

## Characterization of Kallireins and microRNAs in Urine Sediment for the Discrimination of Prostate Cancer from Benign Prostatic Hyperplasia

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### Abstract

**Objectives:** Prostate Cancer (PCa) and Benign Prostatic Hyperplasia (BPH) are frequently coexisting in elderly men. The measurement of serum PSA together with Digital Rectal Examination (DRE) represents the primary diagnostic tool to suspect PCa, whereas definitive diagnosis is achieved by prostate biopsy. The low specificity of PSA and the modest detection rate of biopsy convict the patient to a quite often unnecessary and uncomfortable clinical itinerary. There is a urgent need for new and more accurate methodologies to diagnose PCa. In the present study, the expression of 4 mRNAs and 2 miRNAs was evaluated in post DRE urine cell pellets from patients suffering PCa and age-matched subjects affected by BPH with elevated PSA levels. We also evaluated the diagnostic accuracy of markers in predicting PCa.

**Materials and methods:** The expression levels of 4 mRNAs (3 kallikreins - KLK3, KLK11, KLK13 and a prostate cancer antigen - PCA3) and 2 microRNAs (miR-9-3p and miR-19a-3p) were assayed by means of real-time PCR in post DRE urine of 79 men undergoing prostate biopsy for PSA levels > 3 ng/mL. The diagnostic power of tested markers was evaluated through logistic regression analysis.

**Results:** PCA3 was undetectable in 22 out of 38 BPH subjects. KLK3 and KLK11 were significantly up-regulated in PCa group (p value < 0.001), while miR-9-3p and miR-19a-3p were up-regulated in BPH group (p value < 0.001 and < 0.01, respectively). KLK13 was not differentially expressed between groups. MiR-19a-3p and miR-9-3p reached the highest specificity (64.29%) and sensitivity (81.08%), respectively. The more accurate bivariate logistic model was obtained combining KLK11 with either miR-9-3p and miR-19a-3p.

**Conclusions:** Our findings demonstrated that selected kallikreins and miRNAs proved to be an accurate diagnostic tool for PCa. Urine cells pellets obtained after DRE represent a reliable biological matrix for minimally invasive gene expression assays.

**Keywords:** Prostate cancer; Urine sediment; Benign prostatic hyperplasia; Diagnosis; Biomarker; Kallikrein; microRNA

### Introduction

Prostate cancer (PCa) is the most common cancer in European elderly men. Over 200 cases every 100.000 subjects are diagnosed in Northern and Western Europe and a continuous increase is observed in Eastern and Southern Europe [1]. Similarly, Benign Prostatic Hyperplasia (BPH) is a condition closely related to ageing [2] and consists of a benign enlargement of prostatic adenoma size that gives rise to Lower Urinary Tract Symptoms (LUTS). These urinary disorders can occur in up to 30% of men older than 65 years [3]. These two conditions are frequently coexisting, and up to 20% of BPH patients subjected to trans urethral resection of prostate are incidentally found to harbour PCa [4]. PCa and BPH also share relevant features at the genetic level [5] and inflammation has been suggested to play an important role in both urologic conditions [6]. Nonetheless, they take place in different anatomic sites [7] and BPH does not affect the risk of developing PCa [8]. The molecular mechanisms responsible for benign or malignant growth of prostate epithelial cells are partially unknown, although cellular overgrowth is a common event. The measurement of serum PSA together with digital rectal examination (DRE) represents the primary diagnostic tool to suspect PCa, whereas definitive diagnosis is achieved by prostate biopsy [9]. In young men, serum PSA levels < 2-3 ng/mL are considered normal: beyond this value, higher levels of PSA are associated with higher risk of having PCa [9]. Nevertheless, poorly differentiated forms of PCa could have low serum

levels of PSA as well as high serum PSA levels could be due to benign conditions including BPH [10]. The low specificity of PSA, which is a prostate specific and not a cancer specific marker, is the cause of many unnecessary biopsies. On the other hand, the detection rate of baseline biopsy is only 25-38% [11,12], whereas false-negative amounts to about 23% [13]. When PSA levels remain elevated, rebiopsy is performed and PCa can be detected in 7-22% of cases at the first rebiopsy and 2-10% at the second one [14-16]. Moreover, this maneuver is affected by bleeding, urinary infection risk and pain and discomfort for the patient. Thus, the high false positive rate of PSA together with the low detection rate of biopsy convict the patient to a quite often unnecessary and uncomfortable clinical itinerary. Nevertheless these limitations, prostate biopsy remains the standard tool to confirm the diagnosis

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of PCa. These many limitations of current diagnostic management of PCa demonstrate the urgent need for new and more accurate tools and methodologies to detect cancer. KLK3 is the gene coding PSA and belongs to the family of kallikreins (KLKs), which accounts for 15 highly conserved serin proteases which have been demonstrated to be involved in hormone-dependent diseases including PCa [17,18]. The scientific interest towards kallikreins in cancer biomarker discovery is justified by their alterations in expression in several cancers which was demonstrated at the protein level [19-21]. KLK11 proved to be altered in PCa at the protein level [22], whereas KLK13 has been described as a favorable prognostic marker of ovarian cancer [23], and shares 51% amino acid identity with KLK11. PCA3 is a new biomarker which is detectable in post DRE urine sediments. Its diagnostic accuracy for PCa is higher than total PSA in men with elevated PSA levels. Though many studies have demonstrated the ability of PCA3 to detect PCa, its employment in clinical routine is under debate [24].

There is a growing scientific interest in microRNAs as markers for PCa; these small RNAs preside over many cellular functions and regulate gene expression [25] and their alteration has been observed in cancer [26]. The first profiling of miRNA involved in PCa dates back in 2007 [27]: from that point, many progresses have been made towards the characterization of different sets of miRNAs for PCa diagnosis and prognosis [28]. Many studies have demonstrated the modulation of miR-9 in various cancers, while miR-19a-3p belongs to the oncogenic miR-17-19 cluster, also named oncomiR-1 [29]. Both miR-9-3p and miR-19a-3p presented *in silico* affinity binding for PCA3.

