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Where does your gene come from? Evolution of light-emitting enzymes in luminous organisms

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Abstract

Bioluminescence — the emission of visible light by living organisms — relies on the oxidation of a luciferin substrate catalysed by a luciferase enzyme ([1], for review). This "famous" terminology may give the false idea that all luminous organisms are using identical or homologous molecular tools to achieve bioluminescence. Instead, multiple light emission systems co-emerged independently along the tree of life resulting in a plethora of non-homologous luciferases ([2], for review). To investigate the diversity of known luciferase proteins (including luciferases *stricto sensu* and photoproteins), we analysed a total of 134 sequences coming from 75 species and 11 phyla. The global dataset was analysed using a sequence-similarity-based clustering approach based on BLASTp e-values and using the CLANS software [3]. We identified 12 distinct groups of luciferases, each comprising homologous proteins but with no homology between groups [4]. In addition, non-luciferase - but homologous – enzymes were added to the analyses to illustrate the evolutionary context of each identified group. It appears that phylogenetically related organisms may sometimes use non-homologous luciferases (e.g., case of luminous decapods, ostracods, and copepods within Pancrustacea) but also that phylogenetically distant organisms may use homologous luciferases (e.g., case of the brittle star *Amphiura filiformis* and the sea pansy *Renilla*). Genes coding for luciferases may then have emerged as new genes or have been co-opted from ancestral non-luciferase genes (i.e., with an ancestral function unrelated to bioluminescence). Evolution (and natural selection, in particular) indeed often promotes evolutionary innovation by co-opting preexisting genes for new functions. In this latter case, the homologous gene co-options may occur independently in phylogenetically distant organisms (i.e., parallel evolution) as observed in the case of the brittle star/sea pansy luciferases [5]. As already suggested for other types of proteins (e.g., [6]), our findings suggest that co-option may be an underappreciated process underpinning protein "neofunctionalisation", in particular in the context of luciferase evolution.

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