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#### Unstable tandem repeats in promoters confer transcriptional evolvability.

Vinces MD, Legendre M, Caldara M, Hagihara M, Verstrepen KJ

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##### Walter Schaffner

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Developmental Biology

New Finding

**I find this article fascinating because it reveals another function for "junk" DNA. In yeast, short tandem repeats of the micro-satellite-type are associated with the promoter regions of approximately 25% of all genes. The authors show that variation in repeat length affects the efficiency of gene transcription. Due to the instability of such repeats, they can evolve rapidly and, thus, act as "tuning knobs" for changes of gene expression.**

It has long been known that transcriptional regulatory sequences (namely, "enhancers") in viruses are often organized as tandem repeats. These repeats, which typically contain binding sites for transcription factors, can be generated via duplication upon selection for increased transcription activity. Regulatory sequences of mammalian genes (enhancers/silencers /promoters that contain binding sites for positively or negatively acting transcription factors) typically are not organized as repeats, but cases have been described where promoter-associated micro- or mini-satellites influence gene expression. The article presented here represents a thorough analysis of this effect in yeast. The authors find that 90% of the upstream repeats do not bind transcription factors. Most, but not all, such repeats are A + T rich, located about 200 base pairs upstream of the translational start codon, and apparently affect gene activity by nucleosome positioning. By comparing *Saccharomyces cerevisiae* strains and also looking at related yeast species, they find that expression plasticity is highly correlated with the presence of variable promoter repeats. This keeps us wondering why not all organisms contain such mechanisms to ensure expression plasticity and, similarly, why the other 75% of genes in yeast are not involved in this process. Perhaps there are constraints, especially in sophisticated multicellular organisms, that forbid evolutionary changes that are too rapid. Alternatively, transcriptional programs can also be affected by changes in the transcription factors themselves, and this may be a contributing factor. We have found that repeats within coding regions (such as polyglutamine stretches encoded by CAG repeats), as present in a number of eukaryotic transcription factors, can influence the properties of such regulators (see ref {1}, on which I am an author).

References: {1} Gerber et al. *Science* 1994, 263:808-11 [[PMID:8303297](#)].

**Competing interests:** None declared

Evaluated 19 Jun 2009

[How to cite this evaluation](#)**Yves Van de Peer**Ghent University, Belgium  
Developmental Biology

**In this paper, Vinces et al. show that tandem repeats in promoters, often referred to as 'junk DNA', might actually have important biological functions such as facilitating adaptation to changing environments.**

Vinces et al. discovered that stretches of tandem repeats in the nucleosome-free region directly upstream of genes influence the activity of neighboring genes. The repeats determine how tightly the local DNA is wrapped around the nucleosomes, and this packaging structure dictates to what extent genes can be activated. Interestingly, tandem repeats are very unstable and the number of repeats changes frequently when the DNA is copied. These changes affect the local DNA packaging, which in turn alters gene activity. In this way, unstable 'junk' DNA allows fast shifts in gene activity, which may allow organisms to tune the activity of genes to match changing environments. To test their theory that such repeats are important for adaptation, the researchers conducted a complex experiment aimed at mimicking biological evolution, using yeast cells. Their results show that when a repeat is present near a gene, it is possible to select yeast mutants that show increased activity of this gene. However, when the repeat region was removed, this fast evolution was impossible. This suggests that only cells with the repeats would be able to swiftly adapt to changes in the environment. A preliminary analysis of Homo sapiens promoters reveals a tandem repeat distribution that is comparable to that of yeast, suggesting that the mechanism described might be a universal one in eukaryotic organisms.

**Competing interests:** None declaredEvaluated 26 Jun 2009 **NEW**[How to cite this evaluation](#)**Faculty Comments & Author Responses****How to cite the Faculty of 1000 Biology evaluation(s) for this paper****1) To cite all the evaluations for this article:**Faculty of 1000 Biology: evaluations for Vinces MD et al *Science* 2009 May 29 324 (5931) :1213-6 <http://www.f1000biology.com/article/id/1161222/evaluation>**2) To cite an evaluation by a specific Faculty member:**Walter Schaffner: Faculty of 1000 Biology, 19 Jun 2009 <http://www.f1000biology.com/article/id/1161222/evaluation>Yves Van de Peer: Faculty of 1000 Biology, 26 Jun 2009 <http://www.f1000biology.com/article/id/1161222/evaluation>