Homeobox

Homeobox proteins have been characterized extensively as transcriptional regulators involved in pattern formation in both invertebrate and vertebrate species.

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A homeobox is a DNA sequence, around 180 base pairs long, found within genes that are involved in the regulation of patterns of anatomical development (morphogenesis) in animals, fungi, and plants. These genes encode homeodomain protein products that are transcription factors sharing a characteristic protein fold structure that binds DNA.

The "homeo-" prefix in the words "homeobox" and "homeodomain" stems from the mutational phenotype known as "homeosis", which is frequently observed when these genes are mutated in animals. Homeosis is a term coined by William Bateson to describe the outright replacement of a discrete body part with another body part.

It has been reported that HOXA transcript at the distal tip (HOTTIP) is dysregulated in various cancers. We performed this meta-analysis to clarify its promising functions as a prognosis marker in malignant tumors. METHODS: The electronic databases, including PubMed, Medline, OVID, Cochrane Library, and Web of Science were searched from inception to September 23, 2016. The hazard ratio (HR) and 95% confidence interval (CI) were calculated to explore the relationship between HOTTIP expression and overall survival (OS), which were extracted from the eligible studies. The odds ratio (OR) was calculated to assess the association between HOTTIP expression and pathological parameters by using RevMan5.3 software. RESULTS: Seven studies were included in the study, with a total of 652 patients. The pooled HR suggested that high HOTTIP expression was significantly correlated with poor OS (HR=2.16, 95% CI: 1.69-2.76, P<0.00001) in cancer patients without obvious heterogeneity. The results showed there was a significant difference in the incidence of lymph node metastasis (LNM) between high HOTTIP expression group and low HOTTIP expression group (OR=2.30, 95% CI: 1.58-3.35, P<0.0001). A similar result was observed in the association between HOTTIP expression and distant metastasis (DM), the odds ratio was 3.30 (95% CI: 1.78-6.12, P=0.0001) without obvious heterogeneity. In addition, high HOTTIP expression was significantly associated with high tumor stage (OR=3.30, 95% CI: 0.25-0.64) without heterogeneity. CONCLUSIONS: This meta-analysis demonstrated that high HOTTIP expression significantly predicts poor OS, lymph node metastasis, distant metastasis and tumor stage, suggesting that high HOTTIP expression may serve as a novel biomarker for poor prognosis in cancers $^{1)}$.

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Fan YH, Yan F, Chai Y, Jiang Y, Zhu X, Wang R. Long non-coding RNA HOTTIP as an independent prognostic marker in cancer. Clin Chim Acta. 2017 Aug 1. pii: S0009-8981(17)30292-9. doi: 10.1016/j.cca.2017.07.031. [Epub ahead of print] Review. PubMed PMID: 28778381.

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