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世界初、頭足類のゲノム解読 - タコの全ゲノムを解読

Nature掲載論文: 「The octopus genome and the evolution of cephalopod neural and morphological novelties」

OIST、米シカゴ大学、カリフォルニア大学バークレー校の共同研究チームの研究成果

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<論文要旨>

- ✓脊椎動物の進化に繋がったと考えられているゲノム重複について、タコでゲノム重複が起きたという証拠は見つからなかった。
- ✓タコのゲノムの半分近くは可動遺伝子のトランスポゾンで占められ、タコは動物界において含有量が多い。多くの可動遺伝子がタコの神経系で活発に動いている。他の動物では同じ染色体上にある遺伝子がタコのゲノム上では分散しており、これはトランスポゾン活動の結果と考えられる。

- ✓胚発生に関わっているHox遺伝子は、大部分の動物ではクラスターを成しているが、タコでは断片的に散らばって存在。これが頭足類の多彩な進化を可能にしたものと考えられる。

➔ これまで未知の領域であった頭足類の初のゲノム解読により、動物の複雑な神経ネットワークや生物進化の研究の進展などにつながる可能性。

表紙



LETTER

The octopus genome and the evolution of cephalopod neural and morphological novelties

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Ceoloid cephalopods (squids, cuttlefish and nautilus) are active, neuronal predators with a rich behavioral repertoire¹. They have the largest nervous systems among the invertebrates and possess other striking morphological innovations including camera-like eyes, predatory arms, a highly derived early embryogenesis and a remarkably sophisticated adaptive coloration system². To investigate the molecular basis of cephalopod brain and body innovations, we sequenced the genome and multiple transcriptomes of the California two-spot octopus, *Octopus bimaculoides*. We found no evidence for hypothetical whole-genome duplications in the octopus lineage³. The core developmental and neural gene repertoires of the octopus is broadly similar to that found across invertebrate phyla, except for massive expansions in two gene families previously thought to be uniquely enlarged in vertebrates: the protocadherins, which regulate neuronal development, and the CREB independently of cAMP response element-binding protein (CREB) family of cAMP response element-binding proteins. Extensive messenger RNA editing generates transcript and protein diversity in genes involved in neural excitability, as previously described⁴, as well as in genes participating in a broad range of other cellular functions. We identified hundreds of cephalopod-specific genes, many of which showed elevated expression levels in such specialized structures as the skin, the suckers and the nervous system. Finally, we found evidence for large-scale genomic rearrangements that are closely associated with transposable element expansions. Our analysis suggests that substantial expansion of a handful of gene families, along with extensive remodeling of gene linkage and repetitive content, played a critical role in the evolution of cephalopod morphological innovations, including their large and complex nervous systems. Both invertebrate cephalopods such as the octopus (Fig. 1a) show remarkable morphological diversities from the basic invertebrate body plan.

87% of expressed protein-coding genes and 83% of the estimated 27,916 protein-coding genes (Methods and Supplementary Notes 1–5). The conserved fraction is dominated by high-copy repetitive sequences (Supplementary Note 1). Nearly 47% of the assembled genome is composed of repetitive elements, with two bursts of transposon activity occurring ~25 million and ~36 million years ago (Mya) (Supplementary Note 4). We predicted 3,848 protein-coding genes (Methods and Supplementary Note 6) and found alternative splicing at 2,871 loci, but not more than an unusually high number of splice variants (Supplementary Note 4). As to G. diversification between the assembled genome and transcriptome sequences provided evidence for extensive mRNA editing by adenosine deaminases acting on RNA (ADAR). Many could be cells enriched in neural tissue, and are found in a range of gene families, including transcription factors such as the tubulin, which suggests that RNA editing may have played a previously unrecognized role in cephalopod evolution (Fig. 1 and Supplementary Note 5). Based primarily on chromosome numbers, several researchers proposed that whole-genome duplications were important in the evolution of the cephalopod body plan³, postulating the role played by the independent whole-genome duplications events that occurred early in vertebrate evolution³. Although this is an attractive hypothesis for both gene family expansion and increased regulatory complexity across multiple genes, we found no evidence for a. The gene family expansion present in octopus are predominantly expanded in clusters along the genome, rather than distributed in widely scattered systems as expected for a polyploidized³ (Supplementary Note 4,2). Although genes that regulate development are often maintained in multiple copies after polyploidization in other lineages, they are not generally expanded in octopus relative to lamprey, rat and other vertebrate kinships³ (Table 1 and Supplementary Notes 7 and 8).