The primary aim of the present study was the determination of 4 mRNAs (KLK3, KLK11, KLK13 and PCA3) and 2 miRNAs (miR-9-3p and miR-19a-3p) expression, in post DRE urine cell pellets from patients suffering PCa and age-matched subjects affected by BPH with elevated PSA levels. Secondary aim was to evaluate the diagnostic accuracy of markers in predicting PCa.

## Materials and Methods

### Patients

**Patients** - From June 2012 to April 2013, 41 Caucasian subjects affected by PCa and 38 age-matched subjects with BPH were enrolled. Ethics Committee of the University of Perugia approved the study protocols. All subjects provided written informed consent. PCa group included patients with localized PCa and age < 75 years. Robot assisted radical prostatectomy was performed in all included PCa patients. For PCa group exclusion criteria were age > 75 years, locally advanced or metastatic PCa. BPH group included subjects with negative needle biopsy, PSA levels higher than 3 ng/ml which underwent transurethral prostate resection with confirmed diagnosis of BPH. Exclusion criteria for BPH group were urinary infections, bladder stones, catheterization, age > 75 years. The clinical parameters of all subjects are reported in Table 1. The expression values of KLK3, KLK11, KLK13, miR-9-3p and miR-19a-3p were evaluated in urine sediments and comparisons were made between PCa and BPH groups. Logistic regression analysis was performed to estimate the diagnostic accuracy of markers under analysis in predicting PCa.

### Sample processing

**Urine collection:** First catch voided urine was collected in sterile cups before prostate biopsy and after attentive DRE. Briefly, a firm pressure on the gland from base to apex and from lateral to median side with three strokes for each lobe was performed. Urine was stored at 4°C

and processed within 4 hours. After centrifugation (2000 × g, 10 min, 4°C) cell pellets were washed twice with 1X calcium-free phosphate buffered saline. Cell lysates were obtained adding 300 µL Lysis and Stabilization Buffer (Total RNA Extraction Kit, Norgen Biotek Corp. Ontario, Canada).

**RNA extraction:** Total RNA, including miRNAs, was extracted from cell lysates with Total RNA Extraction Kit (Norgen Biotek Corp. Ontario, Canada) following the manufacturer's recommendations. RNA has been subjected to qualitative and quantitative assessments through Bioanalyzer, Nanodrop and Qubit RNA HS Assay Kit (Life technologies). RNA was stored at -80°C until use.

### Reverse transcription and real-time PCR

**mRNAs:** 15 ng of total RNA were reverse transcribed with SuperScript VILO cDNA Synthesis Kit (Invitrogen, Life Technologies, CA, USA) according to manufacturer's protocol. Real-time PCR assays were performed with Taqman probes (Applied Biosystems, Foster City, CA) on a BioRad iCycler (BioRad, Hercules, CA). The probe sequences used are listed in Table 2. In a total PCR reaction volume of 20 µL, 4 µL of diluted cDNA (1:20) were added. Each sample was run in triplicate and results were averaged. In parallel, negative controls without template were analyzed. The  $\Delta\Delta C_t$  method was used to calculate the

Clinical parameters (total subjects: 79)		PCa (41)	BPH (38)
Median Age		65 (54-75)	66 (48-74)
Median PSA (ng/mL)		7.32 (3.54-50)	7.24 (1.38-21.22)
Clinical Gleason Score	6 (3+3)	32	-
	7 (3+4)	6	
	7 (4+3)	1	
	8 (4+4)	1	
	9 (5+4)	1	
Clinical staging	cT1c	23	-
	cT2a	13	
	cT2c	3	
	cT3a	2	
Pathological Gleason Score	6 (3+3)	29	-
	7 (3+4)	9	
	7 (4+3)	1	
	8 (4+4)	1	
	10 (5+5)	1	
Pathological Staging	pT2a	4	-
	pT2c	28	
	pT3a	6	
	pT3b	3	
Positive Surgical Margin	15%	-	

**Table 1:** Clinical parameters of subjects included in the study.

Gene	Name	Sequence	Exons connected	Amplicon
KLK3	kallikrein-related peptidase 3	NM_001030047.1	1-2	83 bp
	Hs02576345_m1			
KLK11	kallikrein-related peptidase 11	NM_001136032.2	4-5	77 bp
	Hs01100849_m1			
KLK13	kallikrein-related peptidase 13	NM_015596	4-5	82 bp
	Hs01087307_m1			
PCA3	Prostate cancer antigen 3	AF_103907.1	2-3	80 bp
ACTB	Actin beta	NM_001101	2-3	63 bp
	Hs01060665_g1			

**Table 2:** TaqMan Probe sequences used for mRNA analysis.

relative expression of the target genes as follows:  $-\Delta Ct_{\text{target gene}} = -(Ct_{\text{target gene}} - Ct_{\beta\text{actin}})$ .

**microRNAs:** 7.5 ng of total RNA were reverse transcribed with miRCURY LNA™ Universal RT miR PCR, polyadenylation and cDNA synthesis kit (Exiqon) as described in our previous paper [30]. 0.5 µL of RNA spike-in control (UniSp6, provided with the cDNA synthesis kit) was introduced in RT mix (total volume 10 µL) immediately before retrotranscription and served as positive cDNA synthesis control. miRCURY LNA™ specific PCR primer set (Exiqon system) and Exiqon miRCURY LNA Universal RT microRNA PCR SYBR Green master mix were used for real-time PCR amplification. In a total reaction volume of 10 µL, 4 µL of diluted cDNA (1:10). Melting curve analysis was performed at the end of amplification steps (45 cycles). Each sample was run in triplicate and the results were averaged; no-template controls were included in the analysis. For each sample, UniSp6 was used as PCR positive control. PCR reactions were performed on a Bio-Rad iCycler (BioRad, Hercules, CA). MiR-191 was used to normalize data based on the gene stability number obtained from NormFinder algorithm [31]. The  $-\Delta Ct$  method was used to calculate the relative expression of the target genes as follows:  $-\Delta Ct_{\text{target miRNA}} = -(Ct_{\text{target miRNA}} - Ct_{\text{miR-191}})$ .

