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论文

PR/AR基因多态性与上皮性卵巢癌易感性的研究

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摘要：

目的 研究孕激素受体(PR)基因+331G/A(rs10895068)与PROGINS(rs1042838)单核苷酸多态(SNP)以及雄激素受体(AR)基因CAG(GDB:185508)与GGN(GDB:197027)短串联重复(STR)多态与卵巢癌遗传易感性的关系。方法 病例组为40例上皮性卵巢癌患者，对照组为48例健康女性，DNA测序方法分析两组的基因型，并比较不同基因型与卵巢癌发病风险以及分期、分级的相关性。结果 病例组和对照组PR基因+331G/A位点均为GG型，未发现GA和AA型；两组PROGINS均为CC型，未发现CA和AA型；AR基因CAG和GGN重复次数在病例-对照组间无明显差异，但短组GGN重复使卵巢癌发病危险提高2.82倍(P<0.05)；未发现病例组中卵巢癌分级、分期与STR分布相关(P>0.05)。结论 AR基因GGN重复多态与上皮性卵巢癌的发生明显相关，很可能是卵巢癌的致病因素之一。

关键词： 卵巢肿瘤；多态性；孕激素受体；雄激素受体

Association between PR/AR gene polymorphisms and susceptibility to epithelial ovarian cancer

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Abstract:

Objective To study the correlation of genetic susceptibility to epithelial ovarian cancer with two single nucleotide polymorphisms (SNP), +331G/A(rs10895068) and PROGINS(rs1042838), in the progesterone receptor (PR) gene, and two DNA short tandem repeat (STR) polymorphisms, CAG (GDB:185508) and GGN(GDB:197027), in the androgen receptor (AR) gene. Methods Genotypes of 40 patients with epithelial ovarian cancer and 48 healthy controls were analyzed by the DNA sequencing method. The relationship of genotypes with the risk, stages, and grades of ovarian cancer were analyzed. Results No polymorphisms at the position +331 or PROGINS were detected in ovarian cancer patients and healthy controls, only GG type at the position +331 and CC type in PROGINS. There was no significant difference in CAG or GGN repeats of AR between the two groups, while the short set of GGN repeats increased the risk of ovarian cancer by 2.82 times (P<0.05). Neither differentiations nor stages of ovarian cancer were associated with the distribution of STR (P>0.05). Conclusion GGN repeat polymorphism of the AR gene is related to the occurrence of epithelial ovarian cancer, and may be one of the main pathogenic factors.

Keywords: Ovarian neoplasms; Polymorphism; Progesterone receptor; Androgen receptor

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