

The transition between gating states in inward rectifier K⁺ channels

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Potassium channels are integral membrane proteins that facilitate a controlled flow of charge across cell membranes. Electrical activity depends the capacity of the channel to stably adopt alternate physiological conformers – ‘closed’ and ‘open’. Although previous crystal structures of K⁺ channels reveal significant plasticity of the pore, it is unclear whether the conformational differences between individual structures correlate solely with gating state, or if they are representative of familial connections. Two subtly different X-ray structures of a prokaryotic inward rectifier K⁺ channel (KirBac3.1) from *Magnetospirillum magnetotacticum* are presented here. The assembly with the more constricted ion conduction pathway is markedly asymmetric in the intracellular domains, whereas the other channel is sufficiently open to allow insertion of a large polyamine into the conduction pathway. The KirBac3.1 structures complement that of a close homologue, KirBac1.1, crystallised in an unequivocally non-conducting ‘closed’ conformation. By eliminating family-specific differences, the structures define key molecular indicators of gating state. Incremental re-arrangements occurring in the pore and intracellular domains are likely to reflect distinct stages in the closed-to-open transition.