From protein interactions to dynamic networks: cancer membrane protein-regulated networks

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Abstract:

As an increasing number of cancer omics data become available, there is a growing need to integrate these data with the biological networks to reveal cancer mechanisms. However, three open issues remain challenging. First, the interactomes in most of the organisms are still incomplete. Second, the network is usually too complicated to directly use. Third, the static networks cannot reflect the spatiotemporally dynamic behaviors of a cell. To address these issues, we introduced the concepts and strategies of PPI and module families to construct (enlarge) the networks through homologous mapping (across multiple species) [1,2]. For analysis of complex PPI networks, we further proposed the organizational principles of modules for identifying the modules and module-module interaction networks [2,3]. Moreover, we applied these strategies to uncover membrane proteins (MPs) and their regulated pathways in human cancers. A systematically integrated method (SIM) is presented to generate a resource of cancer membrane protein-regulated networks (CaMPNets) [4], containing 64,125 new PPIs for 1,964 MPs, using expression profiles from 5,922 tumors across 15 human cancers. In summary, CaMPNets can reveal the cancer-wide atlas of MPs and their regulated pathways, with significant implications for facilitating the identification of gene set-based prognostic biomarkers as well as therapeutic targets and agents.

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