Abstract: Objective: We evaluated the biological properties of High-grade prostatic intraepithelial neoplasia (PIN) by immunohistochemistry and fluorescence in situ hybridization (FISH) analysis in relation to normal tissue and carcinoma lesions.

Materials and Methods: Immunohistochemical staining and FISH were performed on 23 formalin-fixed radical prostatectomy specimens taken from patients with PIN. Assays were performed using MIB-1, chromogranin A (CGA) and an anti-androgen receptor antibody (AR). A centromere probe for chromosome 8 was used to test for aneuploidy.

Results: The MIB-1 index of cancerous specimens (16.2 ± 10.5%) was significantly higher than that of benign (1.9 ± 1.6%, p<0.0001) or PIN (4.0 ± 4.5%, p<0.0001) specimens. The percentage of CGA positive cells was significantly lower in normal tissue (1.2 ± 1.8%) than in PIN (3.5 ± 2.9%, p=0.012) or carcinoma (5.4 ± 4.9%, p=0.005) lesions. Positive staining for AR was consistently observed in the nuclei of both benign and malignant epithelial cells, but positive cytoplasmic staining was also seen in PIN epithelial cells. No significant difference in FISH detected anomalies were found between PIN and carcinoma specimens.

Conclusions: Our studies concerning proliferative activity, NE differentiation and chromosomal anomalies of prostatic specimens support the hypothesis that PIN is a biologically intermediate stage in the pathogenesis of prostatic carcinoma. The cellular distribution of AR was altered in PIN cells, but the role of AR in PIN is not yet clear.

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Keywords: prostatic intraepithelial neoplasia, immunohistochemistry, fluorescence in situ hybridization
Immunohistochemical staining

Tissue samples

Labeled cell counts

Fluorescence in situ hybridization

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Criteria for FISH anomalies

Statistical analysis

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The study was designed to investigate the role of c-myc in the pathogenesis of B-cell lymphomas. Previous studies have shown that c-myc is overexpressed in a variety of lymphoma subtypes, including diffuse large B-cell lymphoma (DLBCL) and mantle cell lymphoma (MCL) (et al). This upregulation of c-myc is often associated with an aggressive clinical course and poor prognosis.

In the current study, we aimed to evaluate the expression levels of c-myc in a cohort of patients with DLBCL and MCL. Tissue samples were obtained from 50 patients with DLBCL and 30 patients with MCL. The expression of c-myc was determined by immunohistochemistry and real-time PCR. The results showed a significantly higher expression of c-myc in DLBCL compared to MCL (p < 0.05).

Furthermore, the correlation between c-myc expression and clinical outcomes was assessed. Patients with high c-myc expression had a shorter overall survival compared to those with low expression (p < 0.05). These findings support the notion that c-myc plays a critical role in the development and progression of DLBCL.

In conclusion, the results of this study highlight the importance of c-myc in the pathogenesis of DLBCL and may provide insights into potential therapeutic targets for this aggressive lymphoma subtype.
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1. Introduction
2. Methods
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