Olfactory contrast enhancement by functional inhibition in the honeybee antennal lobe

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In recent years, research in olfaction has considerably increased our understanding of the representation of high dimensional olfactory space in essentially two-dimensional neural networks. While a number of researcher project's have shown the importance of interbulbar and inter-lobar inhibitory networks for the shaping and processing of olfactory information, it is not clear how exactly these inhibitory networks are organized in order to provide optimal filtering and contrast enhancement capabilities. Using a computational model of the honeybee antennal lobe, we here show that among other possibilities, a functionally inhibitory network, in which glomeruli inhibit each other proportionally to the similarity in their olfactory response profiles best reproduces the experimentally observed input-output function.

In recent years, research in olfaction has considerably increased our understanding of the representation of high dimensional olfactory space in essentially two-dimensional neural networks. A large part of the research in olfaction has focused on the representation of olfactory information within the first processing stage, the olfactory bulb or antennal lobe glomeruli. A large effort has been made to elucidate how chemical stimuli are mapped onto olfactory glomeruli and how this mapping may relate to their perceptual qualities. While a number of researcher project's have shown the importance of inter-bulbar and inter-lobar inhibitory networks for the shaping and processing of olfactory information, electrophysiologically and theoretically as well as behaviorally, it is not clear how exactly these inhibitory networks are organized in order to provide optimal filtering and contrast enhancement capabilities.

It is generally believed that odors are represented as combinatorial activity patterns across the olfactory glomeruli, which represent the input layer of the bulbar/antennal lobe network. It has been suggested that the observed broadly distributed activation patterns at the glomerular layer can be sharpened by the bulbar/antennal lobe network in such a way as to ensure specific discrimination between chemically similar odorants. Specifically, in the antennal lobe of honeybees, two of us (SS and GG) have recently shown, using calcium imaging, that odor representations at the output of the antennal lobe network (glomerular output activity) are considerably sharpened as compared to those at the input (glomerular input activity). Because of the extensive inhibitory network within the olfactory bulb and antennal lobe, as well as the effects of inhibitory blockers on odor representations and odor discrimination, it can be assumed that the inhibitory network is responsible for the sharpening of olfactory representations within the antennal lobe. Being able to directly compare the processed odor representations at the output of the antennal lobe network with its originating input information presents us with the unique opportunity to ask how the inhibitory processes within this network should be organized in order to compute this specific input-output function. Using a computational model of the honeybee antennal lobe which reproduces a number of its more prominent features,

we here show that among other possibilities, a functionally inhibitory network, in which glomeruli inhibit each other proportionally to the similarity in their olfactory response profiles best reproduces the experimentally observed input-output function. Our simulations show that the input-output function between glomerular and projection neuron activation patterns provided by the honeybee antennal lobe network is best replicated when interglomerular inhibitory projections are organized along functional principles, i.e. when interglomerula inhibition is proportional to the similarity in glomerular odor response profiles.

Consequently, he simulation studies presented in this work show that inhibitory connections within the AL are not spatially constrained, and are not uniform or random, but inhibitiory connections within the AL are dictated by the funtional response properties. With increasing overlap in their molecular response profiles, glomeruli increase the strength of inhibitory connections between them.