POSTERS

CONTROLLING COMPLEMENT FROM IMMUNITY TO DEVELOPMENT

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The complement system is classically regarded as a key effector of innate immunity, whose activity must be tightly regulated to avoid self-damage. Beyond this canonical role, complement components are increasingly recognized as active players in developmental processes, where controlled activation may contribute to selective cell elimination and tissue remodeling.

Here, we investigate the RCA gene repertoire and expression dynamics in the gastropod *Pomacea canaliculata*, focusing on adult hemocytes and early development. We identified seven distinct RCA genes, several of which generate up to four alternative splicing variants, revealing a notable molecular complexity. Transcriptomic analyses show that RCA genes are predominantly expressed in hemocytes, consistent with their role in immune regulation, but are also detectable in other tissues such as the ampulla, posterior kidney, and ganglion. In adult hemocytes, expression levels of all PcRCAs are broadly comparable and similar to those of PcC3, suggesting a coordinated regulatory framework controlling complement activity.

The most informative patterns emerge during early development, within the first 20 days post-fertilization (dpf), prior to hatching. During this period, PcC3 expression progressively increases, while specific RCAs display divergent trends. PcRCA4 is gradually down-regulated, suggesting a reduced protective role and a potential permissive condition for complement-mediated cell elimination. Conversely, PcRCA6 closely follows the PcC3 expression profile, supporting a protective function against C3 activation.

These results, obtained through bioinformatic analyses of Nanopore-generated transcriptomes complemented with publicly available Illumina datasets, highlight a finely tuned and developmentally regulated complement control system in *P. canaliculata*, linking immune regulation to non-canonical roles during development.