

中文題目：肺癌惡性肋膜積水癌細胞顯示葡萄糖代謝基因之異常表現

英文題目：Malignant pleural effusion cells show aberrant glucose metabolism gene expression

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Background: Malignant pleural effusion (MPE) accompanying lung adenocarcinoma indicates poor prognosis and early metastasis. This study aimed to identify genes related to MPE formation.

Methods: Three tissue sample cohorts - seven from healthy lungs, 18 from early stage lung adenocarcinoma with adjacent healthy lung tissue, and 13 from MPE were analyzed by microarray. The identified genes were verified by quantitative real-time polymerase chain reaction (qRT-PCR), immunohistochemical staining, and immunofluorescence confocal microscopy.

Results: Twenty up- or down-regulated genes with a two-fold change in MPE cancer cells compared to healthy tissues were differentially expressed from early- to late-stage lung cancer. Aldolase A, sorbitol dehydrogenase, transketolase, and tuberous sclerosis 1 were related to glucose metabolism. QRT-PCR validated their mRNA expressions in pleural metastatic samples. Immunohistochemical staining confirmed their aberrant expressions in tumor cells. Transketolase regulated the proliferation, VEGF secretion of lung cancer cells *in vitro* and *in vivo*.

Conclusion: Glucose metabolic reprogramming is important in MPE pathogenesis.