profiling.

Introduction

Investigation across diverse eukaryotes has drawn attention to the important role of *cis*-regulatory sequences in the evolution of gene expression (Siepel and Arbiza, 2014; Wittkopp and Kalay, 2011; Wittkopp *et al.*, 2008). However, the *cis*-regulatory sequence differences that accompany—or indeed underpin—species divergence remain largely unknown. One plausible explanation for this is the difficulty in predicting *cis*-regulatory regions from genomic sequence alone. Accurate estimation of promoter positions requires empirical, usually functional genomic evidence. At present, the best high-throughput approach to identify promoters at genome-scale is Transcription Start Site (TSS) profiling, which includes CAGE (Murata *et al.*, ????) and RAMPAGE (Batut and Gingeras, 2013), among others. While TSS profiling methods differ among themselves methadologically, these methods capture the 5'-ends of capped mRNAs, sequence their corresponding cDNAs and align the reads to the genome to identify the TSSs present within a given transcriptome. Clustering gene-adjacent TSSs defines a promoter, transcription start region (TSR), at single base-pair resolution, thereby providing genomic locations for *cis*-regulatory regions within a species (Lenhard *et al.*, 2012; Rach *et al.*, 2009). TSS profling studies in a variety of model organisms has demonstrated that the shape of TSS distributions (*i.e.* promoter shape) at promoters is related to the promoter class and correlates with the function of the associated gene (Carninci *et al.*, 2006; Hoskins *et al.*, 2011; Raborn *et al.*, 2016; Rach *et al.*, 2009). In addition, recent work indicates that promoter shape is itself a quantitative trait (Schor *et al.*, 2017), which has

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important implications for the understanding of the evolution of *cis*-regulatory regions.

Demographic structure

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Methods

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Results

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Discussion

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1) Item 1
2) Item 2
3) Item 3

- Consider a fall in population induced by a decline in the number of births in the economy, taking as given mortality and migration.
- It is well known that a lower population growth raises the capital–labor ratio in the Solow–Swan growth model.
- The same property holds in Diamond's (1965) overlapping generations model, and it enhances welfare as long as the economy is dynamically efficient; i.e., when the interest rate exceeds the population growth rate.

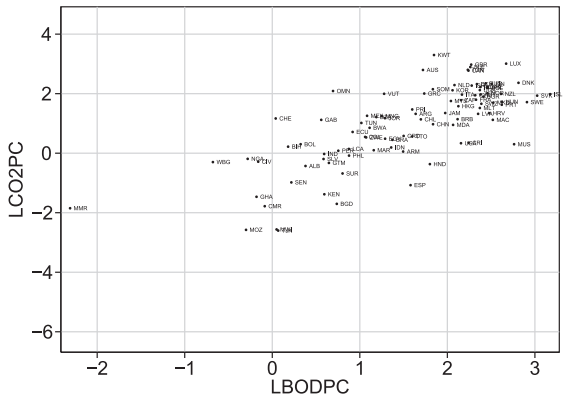

FIG. 1. Fluctuations in Cohort Size N_t over Generations.

A similar trend is observed in the United States and advanced European countries (Gustafsson and Kalwij, 2006), and also in Canada, Australia, and New Zealand (Sardon, 2006). Interestingly, as pointed out by Bongaarts and Feeney (1998), even when the cohort's lifetime fertility rate (the number of children a mother has in her lifetime) does not fall, the delayed childbearing alone leads to a decline in the number of childbirths, measured by the total period fertility rates (TPFRs).

Model

Demographic structure

i.e.:

$$\lambda_t = \begin{cases} 0, \, t < 0, \\ \lambda, \, t \geq 0. \end{cases} \tag{1}$$

Table 1. SH test results on nuclear and mitochondrial phylogenetic trees

Sequence data	Tree	$-\ln L$	SH test P-value
mtDNA	mtDNA	−109219.5	0.5
mtDNA	Nuclear	−61720.8	<0.00001
Nuclear	mtDNA	−113033.1	<0.00001
Nuclear	Nuclear	−60699.9	0.5

where C is a constant term defined as $C \equiv \beta\log\beta-(1+\beta)\log(1+\beta)+\beta\log A\alpha+(1+\beta)\log A(1-\alpha)$. Similarly, long-term welfare in the benchmark economy ($\lambda=0$) can be written as:

$$U^* = (1+\beta)\log[A\alpha(k^*)^{2\alpha-1}+(k^*)^{\alpha}]-\beta(1-\alpha)\log k^*+C. \quad (2)$$

Supplementary Material

Supplementary tables S1?S7 and figures S1?S11 are available at Molecular Biology and Evolution online (http://www.mbe.oxfordjournals.org/).

Acknowledgments

The authors gratefully acknowledge the help of Robert Policastro and Gabriel Zentner at Indiana University Bloomington for technical assistance and use of laboratory facilities.

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