ASSOCIATION OF POLYMORPHISMS IN GENES INVOLVED IN DNA REPAIR AND CELL CYCLE ARREST WITH BREAST CANCER IN A VIETNAMESE CASE-CONTROL COHORT

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Breast cancer (BC) is the most common cancer diagnosis in women worldwide. Among causative BC genes, MRE11, ERCC1, TNRC9 (TOX3), and CASC16 play an important role in DNA damage repair; FGFR2, CCNE1, ZMIZ1, and LSP1 involve in cell cycle checkpoint. A functional polymorphism of these genes may alter DNA repair capacity and genomic stability. Single Nucleotide Polymorphisms (SNPs) can modify the risk of cancer, and thus, SNPs may be considered as potential markers of carcinogenesis. Among them, eight SNPs (rs2981582, rs569550, rs3218035, rs704010, rs2155209, rs3212986, rs12443621 and rs4784227) are significantly associated with BC risk in various populations. This study was conducted to investigate the genetic susceptibility of these SNPs in the development of BC in Vietnamese women. MRE11 rs2155209 and CASC16 rs4784227 were found to be associated with BC risk (CC vs. CT + TT: OR = 0.57, 95% CI 0.34 to 0.97, P = 0.03 and CT vs. CC + TT: OR = 1.43, 95% CI 1.03 to 1.97, P = 0.03; respectively). These findings suggest that SNPs involved in DNA repair genes may affect the susceptibility of BC in Vietnamese women.

Key words: *breast cancer, single nucleotide polymorphism, MRE11, rs2155209, CASC16, rs4784227*

АСОЦІАЦІЯ МІЖ ПОЛІМОРФІЗМАМИ В ГЕНАХ, ЗАЛУЧЕНИХ ДО РЕПАРАЦІЇ ДНК І ТЕРМІНАЦІЇ КЛІТИННОГО ЦИКЛУ, ТА РАКОМ ГРУДЕЙ У КОГОРТНОМУ ДОСЛІДЖЕННІ ТИПУ «ВИПАДОК-КОНТРОЛЬ» У В'ЄТНАМІ

Рак грудей (РГ) – це найпоширеніший діагноз ракового захворювання серед жінок у всьому світі. З-поміж каузативних генів РГ, *MRE11*, *ERCC1*, *TNRC9* (*TOX3*) і *CASC16* відіграють важливу роль у репарації ДНК; *FGFR2*, *CCNE1*, *ZMIZ1* і *LSP1* беруть участь у контрольній точці клітинного циклу. Функціональний поліморфізм цих генів може змінювати здатність до репарації ДНК і стабільність геному. Однонуклеатидні поліморфізми (SNP) можуть модифікувати ризик появи раку, отже, SNP можна розглядати як потенційні маркери канцерогенезу. З-поміж них, вісім SNP (rs2981582, rs569550, rs3218035, rs704010, rs2155209, rs3212986, rs12443621 і rs4784227) тісно асоційовані з ризиком появи РГ у різних популяціях. Це дослідження було проведене з метою вивчення генетичної схильності цих SNP у розвитку РГ серед в'єтнамських жінок. Було виявлено, що *MRE11* rs2155209 і *CASC16* rs4784227 пов'язані з ризиком виникнення РГ (CC vs. CT + + TT: OR = 0,57, 95 % CI 0,34 до 0,97, *P* = 0,03 і CT vs. CC + TT: OR = 1,43, 95 % CI 1,03 до 1,97, P = 0,03; відповідно). Ці результати свідчать про те, що SNP, залучені до генів репарації ДНК, можуть впливати на схильність в'єтнамських жінок до РГ.

Ключові слова: рак грудей, однонуклеатидний поліморфізм, *MRE11*, rs2155209, *CASC16*, rs4784227.

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