Does Maternal Smoking during Pregnancy Moderate the Effect of Genes on Offspring’s Smoking Behavior?

Pamela N. Romero Villela1,2*, Jared C. Balbona1,2, Richard Border, Ph.D.3, Matthew C. Keller, Ph.D.1,2, Luke M. Evans, Ph.D.,1,5, Marissa A. Ehringer, Ph.D.1,4

1Institute for Behavioral Genetics, University of Colorado, Boulder, Colorado, USA
2Department of Psychology, University of Colorado, Boulder, Colorado
3Departments of Neurology and Computer Science, University of California, Los Angeles
4Department of Integrative Physiology, University of Colorado, Boulder, Colorado
5Department of Ecology & Evolutionary Biology, University of Colorado, Boulder, Colorado

* Corresponding Author: Pamela Romero Villela, Institute for Behavioral Genetics, Boulder, CO 80309; pamela.romerovillela@colorado.edu

KEYWORDS: genetics, epigenetics, smoking, GxE, maternal smoking during pregnancy

ABSTRACT:

Maternal smoking during pregnancy (MSP) is a strong predictor of later offspring nicotine use. However, not all children exposed to nicotine prenatally later go on to smoke, suggesting that the effect of MSP may be moderated by genetic factors (Buka, Shenassa, & Niaura, 2003). Due to limited sample sizes and statistical power, few studies have investigated this potential interaction between genetics and maternal smoking during pregnancy. We attempt to address this gap using the UK Biobank to examine potential genetic interactions with maternal smoking to predict a wide range of smoking phenotypes: cigarettes per day, smoking initiation, smoking cessation, and birth weight. We used plink2 (Purcell et al., 2007) to conduct a genome-wide interaction study to assess if genome-wide loci moderated the effect of MSP on unrelated offspring of European descent (n=116,442). Our results failed to find loci that reached genome-wide significance for the interaction with maternal smoking. It is possible that even with a large sample size such as UK Biobank, the power to detect such interactions at the genome-wide level is limited. Future analyses will investigate gene-by-environment and polygenic risk score-by-environment interactions.

References:


GRANT SUPPORT: Not applicable.