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Comparison of TP53 mutation prevalence in human blood cells from lung cancer patients and control subjects

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Early detection and diagnosis of lung cancer is a crucial component of treatment and increasing survival odds. Our previous research demonstrated the utility of mutation prevalence of the TP53 gene in bronchial epithelial cells as an indicator of lung cancer risk. The purpose of our research was to determine if TP53 mutation prevalence in peripheral blood cells is a useful marker for determining lung cancer status. We used genomic DNA (gDNA) extracted from blood cells to examine TP53 mutation status and prevalence in lung cancer and non-cancer (control) groups. Samples from cases and controls were selected as pairs based on age, sex, race, smoking status, and smoking history expressed in pack-years. gDNA was extracted from buffy coat samples, target sequences were amplified via PCR, and two sequencing libraries were created. Both libraries have been sequenced: Approximately 28 million reads were obtained from each library with approximately 94.4% %Q30. Bioinformatic analysis is in progress to enable a comparison of TP53 mutation prevalence in cancer and non-cancer groups. If TP53 mutations are more common in the cancer group, it may suggest that mutation prevalence in gDNA collected from peripheral blood can be used as a marker of lung cancer status.

