PgmNr 3298: Methylation sensitive digital PCR tests for rapidly assessing heavy alcohol consumption and smoking using DNA from blood or saliva.

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Background: Smoking and Excessive Drinking are the 1\textsuperscript{st} and 3\textsuperscript{rd} leading causes of mortality in the world. Unfortunately, there are no existing clinically implementable tests for quantifying the extent of either lifestyle factor. In 2012 and 2014, respectfully, we published the first genome wide study of smoking and heavy alcohol consumption (HAC). Herein, we detail the translation of those genome wide findings to easy to perform quantitative digital PCR (dPCR) tests for both smoking and drinking using DNA from blood or saliva from 233 smokers, 143 HAC and 200 controls. Results: Using DNA from whole blood, we show that dPCR assessment of methylation at cg05575921 has a Receiver Operating Characteristic (ROC) area under the curve (AUC) of 0.995 for predicting smoking with the amount of demethylation at cg05575921 being proportional to daily cigarette consumption. Similarly, a set of 4 dPCR markers specific for HAC has an AUC of 0.95 using DNA from whole blood. By using a recently described dPCR marker capable of correcting for the cellular heterogeneity in saliva, similar AUC values and dose response curves were seen with respect to cigarette and alcohol consumption using DNA prepared from saliva. Conclusions: We conclude that clinically implementable dPCR tools using DNA from blood or saliva can sensitively detect the presence and intensity of both smoking and HAC. Since the methylation signatures for both alcohol and cigarette consumption revert with abstinence, we believe that these easy to perform, rapid digital PCR tools will be useful to clinicians and researchers in assessing and monitoring those enrolled in substance use disorder treatment, employee wellness programs and insurance underwriting.