

## Lifestyle and DNA base composition in polychaetes

Andrea Tarallo,<sup>1</sup> Maria Cristina Gambi,<sup>2</sup> and Giuseppe D'Onofrio<sup>1</sup>

<sup>1</sup>Stazione Zoologica Anton Dohrn, Department of Biology and Evolution of Marine Organisms, Naples, Italy; and <sup>2</sup>Stazione Zoologica Anton Dohrn, Department of Integrative Marine Ecology (Villa Dohrn-Benthic Ecology Center), Ischia, Naples, Italy

Submitted 17 February 2016; accepted in final form 27 September 2016

**Tarallo A, Gambi MC, D'Onofrio G.** Lifestyle and DNA base composition in polychaetes. *Physiol Genomics* 48: 883–888, 2016. First published October 7, 2016; doi:10.1152/physiolgenomics.00018.2016.—A comparative analysis of polychaete species, classified as motile and low-motile forms, highlighted that the former were characterized not only by a higher metabolic rate (MR), but also by a higher genomic GC content. The fluctuation of both variables was not affected by the phylogenetic relationship of the species. Thus, present results further support that a very active lifestyle affects MR and GC at the same time, showing an unexpected similarity between invertebrates and vertebrates. In teleosts, indeed, a similar pattern has been also observed in comparisons of migratory and nonmigratory species. A cause-effect link between MR and GC has not yet been proved, but the fact that the two variables are significantly linked in all the organisms so far analyzed is, most probably, of relevant biological and evolutionary meaning. The present results fit very well within the frame of the metabolic rate hypothesis proposed to explain the DNA base composition variability among organisms. On the contrary, the thermostability hypothesis was not supported. At present, no data about the recombination rate in polychaetes were available to test the biased gene conversion (BGC hypothesis).

GC%; metabolic rate; motility; BGC; teleosts

POLYCHAETES, COMMONLY KNOWN as bristle worms, emerged, according to fossil records, in the early Cambrian Period (26). They represent the most diverse clade within the Annelida (~90% of the known species), mainly living in marine habitats (21, 46). A bilateral metamerism organization, with distinct anterior and posterior segments, characterizes their body plan (26). Despite this simple basic scheme, a tremendous diversity of body forms have been originated, showing a wide array of adaptations related to their various functional aspects, from feeding to reproduction, from behavior to locomotion (21).

Regarding motility, polychaete species have been grouped by Fauchald and Jumars (16) in three categories: 1) motile, grouping organisms showing active burrowing, crawling, and swimming, 2) discretely motile, group burrow-constructing or tube-dwelling organisms, and 3) sessile, grouping organisms permanently and obligatorily living inside the tubes they constructed, generally attached to a hard substrate or inserted in a soft substrate, and unable to survive if removed from the attachment site (21). Lifestyle is well known to affect both the morphology and the physiology of bristle worms (26). Recent phylogenetic analysis showed that the basal branching taxa would include a huge variety of lifestyles, from tubicolous to errant forms (44). Thus the result failed to support the hypoth-

esis that the specialized morphology of the very few sessile families may originate from a simpler motile form (26).

Pioneering physiological investigations between two categories of polychaetes with different degree of motility, i.e., Errantia and Sedentaria, showed that the former were characterized by higher routine oxygen consumption than the latter (29, 30).

The report was of great interest in the light of the metabolic rate hypothesis. Very recently, indeed, an extended analysis of hundreds teleost genomes showed that fishes with energetically expensive lifestyles, such as oceanic migratory species, were characterized not only by higher metabolic rate (MR) than nonmigratory ones, but also by higher gill area extension and higher genomic GC content (33). The results (linking physiology, morphology, and genomics) were in very good agreement within the frame of the MR hypothesis.

The hypothesis, proposed by Vinogradov (39, 42) to explain the evolution of DNA base composition variability among organisms, grounded on the experimental observations that high GC levels confer to the DNA molecule an increased flexibility, or bendability (3, 17). Vinogradov (39, 40, 42), indeed, observed that highly transcribed genes were in DNA regions characterized by low nucleosome formation potential and high GC content, most probably to better tolerate the torsion stress produced during the transcription process. Further analysis carried out on the human genome indicated that GC-rich genes were not only highly expressed than GC-poor ones, but also characterized by shorter introns in order to favor a faster transcription (2, 36, 41). The linkage between gene expression level (or MR) and GC content has been validated by several analyses carried out at intra- and intergenome level (2, 10, 33, 34, 36, 42), and reported to strongly affect the whole genome organization (7).

In the light of the above results from fish (10, 33, 34), and considering the different metabolic rate observed among polychaetes with different degree of motility (29, 30), a number of bristle worms species were here investigated with the aim of testing the prediction of the MR hypothesis. Namely, that polychaetes with active lifestyles compared with those with less active lifestyles should show not only a higher MR than the latter (29, 30), but also a higher genomic GC content.

### MATERIALS AND METHODS

To test the MR hypothesis, and keeping in mind our results from the comparison of migratory vs. nonmigratory teleostean fishes (33), polychaete specimens were split in two groups with markedly different locomotor skills: 1) motile (M), corresponding to the motile group defined by Fauchald and Jumars (16); and 2) low-motile (LM), characterized by lower degree of activity and corresponding essentially to the discretely motile and sessile species defined by Fauchald and Jumars (16).

The analysis of the average genomic base composition, i.e., GC, was performed on specimens collected from different biogeographic

Address for reprint requests and other correspondence: A. Tarallo, Stazione Zoologica Anton Dohrn - Dept. of Biology and Evolution of Marine Organisms, Villa Comunale, 80121, Naples, Italy (e-mail: andrea.tarallo010@gmail.com; andrea.tarallo@szn.it).