### Statistical analysis

GraphPad Prism 6.0 (GraphPad Software, Inc., San Diego, CA) was used to evaluate statistical significance between groups. Gene expression data were expressed as  $-\Delta Ct$ s. The significance threshold was set at 0.05. Mann-Whitney test was used to compare the expression levels of selected genes between groups. XLSTAT (Microsoft) was used to carry out Receiver Operating Characteristics (ROC) and logistic predictive models of selected markers in order to evaluate if their combination could ameliorate the proportion of correctly predicted diagnosis and to define cut-offs in the  $\Delta Ct$  values for a positive test. Logistic regression analysis was performed to estimate the accuracy of selected genes in predicting PCa. Prediction models were based on mRNA and miRNA expression values. First, univariate logistic regression analysis was made for each independent variable; differentially expressed genes between PCa and BPH groups were included. Bivariate logistic regression analysis was performed in order to establish the best combination of independent variables able to predict PCa.

### miRNA target prediction and pathway analysis

Computationally predicted mRNA targets of the miRNAs under analysis were identified by TargetScan Release 6.2 (<http://www.targetscan.org>) [32] and MicroCosm Targets version 5 (<http://www.ebi.ac.uk/enright-srv/microcosm>) [33]. The outputs of these target prediction algorithms were merged and all predicted targets (including overlapping targets) were revealed by Microsoft Visual FoxPro 9.0 (Microsoft Corp.) developer tool using the annotation database downloaded from the Ensembl homepage ([www.ensembl.org](http://www.ensembl.org)) [34,35]. Targets of significantly differentially expressed miRNAs were subjected to pathway analysis in all pair-wise comparisons. DIANA mirPath software [36] analysis was also performed using DIANA-MicroT-4.0 and TargetScan 5 prediction algorithms.

## Results

### Qualitative and quantitative assessment of RNA

Total recovery of RNA was not significantly different among samples. Mean RNA integrity number (RIN) was 8.7 (8.3-9.0) and 260/280 ratio was 1.84 (1.84-2.03). Minimal variations in total RNA

content were corrected during reverse transcription using fixed RNA input (15 ng total RNA for KLK3, KLK11, KLK13; 7.5 ng for miR-9-3p and miR-19a-3p). Relative quantification of real-time PCR data was performed referring the levels of selected targets to housekeeping genes ( $-\Delta Ct$ ). Expression levels with standard deviations are reported in Figure 1 and Supplementary Table 1.

### KLK3, KLK11, KLK13

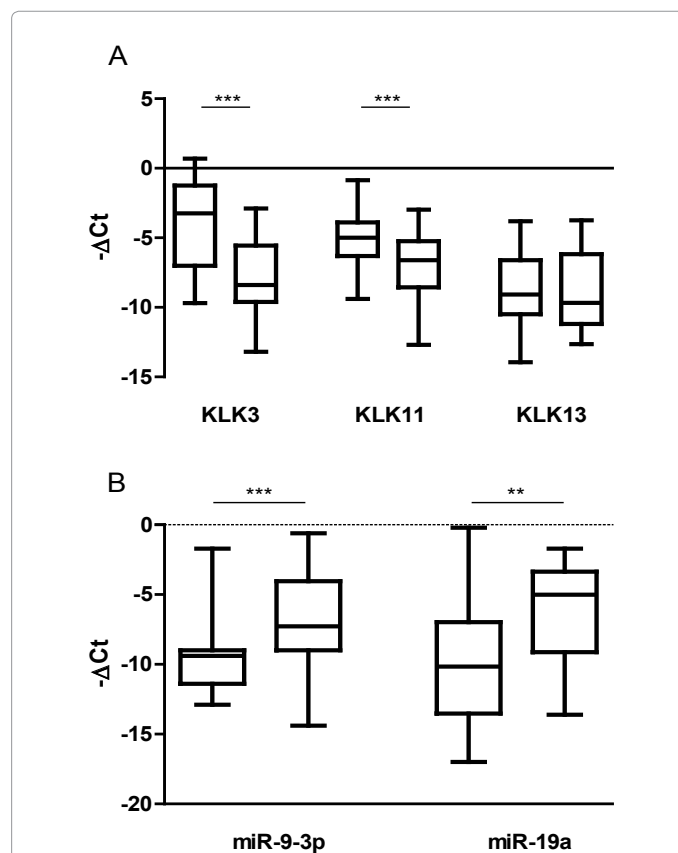
KLK3 and KLK11 were significantly up-regulated in PCa patients with respect to BPH ( $P < 0.001$  and  $P < 0.01$ , respectively) (Figure 1, Panel A). KLK13 was not significantly different between PCa and BPH groups (Figure 1, Panel A). In the univariate logistic regression analysis, KLK11 reached the highest odds ratio (1.579, 95% CI 1.187-2.101) followed by KLK3 (odds ratio 1.575, 95% CI 1.229-2.020).

### PCA3

PCA3 was not determined in 22 out of 38 BPH patients. In PCa group, PCA3 was detectable in all subjects, with mean expression value of  $-6.850 \pm 3.405$ .

