ARRAY-COMPARATIVE GENOMIC HYBRIDIZATION AS A NOVEL HIGH-THROUGHPUT APPROACH IN BLADDER CANCER TREATMENT

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INTRODUCTION

Bladder cancer (BC) is the second most common genitourinary malignancy with high recurrence rates. BC is the sixth tumor with the highest incidence and the eighth one with the highest mortality.

A GLOBAL PROBLEM

BC is the 9th most common cancer worldwide

Despite their high incidence and prevalence, there has been little progress in diagnosis, prognosis and therapy. Since the prognostic tools currently available have limitations and acquired changes in specific genes are thought to be significant in the development of bladder tumours, we needed to improve the research in this field of genetic changes associated with the BC.

AIM: Characterization of the genomic profile of bladder cancer using the array-Comparative Genomic Hybridization (aCGH) technique.

MATERIAL AND METHODS

Samples collection

Patients, after transurethral resection of bladder tumor

Non-cancer donors

Bladder tumor samples

Control - Bladder tissue samples

DNA extraction

Tissue dissociation

Cell lysis

DNA bonding

Wash

Elution

Amp/GEM

Control - Patient

The control DNA and the patient DNA are labeled with fluorescent dyes and applied to the microarray

Fluorescent signals are measured by the microarray scanner

The data are analyzed by the specific software generating the results

Histopathological information from the patients was analyzed and clinical data registered.

RESULTS

(A) Genomic changes identified in one of the patients of the present study:

1q 13q 18q 21q

Gains

1p 3p 5q 8p

Losses

1q 3q 13q 18q 21q

We did not observe a pattern of chromosomal alterations, as, we did not find imbalances in more than 20% of patients.

Additionally, the sizes of aberrations detected for the same chromosome were often variable between patients.

(B) Ideogram representative of all genomic changes identified:

ch. 11 13 18 21

Gains

ch. 6 10 13 20 21 22

Losses

CONCLUSIONS

This approach allowed us to identify altered chromosomal regions in bladder cancer comparing to normal tissues. In this way, is possible to map fundamental genes related to disease initiation and progression. The correlation between molecular and clinical-pathological data will be fundamental to identify recognized biomarkers with possible diagnostic and prognostic interest.

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