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Parallel proteomic analysis in muscle-invasive bladder transitional cell carcinoma and cancer-related stroma

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ABSTRACT. To bring about improvements in cancer biology research and elucidate mechanism-based therapeutic targets, we studied the proteome expression profile of purified normal urothelial cells (cancer cells) and normal stromal cells (cancerous stromal cells). Based on the expression profile, biomarker discovery and the mechanisms of multi-step carcinogenesis were explored. We found that 1412/1403 unique proteins commonly appeared in 4 sets of paired cancer/normal tissue, and 1753 proteins were differentially expressed. Three hundred and forty-one proteins were repeatedly expressed in both cancer and cancer stromal cells; 358 proteins were repeatedly expressed in both normal urothelial and normal stromal cells. Among them, 186/203 proteins were specific repeat

expressions in cancer/normal tissue and thought to play an important role in cancer-stroma interactions. Differential proteins were further analyzed using bioinformatic tools and compared with the published literature. GO enrichment/depletion analysis indicated that carcinogenesis involved all the biological processes and all the cellular components. Five hundred and sixty-eight differential proteins were located in the well-known biological Kyoto Encyclopedia of Genes and Genomes pathways, including metabolic pathways, ribosome spliceosome, and endocytosis. One hundred and thirty-nine of the 186 proteins that displayed specific repeat expressions in cancer tissue were located in the biological Kyoto Encyclopedia of Genes and Genomes pathways and are thought to be candidate biomarkers for targeted therapy.

Key words: Muscle-invasive bladder cancer; Stroma; Biomarker; Pathway analysis