### miR-9-3p and miR-19a-3p

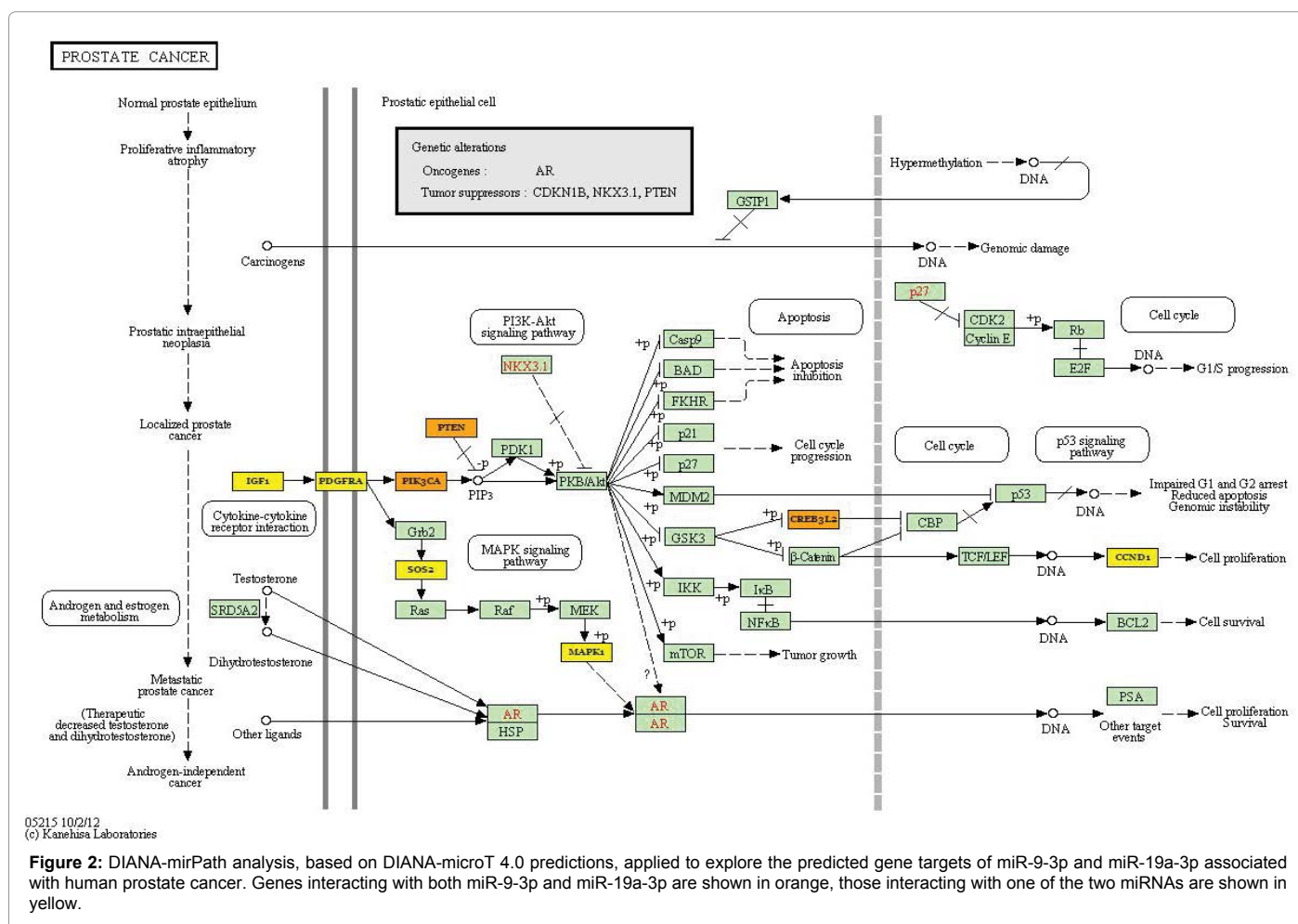
miR-9-3p and miR-19a-3p were downregulated in PCa group with respect to BPH patients ( $P < 0.001$  and  $P < 0.01$ , respectively) (Figure 1, Panel B). In the univariate logistic regression analysis, odds ratios were 0.719 and 0.820 for miR-9-3p and miR-19a-3p, respectively.



**Figure 1:** Expression levels expressed as  $-\Delta Ct$  (median with range and interquartile range) of selected mRNAs (KLK3, KLK11 and KLK13, Panel A) and miRNAs (miR-9-3p, miR-19a-3p, Panel B) between prostate cancer patients (PCa, left) and subjects with benign prostatic hyperplasia (BPH, right). \* $P < 0.05$ ; \*\* $P < 0.01$ ; \*\*\* $P < 0.001$ .

Variable(s)	OR	95% CI	P value	Sensitivity		Hosmer-Lemeshow test (Pr>χ <sup>2</sup> )	β	AUC	
Univariate analysis									
KLK3	1.575	[1.229-2.020]	<0.0001	73.53%	60.87%	0.398	0.851	0.837	
KLK11	1.579	[1.187-2.101]	0.0003	67.65%	62.86%	0.913	0.563	0.739	
miR-9-3p	0.719	[0.588-0.881]	0.0002	81.08%	53.33%	0.359	0.580	0.769	
miR-19a-3p	0.820	[0.718-0.935]	0.001	76.47%	64.29%	0.091	0.494	0.723	
Bivariate analysis									
KLK3+KLK11	KLK3	1.500	[1.167-1.928]	< 0.0001	85.29%	65.22%	0.692	0.758	0.860
	KLK11	1.331	[0.920-1.926]					0.307	
KLK3+miR-9-3p	KLK3	1.631	[1.200-2.216]	< 0.0001	87.10%	72.22%	0.106	0.929	0.877
	miR-9-3p	0.827	[0.612-1.118]					0.293	
KLK3+miR-19a-3p	KLK3	1.833	[1.289-2.607]	< 0.0001	85.71%	72.22%	0.312	1.127	0.880
	miR-19a-3p	0.932	[0.764-1.137]					0.177	
KLK11+miR-9-3p	KLK11	1.420	[1.016-1.985]	0.0001	86.67%	71.43%	0.546	0.404	0.828
	miR-9-3p	0.729	[0.576-0.924]					0.567	
KLK11+miR-19a-3p	KLK11	1.435	[1.006-2.049]	0.0004	78.57%	76.92%	0.500	0.395	0.811
	miR-19a-3p	0.803	[0.688-0.937]					0.529	

