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ТРАНСКРИПТОМИКА

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НЕОБЫЧНАЯ ЗАВИСИМОСТЬ МЕЖДУ ЭКСПРЕССИЕЙ ГЕНОВ
И ОТРИЦАТЕЛЬНЫМ ОТБОРОМ У ИНФУЗОРИЙ РОДА *Euplotes*¹

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У большинства исследованных организмов экспрессия генов связана с рядом эволюционных особенностей, относящихся к белокодирующему последовательностям. В частности, экспрессия генов положительно коррелирует со средней интенсивностью отрицательного отбора и влияет на использование кодонов. Нами изучена связь между экспрессией генов и паттернами отбора у двух видов ресничных простейших рода *Euplotes*. Мы обнаружили, что на использование кодонов влияет экспрессия генов в этих организмах, что указывает на дополнительные эволюционные ограничения на возникновение мутаций в сильно экспрессируемых генах по сравнению с генами, экспрессируемые с меньшей скоростью. В то же время, на уровне синонимичных и несинонимичных замен мы наблюдаем более сильное ограничение на гены, экспрессируемые с более низкой скоростью, по сравнению с генами с более высокой скоростью экспрессии. Наше исследование дополняет дискуссию об общих закономерностях эволюции и ставит новые вопросы о механизмах контроля экспрессии генов у инфузорий.

Ключевые слова: экспрессия генов, отрицательный отбор, инфузории, ресничные простейшие, *Euplotes*, эволюция белокодирующих последовательностей

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Unusual Dependence between Gene Expression and Negative Selection in *Euplotes***M. A. Moldovan¹, * and S. A. Gaydukova²**¹*Skolkovo Institute of Science and Technology, Moscow, 121205 Russia*²*Faculty of Bioengineering and Bioinformatics, Lomonosov Moscow State University, Moscow, 199911 Russia***e-mail: mika.moldovan@gmail.com*

In most of the studied organisms, gene expression is associated with a number of evolutionary features pertaining to the protein-coding sequences. In particular, gene expression positively correlates with the average intensity of negative selection and influences codon usage. Here, we study the connection between gene expression and selection patterns in two species of ciliate protists of the genus *Euplotes*. We find that codon usage is influenced by gene expression in these organisms, pointing at additional evolutionary constraints on mutations in heavily expressed genes relative to the genes expressed at lower rates. At the same time, at the level of synonymous vs. non-synonymous substitutions we observe a stronger constraint on the genes expressed at lower rates relative to those with higher rates of expression. Our study adds to the discussion about the general evolutionary patterns and opens new questions about the mechanisms of control of gene expression in ciliates.

Keywords: gene expression, negative selection, infusoria, ciliates, *Euplotes*, coding constraint