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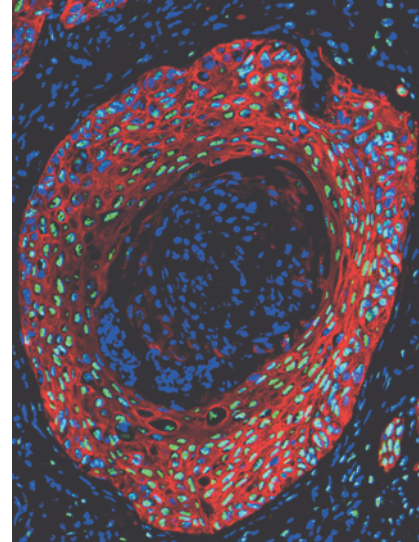
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ABOUT THE COVER

Lung squamous cell carcinoma (SCC) is thought to arise from premalignant lesions in the airway epithelium; therefore, studying these lesions is critical for understanding lung carcinogenesis. RNA sequencing was performed on laser-microdissected representative cell populations along the SCC pathological continuum of patient-matched normal basal cells, premalignant lesions, and tumor cells. Transcriptomic changes and genomic pathways altered with initiation and progression of SCC within individual patients were identified. Immunofluorescent staining confirmed gene expression changes in premalignant lesions and tumor cells, including increased expression of SLC2A1, CEACAM5, and PTBP3 at the protein level and increased activation of MYC via nuclear translocation. The cover micrograph shows merged immunofluorescently stained SCCs (PTBP3, green; KRT5, red; nuclei, blue) showing increased expression of PTBP3 in KRT5-expressing premalignant lesions and SCCs compared to basal cells in normal airway epithelium (not shown). The present study is the first gene expression profiling study of airway premalignant lesions with patient-matched normal airway epithelium and SCC samples, and provides much needed information about the biology of premalignant lesions and the molecular changes that occur during stepwise carcinogenesis of SCC. Importantly, it highlights a novel approach for identifying some of the earliest molecular changes associated with initiation and progression of lung carcinogenesis within individual patients. See the article by Ooi and colleagues (beginning on page 487) for more information.



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