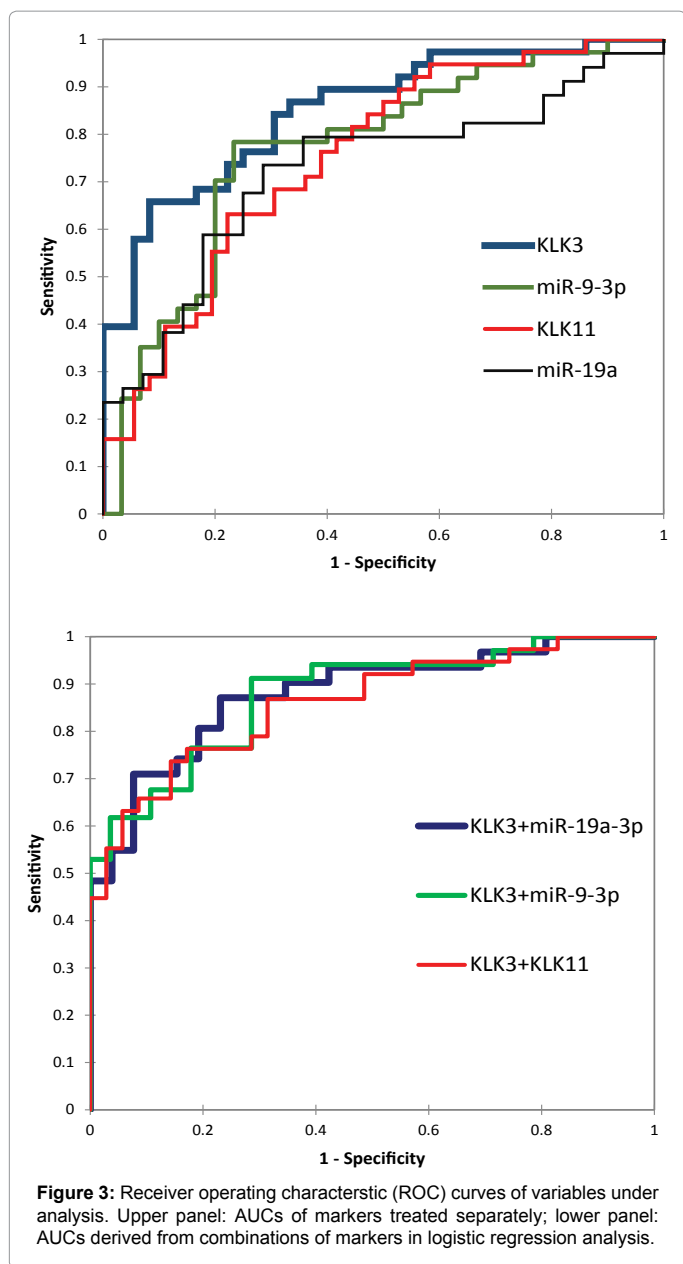
**Table 3:** Logistic regression analysis of variables predicting prostate cancer. Differentially expressed between PCa and BPH group (KLK3, KLK11, miR-9-3p and miR-19a-3p) were included. Prediction models are based on mRNA expression of each gene. |β|, absolute value of regression coefficient; OR, odds ratio; CI, confidence interval; AUC, Area Under Curve.



### Receiver operating characteristics (ROC) and bivariate logistic regression analyses

When treated individually, KLK3 showed the highest AUC

(0,837), followed by miR-9-3p (0,769), KLK11 (0,739) and miR-19a-3p (0,723) (Table 3, Figure 3). The bivariate model which gave the highest specificity (76,92%) and sensitivity (86,67%) were obtained combining KLK11 with miR-19a-3p and miR-9-3p, respectively (Table 3). The



highest AUC (0,880) was reached combining KLK3 with miR-19a-3p (Table 3, Figure 3). Cut-offs of  $\Delta C_t$  values associated with a positive test with corresponding sensitivities and specificities are shown in Supplementary Table 2.

### miRNA target prediction and pathway analysis

Computational target prediction of the 2 differentially expressed miRNAs has been performed with two algorithms: Target Scan Release 6.2 and Micro Cosm Targets Version 5. Among these predictions, 774 (for miR-9-3p) and 1044 (for miR-19a-3p) have been given by MicroCosm. 1237 (for miR-9-3p) and 1171 (for miR-19a-3p) transcripts with conserved sites were found in TargetScan. mRNA targets of differentially expressed miRNAs in all pair-wise comparisons have been subjected to pathway analysis to decipher the function of predicted miRNA targets in biological processes and to identify

pathogenetic pathways potentially modified by posttranscriptional regulation. Results are shown in Figure 2.

### Discussion

The early diagnosis of PCa is of crucial importance to allow for an effective treatment, which could improve cancer-specific survival [37]. Currently, diagnosis of PCa is performed through needle biopsy, whose indications are an elevated PSA level and/or a suspicious DRE [7]. The increase in PSA levels also occurs in benign conditions such as BPH, and this fact leads subjects with BPH and altered PSA levels to be subjected to useless and often repeated biopsies, with discomfort for the patient and high impact on sanitary costs. Both PCa and BPH are ageing-related conditions; this issue is particularly relevant considering the increasing age of population. The molecular mechanisms discriminating benign from malignant growth of prostate epithelial cells are partially unknown, although cellular overgrowth is a common event. The characterization of gene expression signatures exclusive for one of these two urological conditions could greatly improve the clinical management of PCa.

