

Poster presentation

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Comparative evolutionary computational analysis of cerebellar purkinje cell structure and function

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Most computational efforts to understand the functional significance of neurons and networks are based on data obtained in a single species. In this report, we describe the use of comparative computational analysis to test a specific hypothesis arising from our computational studies of the mammalian cerebellum. Specifically, our previous experimental and model-based investigations have suggested that the inhibitory basket connections to the Purkinje cell (PC) serve functionally to limit the influence of parallel fiber activity on somatic output [1]. Because basket connections are not found in non-mammalian vertebrates, we hypothesized that either the electrical properties and/or some aspect of PC relationships to the parallel fibers would differ between mammals and non-mammals.

Reconstructing several single PCs in fish, frogs, turtles, and birds, we find that while all PC dendrites are isoplanar branched structures, mammalian PCs have many more branches with a much shorter tip length from the soma. Non-mammals, especially turtles, also have larger diameter dendrites. Using compartmental single cell models to examine passive electrical properties, we found that the time to peak in somatic voltage following discrete dendritic synaptic input is longer for non-mammalian PCs. Our analysis of the morphology of PC dendrites also suggests an evolutionarily progressive increase in surface area of the Purkinje cell expected to receive parallel fiber inputs (i.e. the spiny branchlets). Thus, mammalian PCs

also appear to have a much larger number of parallel fiber inputs than do non-mammalian PCs.

This is consistent with cell sorting results that will also be reported obtained in collaboration with Dr. Suzanaerculano-Houzel at the Federal University in Rio Janeiro, Brazil. This work shows a progressive increase in the ratio of granule cells to Purkinje cells in fish, frogs, turtles, birds and mammals. In summary, the quantitative and computational analysis of PCs in multiple species experiments suggest that mammalian PCs are electrically more compact and "faster", and have a larger number of parallel fiber inputs than do non-mammalian PCs. This in turn supports our previous hypothesis for the role of basket inhibitory input, and suggests that this input was added to mammalian cerebellar cortical circuitry to control the influence of parallel fibers on somatic output. To our knowledge, this is the first use of comparative computational analysis to examine evolutionary trends in the structure of biological neuronal networks.

References

1. Santamaria, et al.: *J Neurophys* 2007, **97**:248.