Evolution and adaptation of single-pass transmembrane proteins

Irina D. Pogozheva, Andrei L. Lomize

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Evolution and adaptation of single-pass transmembrane proteins

Irina D. Pogozheva and Andrei L. Lomize†

Department of Medicinal Chemistry, College of Pharmacy, Ann Arbor, MI 48109-1065

† corresponding author; address: College of Pharmacy, University of Michigan, 428 Church St., Ann Arbor, MI 48109-1065; phone: 1-734-615-7194.

Email addresses: irinap@umich.edu; almz@umich.edu

HIGHLIGHTS

- Sizes, topologies, localizations, and functions of bitopic proteins were analyzed
- Physical properties of TM helices of bitopic proteins of 6 organisms were compared
- TM segment length, thickness, stability and hydrophobicity are organelle-specific
- Computational models of 2,129 TM α-helical homodimers were analyzed
- Dimerization propensity is higher for receptors of multicellular organisms

Abstract

A comparative analysis of 6,039 single-pass (bitopic) membrane proteins from six evolutionarily distant organisms was performed based on data from the Membranome database. The observed repertoire of bitopic proteins is significantly enlarged in eukaryotic cells and especially in multicellular organisms due to the diversification of enzymes, emergence of proteins involved in vesicular trafficking, and expansion of receptors, structural, and adhesion proteins. The majority of bitopic proteins in multicellular organisms are located in the plasma membrane (PM) and involved in cell communication. Bitopic proteins from different membranes significantly diverge in terms of their biological functions, size, topology, domain architecture, physical properties of transmembrane (TM) helices and propensity to form homodimers. Most proteins from eukaryotic PM and endoplasmic reticulum (ER) have the N-out topology, while other proteins display the N-in topology. The predicted lengths of TM helices and hydrophobic thicknesses, stabilities and hydrophobicities of TM α-helices are the highest for proteins from eukaryotic PM, intermediate for proteins from prokaryotic cells, ER and Golgi apparatus, and lowest for proteins from mitochondria, chloroplasts, and peroxisomes. Tyr and Phe residues accumulate at the cytoplasmic leaflet of PM and at the outer leaflet of membranes of bacteria, Golgi apparatus, and nucleus. The propensity for dimerization increases from unicellular to multicellular eukaryotes, from enzymes to receptors, and from intracellular membrane proteins to PM proteins. More than