In the present report, the expression levels of 4 mRNAs (three kallikreins - KLK3, KLK11, KLK13 - and a PCa marker - PCA3) and 2 miRNAs (miR-9-3p, miR-19a-3p) were assayed in post DRE urine of men suffering PCa and compared with age-matched subjects with BPH. In these two categories of subjects, serum PSA levels were similar (p value 0.49), demonstrating that they do not represent a reliable discrimination tool. To our knowledge, this is the first report evaluating these molecules in post DRE urine sediments of PCa and BPH patients. We found a significant upregulation of KLK3 and KLK11 in cancer group, while KLK13 did not show significant differences. Higher levels of KLK3 and KLK11 mRNAs were positively correlated with risk of harboring PCa, as showed by univariate logistic regression analysis. A recent study on KLK3 mRNA levels in expressed prostatic secretions showed an increase in specimens obtained from PCa patients [38]. Contrary to these findings, the expression of KLK3 has been reported to be decreased in cancerous prostate tissue [39]. KLK11 and, to a lesser extent, KLK13, are both expressed at the mRNA and protein level in normal prostate tissue [40,41] and KLK11 mRNA is much present in PCa tissues with respect to BPH [42]. Higher KLK13 mRNA levels were demonstrated to be an independent favourable prognostic marker for breast carcinoma [43]. In contrast, another study reported the increase in expression of KLK13 as indicator of poor prognosis in epithelial ovarian carcinoma [44]. PCA3 gene, originally named DD3, was discovered in 1990s [45]. Its deregulation in PCa has been evaluated at the tissue level [45,46] and in post DRE urine sediments [46-48] also compared to subjects with BPH [49]. These studies also revealed that the use of this test might raise the specificity of diagnosis of PCa. In our study, PCA3 mRNA was detectable in all subjects of PCa group, whereas it was undetectable in 22 out of 38 patients with BPH. This issue made statistical comparisons between groups unfeasible.

MicroRNAs represent another growing branching the research field of non-invasive diagnostic/prognostic cancer markers [26], because of their intrinsic stability in body fluids such as blood and urine [50]. The convergent alteration of the same sets of miRNAs in much pathology reflects their involvement in many crucial steps of carcinogenesis (Figure 2). miRNAs can act either as oncogenes or oncosuppressors, although their behaviour cannot be generalized to every type of cancer [51]. Several molecular events are potentially responsible for the alteration of miRNAs in cancer: among all, the imbalance of post-transcriptional regulation, genetic modifications

and epigenetic alterations seem to play a major role. It is difficult to establish if a particular miRNA exerts its action as a tumor suppressor or oncogene, since this depends on many factors which vary according to tumor characteristic and other unknown contextual factors. We found both miR-9-3p and miR-19a-3p to be up-regulated in urine sediments from BPH group with respect to PCa patients. Many studies have demonstrated the epigenetic silencing of miR-9 loci in gastric tumors [52], breast cancer [53], non-small-cell lung cancer [54], oral squamous cell carcinoma [55] and renal cancer [56]. Contrary to these findings, miR-9 has been shown to increase in Hodgkin's lymphoma [57] and c-myc-induced mammary tumors [58]; this is an interesting issue, since MYC is responsible for the balanced expression of many miRNAs, such as the oncogenic miR-17-19 cluster, also named oncomiR-1 [26]. The miR-19 family belongs to the miR-17-92 cluster. The overexpression of miR-19a has been observed in prostate tumor tissues compared to adjacent benign tissue [59]. In prostate cancer cell lines, an upregulation has been shown in PC3 androgen-independent cell lines, whereas a downregulation was recorded in LNCaP androgen-dependent strain, compared to normal prostatic epithelial (PrEC) cells [60]. Recently, miR-19a was found to directly repress RAB13, which is able to tight cellular junctions, favouring metastasis formation in PCa [61]. These findings support our results since cancer patients included in the present study all harboured androgen-responsive and organ-confined tumors.

In our univariate logistic regression analysis, all differentially expressed genes between PCa and BPH groups showed acceptable confidence intervals (CI) of odds ratios. *KLK3* and *KLK11* mRNA levels positively correlated with risk of PCa (odds ratios > 1), whereas higher levels of miR-9-3p and miR-19a-3p transcripts were inversely correlated with cancer outcome (odds ratios < 1). The highest sensitivity and specificity was reached by miR-9-3p and miR-19a-3p, respectively. Bivariate logistic regression models were made in order to verify if a combination of variable could improve predictive power for PCa. The best model was obtained combining *KLK11* with either miR-19a-3p or miR-9-3p, which significantly improved specificity (+14.06%) and sensitivity (+19.02%) of *KLK11* alone. The highest AUC was reached combining *KLK3* with miR-19a-3p. Our findings demonstrated that selected kallikreins and miRNAs proved to be an accurate diagnostic tool for PCa. Urine cells pellets obtained after DRE represent a reliable biological matrix for minimally invasive gene expression assays. We did not perform a stratification of PCa patients into low, intermediate and high risk subgroups since the vast majority of them were affected by low risk disease.

