

21st World Congress on

RADIOLOGY & CANCER RESEARCH

August 27-28, 2018 | Toronto, Canada

XRCC1 gene polymorphisms and chromosomal instability in esophageal cancer patients

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Background: Faulty DNA repair due to mutations or polymorphism in XRCC1 (19q13.2), plays a predominant role in both single-strand break repair and base excision repair, which may lead to genomic instability and cancer.

Objectives: The present study evaluated three polymorphisms of XRCC1, p.Arg399Gln, p.Arg194Trp, p.Arg280His and chromosomal instability in esophageal cancer (EC) patients from Punjab, India, and their association with esophageal cancer risk and tumor aggressiveness.

Material and Methods: Cytogenetic analysis and genotyping for Arg399Gln, Arg194Trp and Arg280His polymorphisms by PCR-RFLP method were done in 215 esophageal cancer patients (89 males and 126 females) and 265 controls (95 males and 170 females).

Results: The Arg399Gln polymorphism AA genotype and recessive model (OR=0.57, 95%CI= 0.33-0.98; p=0.038) was associated with an increased risk of EC. No significant difference was found in genotype and allele frequencies for other two polymorphisms. Patients with GA genotype of Arg399Gln polymorphism had a higher frequency of chromosomal aberrations than controls. Patients had higher frequencies of structural and numerical aberrations along with some constitutional aberrations as compared to controls.

Conclusion: The XRCC1 Arg399Gln polymorphism was associated with an increased risk of esophageal cancer. Specific chromosomal anomalies related to tumor progression in patients indicated a poor prognosis. Identification of inherited genomic changes and their association with chromosomal instabilities might help in identifying subjects with aggressive tumors and selection of suitable therapy for personalized medicine.

Biography

Jagjeet Kaur, currently doing Ph.D in Human Genetics, from Guru Nanak Dev University, Amritsar on esophageal cancer, topic of research is DNA repair genes XRCC1, XRCC2, XRCC3 and OGG1 in esophageal cancer patients.

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