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Classification of neuroblastomas based on an analysis of the expression of genes related to prognosis.

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Abstract

PURPOSE: To select the optimal treatment according to the grade of malignancy of neuroblastoma (NB), it is essential to accurately and rapidly identify genetic abnormalities associated with the prognosis. We have identified BIN1 and **neuronatin** beta as the novel prognosis-related genes for NBs. This study aims to assess the correlation between the combination of the expression level of prognosis-related genes and the outcome of NB.

METHODS: In 44 NB samples, the expression levels of TrkA, BIN1, and **neuronatin** beta were determined using quantitative reverse transcriptase-polymerase chain reaction; furthermore, the correlation between the expression of these genes' expression levels and the clinical progression of NB were assessed.

RESULTS: It was possible to classify 44 NBs into 4 groups regarding the grade of malignancy of NB. These 4 groups were all significantly associated with the clinical stages international NB staging system as well as the outcomes of the patients ($P < .001$, according to the trend test by Kruskal-Wallis exact test).

CONCLUSION: The combination of the expression levels of these genes using quantitative reverse transcriptase-polymerase chain reaction is indicated as the effective method to quickly and accurately evaluate the grade of malignancy of NBs.

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