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#### References

1. Arnold M, Karim-Kos HE, Coebergh JW, Byrnes G, Antilla A, et al. (2013) Recent trends in incidence of five common cancers in 26 European countries since 1988: Analysis of the European Cancer Observatory. *Eur J Cancer*.
2. Chute CG, Panser LA, Gorman CJ, Oesterling JE, Guess HA, et al. (1993) The prevalence of prostatism: a population-based survey of urinary symptoms. *J Urol* 150: 85-89.
3. Chapple CR (1999) BPH Disease Management. Introduction and concluding remarks. *Eur Urol* 36 Suppl 3: 1-6.
4. Otto B, Barbieri C, Lee R, Te AE, Kaplan SA, et al. (2014) Incidental prostate cancer in transurethral resection of the prostate specimens in the modern era. *Adv Urol* 2014: 627290.
5. Shah US, Getzenberg RH (2004) Fingerprinting the diseased prostate: associations between BPH and prostate cancer. *J Cell Biochem* 91: 161-169.
6. De Nunzio C, Kramer G, Marberger M, Montironi R, Nelson W, et al. (2011) The Controversial Relationship Between Benign Prostatic Hyperplasia and Prostate Cancer: The Role of Inflammation. *Eur Urol* 60: 106-117.
7. McNeal JE, Redwine EA, Freiha FS, Stamey TA (1988) Zonal distribution of prostatic adenocarcinoma. Correlation with histologic pattern and direction of spread. *Am J Surg Pathol* 12: 897-906.
8. De Marzo AM, Coffey DS, Nelson WG (1999) New concepts in tissue specificity for prostate cancer and benign prostatic hyperplasia. *Urology* 53: 29-39.
9. Heidenreich A, Bellmunt J, Bolla M, Joniau S, Mason M, et al. (2011) EAU guidelines on prostate cancer. Part 1: screening, diagnosis, and treatment of clinically localised disease. *Eur Urol* 59: 61-71.
10. Thompson IM, Pauler DK, Goodman PJ, Tangen CM, Lucia MS, et al. (2004) Prevalence of prostate cancer among men with a prostate-specific antigen level < or =4.0 ng per milliliter. *N Engl J Med* 350: 2239-2246.
11. Lui PD, Terris MK, McNeal JE, Stamey TA (1995) Indications for ultrasound guided transition zone biopsies in the detection of prostate cancer. *J Urol* 153: 1000-1003.
12. Terris MK (2000) Extended field prostate biopsies: too much of a good thing? *Urology* 55: 457-460.
13. Murphy AM, McKiernan JM, Olsson CA (2004) Controversies in prostate cancer screening. *J Urol* 172: 1822-1824.
14. Postma R, Roobol M, Schröder FH, van der Kwast TH (2004) Lesions predictive for prostate cancer in a screened population: first and second screening round findings. *Prostate* 61: 260-266.
15. Mian BM, Naya Y, Okihara K, Vakar-Lopez F, Troncoso P, et al. (2002) Predictors of cancer in repeat extended multisite prostate biopsy in men with previous negative extended multisite biopsy. *Urology* 60: 836-840.
16. Antunes AA, Freire Gde C, Aiello Filho D, Cury J, Srougi M (2006) Analysis of the risk factors for incidental carcinoma of the prostate in patients with benign prostatic hyperplasia. *Clinics (Sao Paulo)* 61: 545-550.
17. Borgoño CA, Diamandis EP (2004) The emerging roles of human tissue kallikreins in cancer. *Nat Rev Cancer* 4: 876-890.
18. Pampalakis G, Sotiropoulou G (2007) Tissue kallikrein proteolytic cascade pathways in normal physiology and cancer. *Biochim Biophys Acta* 1776: 22-31.
19. Diamandis EP, Yousef GM, Soosaipillai AR, Bunting P (2000) Human kallikrein 6 (zyme/protease M/neurosin): a new serum biomarker of ovarian carcinoma. *Clin Biochem* 33: 579-583.
20. Obiezu CV, Scorilas A, Katsaros D, Massobrio M, Yousef GM, et al. (2001) Higher human kallikrein gene 4 (KLK4) expression indicates poor prognosis of ovarian cancer patients. *Clin Cancer Res* 7: 2380-2386.
21. Yousef GM, Scorilas A, Jung K, Ashworth LK, Diamandis EP (2001) Molecular cloning of the human kallikrein 15 gene (KLK15). Up-regulation in prostate cancer. *J Biol Chem* 276: 53-61.
22. Diamandis EP, Okui A, Mitsui S, Luo LY, Soosaipillai A, et al. (2002) Human kallikrein 11: a new biomarker of prostate and ovarian carcinoma. *Cancer Res* 62: 295-300.
23. Scorilas A, Borgoño CA, Harbeck N, Dorn J, Schmalfeldt B, et al. (2004) Human kallikrein 13 protein in ovarian cancer cytosols: a new favorable prognostic marker. *J Clin Oncol* 22: 678-685.
24. Auprich M, Bjartell A, Chun FK, de la Taille A, Freedland SJ, et al. (2011) Contemporary role of prostate cancer antigen 3 in the management of prostate cancer. *Eur Urol* 60: 1045-1054.
25. Reinhart BJ, Slack FJ, Basson M, Pasquinelli AE, Bettinger JC, et al. (2000) The 21-nucleotide let-7 RNA regulates developmental timing in *Caenorhabditis elegans*. *Nature* 403: 901-906.
26. Jansson MD, Lund AH (2012) MicroRNA and cancer. *Mol Oncol* 6: 590-610.
27. Porkka KP, Pfeiffer MJ, Waltering KK, Vessella RL, Tammela TL, et al. (2007) MicroRNA expression profiling in prostate cancer. *Cancer Res* 67: 6130-6135.

