

临床研究

TRAIL 基因 1595C/T 多态性和 LDD 血瘀证、LDD 风险及严重程度相关研究

安勤德¹* 李云云²

(1. 宝鸡市金台医院骨科, 陕西 宝鸡 721000; 2. 宝鸡市解放军第三医院骨科, 陕西 宝鸡 721000)

摘要:目的 研究肿瘤坏死因子相关凋亡诱导配体 (TRAIL) 基因 1595C/T 多态性与腰椎间盘突出症血瘀证、腰椎间盘突出退变 (LDD) 的发病风险及严重程度的关联性。方法 本研究共纳入了 LDD 患者 230 例和健康对照者 197 例。采用核磁共振施耐德曼分型标准对椎间盘退变进行分级。采用比值比 (OR) 和 95 % 置信区间 (95 % CI) 表示风险比。结果 与对照组相比, LDD 组中 CT 和 TT 基因型频率较低 ($\chi^2 = 11.292, P = 0.004$)。与 CC 基因型相比, CT 和 TT 基因型与 LDD 发病呈负相关 (OR = 0.517, 0.315 - 0.649, $P = 0.009$; OR = 0.397, 0.229 - 0.689, $P = 0.001$)。T 等位点频率与 LDD 患病风险呈负相关 (OR = 0.632, 0.482 - 0.829, $P = 0.001$)。基因型为 CT 和 TT 的患者, 其椎间盘退变分级要低于 CC 基因型患者 ($\chi^2 = 19.452, P < 0.001$)。血瘀证患者椎间盘退变程度比非血瘀证患者更严重 ($P < 0.05$)。另外, 椎间盘退变分级越高, T 等位基因频率越低 ($Z = -4.035, P < 0.001$)。结论 在中国汉族人群中 TRAIL 基因 1595C/T 多态性与 LDD 患病和严重性相关联, 患血瘀型腰椎间盘突出症的可能性更大。

关键词: 肿瘤坏死因子相关凋亡诱导配体; 腰椎间盘突出退变; 血瘀证; 基因多态性

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TRAIL Gene 1595C/T of Polymorphism and LDD Syndrome of Blood Stasis. Risk of LDD and Study on Order of Severity

An Qinde¹ Li Yunyun²

(1. Department of orthopaedics in Jintai Hospital, Baoji, Shaanxi, 72100;

2. Department of orthopaedics in Jiefangjun Third Hospital, Baiji, Shaanxi, 712000)

Abstract Objective Research on tumor necrosis factor - related apoptosis - inducing ligand (TRAIL), Gene 1595C/T in polymorphism and stagnation of blood in prostrution of lumbar intervertebral disc, the risk of attack to lumbar, degeneration and coherence of severity. **Methods** This study bring 230 LDD patient and 197 healthy controls (HC). Adapt nuclear magnetic resonance Schneiderman classification oriterion grading lumbar degeneration. Adapt odds ratio and 95% of confidence interval (95% CT) present risk ratio. Consequence: compare with contrast, from LDD and genotype TT have lower frequency ($\chi^2 = 11.292, P = 0.004$). Compare with genotype CC, CT and genotype TT present negative correlation with the risk of attacking to LDD (OR = 0.517, 0.315 - 0.649, $P = 0.397$, 0.229 - 0.689, $P = 0.001$). Isopotential rate T present negative correlation with genotype CT and genotype TT, their classification of lumbar degeneration lower than patient with genotype CC ($\chi^2 = 19.452, P < 0.001$). Patients with stagnation of blood ($P < 0.05$).