

Research on the Adaptability of Apple Snails: Transcriptomic Analysis in Low-Temperature Environments

The apple snail (*Pomacea app.*) is an invasive mollusk species renowned for its exceptional ecological adaptability and swift acclimatization to new environments, enabling it to establish a widespread presence in invaded regions. Environmental temperature stands out as a pivotal factor influencing the distribution and proliferation of apple snails. However, in the wake of global climate change, the gradual rise in temperatures is poised to facilitate their expansion further. Against this backdrop, comprehending the mechanisms through which apple snails adapt to low-temperature environments assumes paramount significance.

Originally introduced to Asia from Taiwan in the 1980s, apple snails were initially cultivated for their edible attributes. Nevertheless, due to a diminishing commercial appeal, many apple snails were abandoned and subsequently found their way into the wild. The extraordinary environmental adaptability of apple snails empowered them to rapidly establish populations, solidifying their status as one of the prevalent invasive species in the southern rice-growing regions of China.

Research indicates that non-biological factors, particularly environmental temperature, exert a more substantial influence than biological factors on the successful proliferation of invasive species. Harsh winter cold is a pivotal constraint limiting the northward expansion of apple snails. Nevertheless, within the context of global warming, the escalating temperatures are likely to favor the further intrusion of apple snails into northern China. Consequently, there is substantial interest in deciphering apple snails' cold resistance and low-temperature adaptability.

Existing research has predominantly centered on environmental factors and low-molecular-weight compounds, with relatively limited insights into the molecular mechanisms. The regulation of heat shock proteins (HSPs) gene expression is a recognized adaptive mechanism of apple snails in response to low-temperature environments. However, research on other genes remains an area ripe for deeper exploration.

To delve more profoundly into apple snails' physiological and molecular adaptive mechanisms in low-temperature settings, we embarked on a series of studies. Initially, we reared apple snails under both standard and low-temperature conditions, followed by RNA extraction and transcriptome sequencing. This approach enabled us to pinpoint genes associated with temperature adaptation. Subsequently, we harnessed GO annotation and KEGG pathway enrichment analysis to unveil the functions and pathways of these genes. This research contributes to unraveling the physiological and biochemical mechanisms

underpinning apple snail adaptation to low temperatures, thus augmenting our initial understanding of their ecological adaptation patterns in cold environments.

Moreover, to holistically explore apple snail responses to low-temperature stress, we analyzed differentially expressed genes under low-temperature conditions, encompassing various functional sets and pathways. These included the antioxidant system, energy metabolism, cell proliferation, and cellular, tissue, organ, and biological membrane systems. This study provides theoretical support for gaining further insights into the molecular mechanisms underpinning apple snail tolerance to low temperatures. It aids in projecting the expansion trends of apple snails and furnishes a more scientifically grounded basis for their prevention and control.

In summation, through an in-depth examination of the adaptability mechanisms of apple snails in low-temperature environments, we aspire to achieve a more profound comprehension of their invasion mechanisms and the constraining factors related to low temperatures. This research dispenses comprehensive insights that inform ecology and environmental conservation endeavors, ultimately advancing our capacity to prevent and manage apple snail proliferation effectively.