

Transcriptomic study of early developmental stages of *Octopus vulgaris*

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The common octopus *Octopus vulgaris* has been proposed as a good candidate for aquaculture operations due to its fast growth and short life cycle. Settlement of animals has been the main bottleneck to reach the adult stage under captivity. However, recent achievements allowed the obtaining of samples to decipher the molecular basis that regulates the intricate early stages in this species.

In this study, *O. vulgaris* samples at different stages were sequenced by RNA-seq for a massive *de-novo* transcriptomic analysis following the TRINITY protocol. Four main comparisons were carried out considering a mix of different embryonic stages and paralarvae at 0, 10, 20 and 40 days post-hatching (dph). A total of 2300 up-regulated transcripts were found in newly hatched paralarvae (0 dph) compared to embryo whereas the number of overexpressed transcripts reached 2336, 3013 and 2580 in 10, 20 and 40 dph paralarvae, respectively, compared to newly hatched animals. Gene ontology enrichment analysis revealed common terms at all ages such as chitin metabolism and peptidase related activities. Terms related to proteolysis and catabolism were significantly more represented in 0, 10 and 20 dph paralarvae whereas mobilization of proteins into the nucleus was more represented at 40 dph. Neural development and response to stimulus and activation of immune response were also differently represented attending to the age of the animals.

Altogether these results represent an overview of the different biological functions at paralarvae stage and will help to decipher at what age relevant functions are activated.

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