

P1. EVOLUTION OF NEURONAL NOS GENE IN CNS OF FISH

G. Annona¹, J.L. Ferran², I. Conte³, J. Postlethwait⁴, and S. D'Aniello¹

¹*Biology and Evolution of Marine Organisms, Stazione Zoologica Anton Dohrn di Napoli, 80121, Napoli, Italy;*

²*Institute of Biomedical Research of Murcia (IMIB), Virgendela Arrixaca University Hospital, University of Murcia, Murcia, Spain;*

³*Telethon Institute of Genetics and Medicine, 80078, Pozzuoli - Napoli, Italy;*

⁴*Institute of Neuroscience, University of Oregon, Eugene, OR 97403, USA*

Nitric Oxide, a gaseous signaling molecule, is probably one of the oldest bio-regulatory elements playing key roles in metazoan physiology. In tetrapods, three *Nos* paralogs were described based on their expression profiles: two constitutive, namely the neuronal *Nos* (*nNos*) and the endothelial *Nos* (*eNos*), and one inducible *Nos* (*iNos*) involved in immune responses. In fish, due to the evolutionary tetraploidization and rediploidization events, the *Nos* repertoire results more complex. Indeed, differential loss of *Nos* gene duplicates have been involved in the generation of fish variability. Interestingly, the *nNos* gene has been maintained in a single copy and is considered the predominant source of NO in neurons. Expressed in several areas of the central and peripheral nervous systems, it participates in the elaboration of olfactory, visual and neuroendocrine stimuli. *nNos* promotes learning and memory and is involved in the control of adult CNS neurogenesis. *Nos* genes share a very similar genomic structure, but the open question is whether this conservation has also a functional meaning. In this work we investigate the *nNos* expression profile in three fish species that occupy key phylogenetic positions in the evolution and show a different *Nos* gene repertoire: *Oryzias latipes* (1 *nNos*), *Danio rerio* (1 *nNos* and 2 *iNos* (a/b)), and *Lepisosteus oculatus* (1 *nNos*, 1 *eNos* and 1 *iNos*). Our results demonstrated that *nNos* expression profile increases in brain areas during the embryo development. Most remarkably, we identified homologous territories as well as specie-specific regions of *nNOS* expression in the CNS, suggesting a complex scenario.

