Comparative study of the ion flux pathway in stator units of proton- and sodium-driven flagellar motors

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Flagellar motor proteins, MotA/B and PomA/B, are essential for the motility of Escherichia coli and Vibrio alginolyticus, respectively. T hose complexes work as a H+ and a Na+ channel, respectively and play important roles in torque generation as the stators of the flagellar mo tors. Although Asp32 of MotB and Asp24 of PomB are believed to function as ion binding site(s), the ion flux pathway from the periplasm t o the cytoplasm is still unclear. Conserved residues, Ala39 of MotB and Cys31 of PomB, are located on the same sides as Asp32 of MotB an d Asp24 of PomB, respectively, in a helical wheel diagram. In this study, a series of mutations were introduced into the Ala39 residue of Mot B and the Cys31 residue of PomB. The motility of mutant cells were markedly decreased as the volume of the side chain increased. The los s of function due to the MotB(A39V) and PomB(L28A/C31A) mutations was suppressed by mutations of MotA(M206S) and PomA(L183 F), respectively, and the increase in the volume caused by the MotB(A39V) mutation was close to the decrease in the volume caused by th e MotA(M206S) mutation. These results demonstrate that Ala39 of MotB and Cys31 of PomB form part of the ion flux pathway and pore wi th Met206 of MotA and Leu183 of PomA in the MotA/B and PomA/B stator units, respectively.

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