Fueling the MATE transporter

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Evolutionarily conserved transport proteins, such as those belonging to the multidrug and toxic compound extrusion (MATE) superfamily, protect cells against toxic chemicals and contribute to multidrug resistance in cancer and bacterial cells.

Understanding how such transporters harness the energy of ion gradients to facilitate drug export is critical in developing novel anti-cancer and anti-bacterial drugs that can overcome resistance.

Reporting last month in the *Proceedings of the National Academy of Sciences*, Hassane Mchaourab, PhD, and colleagues used DEER (double-electron electron resonance) spectroscopy to show how some conserved amino acid residues in NorM, a MATE transporter from the cholera pathogen, mediate the structural changes involved in drug efflux.

By measuring distances between spin labels in NorM, they found that a network of residues in the N-terminal domain is critical for ion-dependent conformational changes, while residues in the C-terminal domain mediate drug binding.

Their work also illustrates how sodium ions and protons drive the conformational cycle to power the transport mechanism.

More information: Derek P. Claxton et al. Sodium and proton coupling in the conformational cycle of a MATE antiporter fromVibrio cholerae, *Proceedings of the National Academy of Sciences* (2018). DOI: 10.1073/pnas.1802417115