

## الإنتاج العلمى لمركز بحوث العلوم الصحية





Association of genetic polymorphisms in DNA repair genes ERCC2 Asp312Asn (rs1799793), ERCC2 Lys 751 Gln (rs13181), XRCC1 Arg399 Gln (rs25487) and XRCC3 Thr 241Met (rs861539) with the susceptibility of lung cancer in Saudi population

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This study demonstrated the association of polymorphisms in *ERCC2* (Asp312Asn) rs13181, *XRCC1* (Arg399Gln) rs1799793, *ERCC*2 (Lys751Gln) and XRCC3(Thr241Met) rs861539 polymorphisms with a susceptibility of lung cancer (LC) onset in the Saudi population. The study was performed on 134 LC patients and 270 controls. The data revealed that there was no significant association of LC with subtype squamous cell carcinoma (SCC), small cell lung cancer (SCLC) and adenocarcinoma with the ERCC2 rs1799793 polymorphism. The data showed that the CC genotype for ERCC2 rs13181, the AA genotype for XRCC1 rs25487, and the genotype TT for XRCC3 rs861539 were significantly associated with SCC susceptibility (p < 0.05). Similarly, the CC genotype for ERCC2 rs13181 and the AA genotype for XRCC1 rs25487 were significantly associated with adenocarcinoma susceptibility (p < 0.05). Whereas, the TT genotype for XRCC3 rs861539 was significantly associated with SCLC susceptibility (p = 0.005). In total, significant association of LC susceptibility was found in the following combination models of recessive genotypes: AC heterozygous for ERCC2 rs13181 + AA homozygous for XRCC1 rs25487, CC homozygous for ERCC2 rs13181 + GA heterozygous for rs25487, CC homozygous for rs13181 + AA homozygous for XRCC1 rs25487, CC homozygous for ERCC2 rs13181 + TT homozygous for XRCC3 rs861539, GA heterozygous for XRCC1 rs25487 + CT heterozygous for XRCC3 rs861539, GA heterozygous for XRCC1 rs25487 + TT homozygous for XRCC3 rs861539, AA homozygous for XRCC1 rs25487 + heterozygous for XRCC3 rs861539, AA homozygous for XRCC1 rs25487+ homozygous for XRCC3 rs861539. These data clearly demonstrated that the combination of recessive genotypes may be associated with susceptibility of LC onset (p < 0.05). In short, the data indicated that DNA repair genes increase LC risk via genegene interaction rather than independent variants.

