IDENTIFICATION OF BIOMARKERS OF ADVANCED PROSTATE CANCER USING MACHINE-LEARNING TOOLS



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Introduction

There are several challenges in the prognosis of prostate cancer owing to its histologic and genetic heterogeneity. Nowadays, there are few accurate tissue-based biomarkers for prostate cancer aggressiveness. Intelligent processing of accumulated knowledge in the era of artificial intelligence is very promising. Machine learning is a subset of artificial intelligence. Its characteristics could be especially helpful in the management of prostate cancer, especially in digital pathology studies.

Objectives

To investigate the role of decision-support applications of machine learning in prostate cancer biomarker identification. We thought to evaluate the utility of the identified biomarkers and their combinations by developing a highly specific computer-aided algorithm.

Material and methods

Formalin fixed paraffin embedded tissues of 101 prostate carcinomas were stained immunohistochemically for Skp2, Slug, Ki67, p53, AR, PSA, E-cadherin, beta-catenin, CD151, vimentin, periostin and versican, and scored. Carcinomas were classified into localized, advanced and metastatic groups, and ISUP gleason grade groups. (Figure 1). Statistical analysis was performed by SPSS.

Results

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After biomarker evaluation and scoring, conditional target variable composited by patients cases with metastatic stage and high gleason grade group was created. Further, a decision tree (Figure 3) was developed with sets of characteristic rules (Figure 2) that display decision algorithms with their possible consequences, including events with a metastatic stage combined with a high GSgroup e.g. "true (T)" event - if both of these conditions are true and the "false (F)" event without either of these conditions. ROC curve and logistic regression models showed E-cadherin and Ki-67 as independent predictors with significance values of 0,018 and 0,048, respectively. (Figures 4a,b).

Conclusion

We were first to show possible use of machine learning algorithms in prediction of advanced prostate cancer, based on validated and novel tissue biomarkers.





Rule I for F if Ki67= Iow and Ecadherin <= 75 and Ki67 <= 7 then F Rule 2 for F if Ki67 = Iowand Ecadherin <= 75 and PSAtotal > 13,600 and beta catnucl = low then F Rule 3 for F if Ki67= low and Ecadherin > 75 and periostin cyt = lowand beta cat cyt <= 20 then F Rule 4 for F if Ki67= low and Ecadherin > 75 and periostin cyt = low and beta cat cyt >20and <= 35 and Skp2str = 0 then F Rule 5 for F if Ki67= low and Ecadherin > 75 and periostin cyt= low and beta cat cyt > 35then F Rule 6 for F if Ki67 = Iowand Ecadherin > 75 and periostin cyt = high then F

if Ki67= high and Ecadherin = Iow and Skp2str > 0 then F Rule 8 for F if Ki67= high and Ecadherin = high then F RULES FOR T (TRUE) Rule I for T if Ecadherin <= 75 and Ki67> 7 and PSAtotal <= 13,600 then T Rule 2 for T if Ecadherin <= 75 and Ki67> 7 and PSAtotal > 13,600 and betacatnucl = high then T Rule 3 for T if Ki67= low and Ecadherin > 75 and periostincyt = low and betacat cyt> 20and<= 35 and Skp2str > 0 then T Rule 4 for T if Ki67 = highand Ecadherin= Iow and Skp2str <= 0 then T



Figure 1. ISUP 2014 Gleason grade groups.

Figure 2. Decision algorithm rules for "true (T)" event - if both conditions
(metastatic stage and high gleason group) are true and the "false (F)" event without either of these conditions.

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