Lux operon conservation patterns reveal specific structural properties relevant to functioning of the bacterial bioluminescent system

Anna Deeva^{*†1}, Evgenia Zykova^{2,3}, Elena Nemtseva^{4,1}, and Valentina Kratasyuk^{1,4}

¹Siberian Federal University (SibFU) – 79 Svobodny pr., 660041 Krasnoyarsk, Russia, Russia

²Institute of Cell Biophysics RAS (ICB RAS) – Institutskaya 3, Pushchino, Moscow region, 142290, Russia, Russia

³State Institute of Information Technologies and Telecommunications (SIITT "Informika") – Bryusov lane 20, Moscow, 125009, Russia, Russia

⁴Institute of Biophysics SB RAS, Federal Research Center "Krasnoyarsk Science Center SB RAS" (IB SB RAS) – Akademgorodok, Krasnoyarsk, 660036, Russia, Russia

Abstract

Continuous light production in luminous bacteria is maintained by coexpressed and conserved set of genes forming lux operon. Due to their joint arrangement and regulation, selection pressure acts on the whole region. Evaluation of lux operon conservation might contribute to explain the functional characteristics of bioluminescent system driven by evolution and speciation of luminous bacteria.

We analyzed complete genomes, scaffolds and contigs of 23 species of luminous bacteria from NCBI database in order to identify amino acid sequences of enzymes involved into bioluminescent reaction, namely bacterial luciferases and oxidoreductases. Phylogenetic analysis of the obtained dataset showed that luciferase sequences split into two clades that is in good agreement with the experimentally characterized groups of "fast" and "slow" luciferases, depending on decay rate of light emission. The distribution of the conservative residues was found to differ for luciferase subunits reflecting their distinct functions. The substantial part of the conservative residues of the alpha-subunit is located in the active site, while on the beta-subunit it is involved into intersubunit interaction. This confirms the role of the latter in stabilisation of luciferase active conformation.

The sequences of oxidoreductases encoded in the lux-operon (LuxG) displayed less conservation, however the division into two clades still could be observed. Comparative study with close homolog, Fre-like oxidoreductase, revealed that LuxG evolution as a part of lux-operon resulted in broadened specificity to flavin substrate.

Weaker conservation of structural features of enzymes involved into bioluminescent reaction except for luciferase may be attributed to the presence of analogous enzymes that could also effectively work with bacterial luciferase. Moreover, the ability of bacterial luciferase to utilize different aliphatic components as one of the substrates may also affect the selective forces.

*Speaker

 $^{^{\}dagger}\mathrm{Corresponding}$ author: a deeva@sfu-kras.ru

The reported study was funded by projects 16-34-00746 mol_a and 6.7734.2017.

Keywords: bacterial bioluminescence, lux operon