SUMMARY AND CONCLUSION
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The following points have come out of the present study:

1. The study population was recruited from All India Institute of Medical Sciences, AIIMS, New Delhi. The majority of study participants were manual workers and smokers.

2. The study pertained to evolution of role of polymorphism in the CYP1A2, SULT1A1, NAT2 and DNA repair gene XRCC1 in the risk for lung cancer. Of these SULT1A1 (mutant) and NAT2*6 (6/6) alleles have been found to be associated with an increased risk of lung cancer.

3. NAT2*5 (*5/wt/*5/*5) and XRCC1 (Arg/Gln/Gln/Gln) are significantly decreased the risk of lung cancer.

4. No association with CYP1A2, NAT2*7 and XRCC1 194 genotype and lung cancer is there.

5. With regard to tumour histology:
   a) CYP1A2 (mutant), SULT1A1 (mutant) and NAT2*6(*6/*6) alleles are associated with elevated risk for SQCC.
   b) The risk is also increased for patient having AC for CYP1A2 (mutant) and NAT2*6 (*6/*6) genotypes.
   c) NSCLC is associated with significant increased risk for CYP1A2 (mutant) and XRCC1 194 (mutant) genotype.
   d) SULT1A1, NAT2*6 and XRCC1 194 are associated with increased risk for poorly differentiated carcinoma.
   e) Only SULT1A1, shows positive association with SCLC.
   f) NAT2*7 and XRCC1 399 do not show any association with histological subtypes.

6. As regards the impact of smoking, XRCC1 399 shows significant association with lung cancer, but with
reduced risk. Increased risk has been observed among non-smokers in CYP1A2 and NAT2*6.

7. On combining the genotypes, following points are evident:
   a) An interaction of CYP1A2 with NAT2*5 and XRCC1 399 significantly reduces the risk of lung cancer.
   b) The combination of SULT1A1 and NAT2*5 significantly increases the risk of lung cancer.
   c) Combination of XRCC1 399 with NAT2*5 and NAT2*7 genotype also elevates the risk.
   d) Various combinations of CYP1A2, SULT1A1, NAT2 and XRCC1 genotype influence the risk of developing lung cancer in all histological groups.

Investigations on the role of polymorphic genes as susceptibility factor for complex diseases like cancer in the inter-ethnic differences of polymorphic trait, smoking and dietary habits, may lead to different results in different populations. Based on above data, which still requires configuration by a larger study, consideration of gene-gene environment interactions and the possibility of identifying in parallel a number of SNPs, using modern genotyping technique, will help us to elucidate the impact of these polymorphisms on the lung cancer.