

## Conservation of non-consensus nucleotides in transcription factor binding sites

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The phenomenon of conserved non-consensus nucleotides was observed by our colleagues [1]. It has several explanations:

- Transcription factor binding sites overlap and conservative "non-consensus" is consensus for unknown regulatory elements;
- Replacement of a non-consensus base with a consensus one changes the affinity of the regulator to the site, and hence the level of gene transcription. That is, if a non-consensus base once began to provide the desired level of regulation, then it cannot "move" to another position.

In this work we are trying to find conservative non-consensus nucleotides or positions in orthologous sites, compare their conservation with neutrally (or almost neutrally) evolving elements and try to explain this phenomenon. We considered the CspA regulator, which provides a transcriptional response to the appearance of fast-absorbing hydrocarbons in the medium [2]. In order to estimate the conservation of non-consensus nucleotides, we compared their conservation with conservation of the same nucleotides in the synonymous positions of corresponding genes. Our approach did not reveal non-consensus nucleotides to be more conserved but it seems to be caused by insufficient sites alignments. We plan to obtain larger sites alignments and repeat our approach.

One of the explanations of conserved non-consensus nucleotides in sites is the sites need to keep certain affinity to the transcriptional factor, i. e. certain weight. In order to estimate weight conservation in orthologous sites, we compared their weight standard deviation with those of randomized sites. The standard deviation of real sites' weight appeared to be lower but such an effect can be explained both with our hypothesis of sites' weight kept at a specific level due to non-consensus nucleotides and with common standard deviation growth after randomizing. Next, we are going to distinguish these two effects by changing a weight threshold for sites.

### Источники и литература

- 1) Kotelnikova, E., Makeev, V., Gelfand, M.: Evolution of transcription factor DNA binding sites. *Gene* 347(2):255-63 (2005)
- 2) RegPrecise, <http://regprecise.lbl.gov/RegPrecise/index.jsp>