Functional coupling of a bacterial binding protein with the channel pore of an ionotropic glutamate receptor

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Prokaryotic solute binding proteins (SBP) facilitate chemotaxis and substrate uptake of a large variety of small molecules and ions by binding their ligands with high specificity and affinity[1,2]. Despite a low sequence identity, SBP are structural homologous to the ligand binding domain (LBD) of ionotropic glutamate receptors (iGluR) and share a common ligand binding mechanism. SBP and LBD consist of two lobed domains connected by a hinge forming a clamshell like structure. Ligand binding takes place at the interface between the two domains, inducing a domain closure. This conformational change function as a key element in the transition of ligand recognition and ion channel gating in iGluR[3,4]. Due to the wide range of recognised ligands and the conserved binding mechanism, SBP may function as a component for analyte recognition in the design of a new class of biosensors. Here we describe an approach to design novel ligand activated ion channels by substituting the LBD of iGluRs with SBP. Substitution of the LBD of the prokaryotic iGluR GluR0 with the ectoine binding protein EhuB resulted in ectoine-activated channels with nanomolar affinity. Thus, by functional linking of a bacterial binding protein to the channel pore of an iGluR, our results substantiate the compatibility of SBPs and the pore structures of iGluR channels for the design of new BioSensors for specific analyte recognition.

References

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