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Molecular alterations associated with chronic exposure to cigarette smoke and chewing tobacco in normal oral keratinocytes

Pavithra Rajagopalan^{1,2}, Ankit P. Jain^{1,2}, Krishna Patel^{1,3}, Vishalakshi Nanjappa¹, Kiran K. Mangalparthi^{1,3}, Anjali Kumari⁴, Malini Manoharan⁴, Coral Karunakaran⁴, Saktivel Murugan⁴, Bipin Nair³, T.S. Keshava Prasad^{1,5,6}, Premendu P. Mathur², Ravi Gupta⁴, Rohit Gupta⁴, Arati Khanna-Gupta⁴, David Sidransky⁷, Harsha Gowda^{1*} and Aditi Chatterjee^{1*}

¹Institute of Bioinformatics, International Tech Park, Bangalore, INDIA

²School of Biotechnology, KIIT University, Bhubaneswar, INDIA

³Amrita School of Biotechnology, Amrita University, Kollam, INDIA

⁴Medgenome Labs Pvt. Ltd., Bangalore, INDIA

⁵NIMHANS-IOB Bioinformatics and Proteomics Laboratory, Neurobiology Research Centre, National Institute of Mental Health and Neurosciences, Bangalore, INDIA

⁶YU-IOB Center for Systems Biology and Molecular Medicine, Yenepoya University, Mangalore, INDIA

⁷Department of Otolaryngology-Head and Neck Surgery, Johns Hopkins University School of Medicine, Baltimore, MD, USA *Corresponding author: <u>aditi@ibioinformatics.org</u>

Abstract

Tobacco usage is a known risk factor associated with development of oral cancer. It is mainly consumed in two different forms (smoking and chewing) that vary in their composition and methods of intake. Despite being the leading cause of oral cancer, molecular alterations induced by tobacco are poorly understood. To investigate the adverse effects of cigarette smoke/chewing tobacco exposure in oral keratinocytes, we developed two cellular models where normal oral keratinocytes were chronically exposed to cigarette smoke and chewing tobacco for a period of 8 months. Cellular assays reveal that OKF6/TERT1 cells acquire an oncogenic phenotype after chronic exposure to cigarette smoke/chewing tobacco. We employed both whole exome sequencing (WES) and quantitative proteomics approaches to investigate the molecular alterations in oral keratinocytes (OKF6/TERT1) chronically exposed to smoke and chewing tobacco. Exome sequencing revealed a much higher rate of C>A transversions in smoke exposed cells in conjunction with previous studies. In contrast, C>G transversions were observed to be higher in chewing tobacco exposed cells. Diverse mutations in both treated cells further highlight the distinct effects of each exposure. Distinct proteomic alterations were observed in smoke and chewing tobacco exposed cells compared to parental cells. In addition, we observe enrichment of different signaling cascades in transformed oral cells upon chronic exposure to either cigarette smoke or chewing tobacco. Current analysis defines a clear distinction in the molecular dysregulation in oral cells in response to different tobacco-based insults. Future studies are needed to validate some of the genetic and proteomic alterations unique to each form of tobacco exposure. This study can serve as a reference for fundamental damage on oral cells as a consequence of exposure to different forms of tobacco.

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