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Opinion Article

Application of Trans Membrane Proteins (TMEMs) in Evolutionary and Behavioral Ecology

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DESCRIPTION

Proteomics has only lately been successfully applied to the closely related sciences of molecular evolution and genetics, and there has been very limited application to the domains of behavioral genetics, evolution, ecology, and population dynamics. A particular class of protein known as a transmembrane protein (TMEM) traverses biological membranes. Some of them are found near the membrane of organelles, whereas others extend across the lipid bilayer of the plasma membrane. The proteins of the TMEM family are generally uncharacterized. Proteomics can support, enhance, and even broaden the study of functional ecology including population genetics, the primary tool used in ecological studies, with a focus on metapopulation structure analysis. However, there is significant potential for proteomics to have an impact in functional ecology-related fields. Proteomics can also serve as the basis for a systems-level integration strategy that can improve ecological studies when combined with related bioinformatics and molecular evolutionary technologies. Since genes pass on phenotypic features from one generation to the next and DNA mutations and recombination create the genetic diversity necessary for evolutionary processes, evolutionary ecologists have typically concentrated on genes. Proteomics is expected to offer significant new knowledge on topics related to metapopulation biology and adaptive processes in nature. Although DNA contains the basic instructions for life, proteins, complexes they make with lipids, carbohydrates, and nucleic acids, and higher order structures they form are responsible for carrying out the genetic plan. Proteins make up the foundation of life, thus it makes sense that selection affects the structures that proteins form. But now that whole genome molecular and bioinformatics analyses are available, measuring selection at the molecular level nearly solely involves examining DNA sequence variation. An important tool for understanding cellular function across a wide variety of plant and animal species is the use of MS-based techniques for the qualitative and quantitative investigation of cellular proteomes, frequently from complicated mixtures. The basis of population biology and functional ecology is the investigation of the interactions between genetic and environmental factors. A relevant issue is the prevalence of non-model species in behavioral ecology studies, for which there is limited genetic data. Protein identification in these species must rely on either transcript sequences or de novo protein sequencing. Transmembrance proteins (TMEMs) are said to be the biomarkers used for the prediction. Potential predictive biomarkers for lung cancer include transmembrane protein like TMEM48 and TMEM97. It is predicted that the proteins in this family will be found in a variety of cell membranes, including those in the mitochondria, endoplasmic reticulum, lysosomes, and Golgi. Numerous cell types include TMEMs, which carry out crucial physiological processes such epidermal keratinization, autophagy, smooth muscle contraction. Differential regulation of the expression of TMEMs has been seen in a variety of malignancies, including lymphomas (TMEM176), colorectal cancer (TMEM25), hepatic cancer (TMEM7), and lung cancer (TMEM48). Typically, tumour tissue exhibits a down regulation of their expression when compared to nearby healthy tissue. TMEM25 protein belongs to the immunoglobulin superfamily and functions in cell adhesion, growth factor signaling, and immune response. TMEM97 is the final protein discussed in this section. This protein, also known as MAC30, belongs to the class of proteins that bind insulin-like growth factors. In contrast to pancreatic and renal malignancies, which both show modest expression levels of TMEM97 protein and mRNA, many cancer types exhibit higher expression of TMEM97. With 275 amino acids and a predicted five to seven transmembrane domains, TMEM45A is a TMEM that is found in the trans Golgi apparatus. Breast cancer, liver cancer, renal cancer, glioma, head and neck cancer, ductal carcinoma, and ovarian cancer are among the malignancies in which this protein is overexpressed. Higher expression levels of TMEM45A have been linked to worse patient overall survival in studies of breast cancer and cervical lesions, suggesting that TMEM45A may be a biomarker for the aggressiveness of these diseases. Chemotherapy resistance can emerge from the tumor environment as well as the cancer cells' own adaptability. In addition, the mechanisms causing treatment resistance can vary depending on the kind of cancer and the chemotherapeutic medication. Although TMEM proteins have a variety of roles and are found in many locations, most of them are connected to cancer. Some of them can serve

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as biomarkers or classifiers because of their correlation with patient survival and disease phases. Others play a part in the development of cancer and tumours, but it is yet unclear how many of them work. A more thorough analysis of these proteins might make it easier to comprehend how they relate to cancer. They could be exploited as new therapeutic targets to increase the effectiveness of chemotherapies because some of them are even involved in chemoresistance. Proteomic research likely focuses primarily on the protein categories important to behavioral ecology that have reproductive activities. The main obstacle to using proteomics in behavioural ecology is getting access to the necessary tissues. Proteomic techniques avoid some of the drawbacks of other genomic methodologies, including microarray and EST analysis, by providing a direct assessment of gene expression. Determine the spatial and temporal expression of proteins in cells, organs, and entire organisms using proteomics, a relatively young scientific field that combines protein biochemistry, genome biology, and bioinformatics. Proteomics typically calls for disruptive sampling, which can conflict with research of behavioral ecology. Protein expression patterns in several species' tissues as well as reproductive organs and related secretions (such as sperm, seminal fluid, and oocytes) have been studied. Future research in these fields will be greatly impacted by proteomics, but how much will depend on how analytical MS, 2DGel technology, and equipment costs continue to advance.