SUMMARY AND CONCLUSIONS

The following points have emerged from the present study:

- Histopathologically confirmed bladder cancer patients were recruited, from the Post-graduate Institute of Medical Education and Research (PGIMER).
- As most of patients were above 56 years of age with mean 57.42, it was evident that bladder cancer is a disease of middle and old ages.
- No statistically significant association was found between alcohol consumption and risk of bladder cancer.
- No association was found between types of the food and risk of bladder cancer.
- Cigarette smoking had shown significant association with an increased risk of bladder cancer.
- High risk jobs status had shown significant association with 2.4 fold increased risk of bladder cancer.
- The polymorphic forms of TAP1 and IL-6 did not show any association with the risk of bladder cancer.
- TAP2 GG genotype was associated with statistically significant increased risk of bladder cancer. Moreover, IL-12β1 AC genotype was associated with significant risk of bladder cancer.
WITH REGARD TO SMOKING STATUS, THE FOLLOWING POINTS COULD BE HIGHLIGHTED.

I. Statistically significant increased risk of bladder cancer was observed for the following genotypes in smokers:
   - IL-6 (CC) and (GC) and (GC+CC)
   - TAP2 (AG) and (GG) and (AG+GG)
   - IL-12β (AC) and (AC+CC)

II. Statistically insignificant association was observed for the TAP1 genotype with the risk of bladder cancer.
   - When derived into histological subtypes, increased significant association for TCC superficial stage was found in patients carrying TAP1 CT and 3 fold increased risk for combined CT+TT genotypes as compared to invasive carcinoma.

WITH REGARD TO JOB STATUS, THE FOLLOWING POINTS EMERGED OUT

Statistically significant increased risk of bladder cancer was observed for the following genotypes with high risk job:
   - IL-6 (GC) and (GC+CC)
   - TAP2 (AG) and (GG) and (AG+GG)
   - IL-12β (AC) and (AC+CC)

II. Statistically insignificant association was observed for the TAP1 genotype with risk of bladder cancer.
   - On studying gene-gene interactions, following GENE combinations were not found to be associated with risk of bladder cancer:
     i) IL-12β and IL-6
Summary and Conclusion

v) Superficial tumour stage showed significant association with protective effect on p14 promoter hypermethylation in blood samples of bladder cancer patients.

vi) Of the bladder tumour samples amplified, 32 (40%) presented p16\textsuperscript{INK4a} promoter hypermethylation, of these, 12 (37.5%) showed p16\textsuperscript{INK4a} promoter hypermethylation in plasma samples.

vii) Muscle invasive tumour stage showed significant association with increased risk of p16 promoter hypermethylation in tissue samples.

viii) High risk jobs status had shown significant association with increased risk of p16 hypermethylation in bladder cancer blood samples.

ix) Non muscle invasive tumour stage showed significant association with protective affect on p16 promoter hypermethylation in blood samples of bladder cancer patients.

The role for aberrant methylation in human bladder tumourigenesis may be particularly important for bladder cancer with the clear cell phenotype. Therefore, identification of additional novel CpG islands that are specifically associated with bladder cancer will be needed to construct a panel with higher sensitivity that maintains high specificity, and studies examining detection of such a panel of genes using recently developed quantitative assays should be undertaken. In addition, assays that are based on the identification of changes in the function of genes central to the maintenance of genetic stability will offer the possibility of identifying the subset of precursor lesions that carry a high risk of progression to invasive bladder carcinoma. More studies using a much larger sample size are needed to further define the potential role of methylated DNA marker in bladder cancer management.

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