28. Hassan O, Ahmad A, Sethi S, Sarkar FH (2012) Recent updates on the role of microRNAs in prostate cancer. *J Hematol Oncol* 5: 9.
29. He L, Thomson JM, Hemann MT, Hernando-Monge E, Mu D, et al. (2005) A microRNA polycistron as a potential human oncogene. *Nature* 435: 828-833.
30. Egidi MG, Cochetti G, Serva MR, Guelfi G, Zampini D, et al. (2013) Circulating microRNAs and kallikreins before and after radical prostatectomy: are they really prostate cancer markers? *Biomed Res Int* 2013: 241780.
31. Vandesompele J, De Preter K, Pattyn F, Poppe B, Van Roy N, et al. (2002) Accurate normalization of real-time quantitative RT-PCR data by geometric averaging of multiple internal control genes. *Genome Biol* 3: RESEARCH0034.
32. Lewis BP, Burge CB, Bartel DP (2005) Conserved seed pairing, often flanked by adenosines, indicates that thousands of human genes are microRNA targets. *Cell* 120: 15-20.
33. Enright AJ, John B, Gaul U, Tuschl T, Sander C, et al. (2003) MicroRNA targets in *Drosophila*. *Genome Biol* 5: R1.
34. Tömböl Z, Szabó PM, Molnár V, Wiener Z, Tölgyesi G, et al. (2009) Integrative molecular bioinformatics study of human adrenocortical tumors: microRNA, tissue-specific target prediction, and pathway analysis. *Endocr Relat Cancer* 16: 895-906.
35. Peter MS, Zsofia T, Viktor M, Andras F, Karoly R, et al. (2010) MicroRNA target prediction: problems and possible solutions. *Curr Bioinform* 5: 81-88.
36. Papadopoulos GL, Alexiou P, Maragkakis M, Reczko M, Hatzigeorgiou AG (2009) DIANA-mirPath: Integrating human and mouse microRNAs in pathways. *Bioinformatics* 25: 1991-1993.
37. Bill-Axelson A, Holmberg L, Garmo H, Rider JR, Taari K, et al. (2014) Radical prostatectomy or watchful waiting in early prostate cancer. *N Engl J Med* 370: 932-942.
38. Whelan C, Crocitto L, Kawachi M, Chan K, Smith D, et al. (2013) The influence of PSA-RNA yield on the analysis of expressed prostatic secretions (EPS) for prostate cancer diagnosis. *Can J Urol* 20: 6597-6602.
39. Väänänen RM, Lilja H, Cronin A, Kauko L, Rissanen M, et al. (2013) Association of transcript levels of 10 established or candidate-biomarker gene targets with cancerous versus non-cancerous prostate tissue from radical prostatectomy specimens. *Clin Biochem* 46: 670-674.
40. Petraki CD, Papanastasiou PA, Karavana VN, Diamandis EP (2006) Cellular distribution of human tissue kallikreins: immunohistochemical localization. *Biol Chem* 387: 653-663.
41. Stavropoulou P, Gregorakis AK, Plebani M, Scorilas A (2005) Expression analysis and prognostic significance of human kallikrein 11 in prostate cancer. *Clin Chim Acta* 357: 190-195.
42. Scorilas A, Gregorakis AK (2006) mRNA expression analysis of human kallikrein 11 (KLK11) may be useful in the discrimination of benign prostatic hyperplasia from prostate cancer after needle prostate biopsy. *Biol Chem* 387: 789-793.
43. Chang A, Yousef GM, Scorilas A, Grass L, Sismondi P, et al. (2002) Human kallikrein gene 13 (KLK13) expression by quantitative RT-PCR: an independent indicator of favourable prognosis in breast cancer. *Br J Cancer* 86: 1457-1464.
44. White NM, Mathews M, Yousef GM, Prizada A, Popadiuk C, et al. (2009) KLK6 and KLK13 predict tumor recurrence in epithelial ovarian carcinoma. *Br J Cancer* 101: 1107-1113.
45. Bussemakers MJ, van Bokhoven A, Verhaegh GW, Smit FP, Karthaus HF, et al. (1999) DD3: a new prostate-specific gene, highly overexpressed in prostate cancer. *Cancer Res* 59: 5975-5979.
46. Hessels D, Klein Gunnewiek JM, van Oort I, Karthaus HF, van Leenders GJ, et al. (2003) DD3(PCA3)-based molecular urine analysis for the diagnosis of prostate cancer. *Eur Urol* 44: 8-16.
47. Hessels D, Schalken JA (2009) The use of PCA3 in the diagnosis of prostate cancer. *Nat Rev Urol* 6: 255-261.
48. van Gils MP, Hessels D, van Hooij O, Jannink SA, Peelen WP, et al. (2007) The time-resolved fluorescence-based PCA3 test on urinary sediments after digital rectal examination; a Dutch multicenter validation of the diagnostic performance. *Clin Cancer Res* 13: 939-943.
49. Moradi Sardareh H, Goodarzi MT, Yadegar-Azari R, Poorolajal J, Mousavi-Bahar SH, et al. (2014) Prostate cancer antigen 3 gene expression in peripheral blood and urine sediments from prostate cancer and benign prostatic hyperplasia patients versus healthy individuals. *Urol J* 11: 1952-1958.
50. Mall C, Rocke DM, Durbin-Johnson B, Weiss RH (2013) Stability of miRNA in human urine supports its biomarker potential. *Biomark Med* 7: 623-631.
51. Fabbri M, Ivan M, Cimmino A, Negrini M, Calin GA (2007) Regulatory mechanisms of microRNAs involvement in cancer. *Expert Opin Biol Ther* 7: 1009-1019.
52. Tsai KW, Liao YL, Wu CW, Hu LY, Li SC, et al. (2011) Aberrant hypermethylation of miR-9 genes in gastric cancer. *Epigenetics* 6: 1189-1197.
53. Lehmann U, Hasemeier B, Christgen M, Müller M, Römermann D, et al. (2008) Epigenetic inactivation of microRNA gene hsa-mir-9-1 in human breast cancer. *J Pathol* 214: 17-24.
54. Kitano K, Watanabe K, Emoto N, Kage H, Hamano E, et al. (2011) CpG island methylation of microRNAs is associated with tumor size and recurrence of non-small-cell lung cancer. *Cancer Sci* 102: 2126-2131.
55. Minor J, Wang X, Zhang F, Song J, Jimeno A, et al. (2012) Methylation of microRNA-9 is a specific and sensitive biomarker for oral and oropharyngeal squamous cell carcinomas. *Oral Oncol* 48: 73-78.
56. Hildebrandt MA, Gu J, Lin J, Ye Y, Tan W, et al. (2010) Hsa-miR-9 methylation status is associated with cancer development and metastatic recurrence in patients with clear cell renal cell carcinoma. *Oncogene* 29: 5724-5728.
57. Leucci E, Zriwil A, Gregersen LH, Jensen KT, Obad S, et al. (2012) Inhibition of miR-9 de-represses HuR and DICER1 and impairs Hodgkin lymphoma tumour outgrowth in vivo. *Oncogene* 31: 5081-5089.
58. Sun Y, Wu J, Wu SH, Thakur A, Bollig A, et al. (2009) Expression profile of microRNAs in c-Myc induced mouse mammary tumors. *Breast Cancer Res Treat* 118: 185-196.
59. He HC, Han ZD, Dai QS, Ling XH, Fu X, et al. (2013) Global analysis of the differentially expressed miRNAs of prostate cancer in Chinese patients. *BMC Genomics* 14: 757.
60. Albertini MC, Olivieri F, Lazzarini R, Pilolli F, Galli F, et al. (2011) Predicting microRNA modulation in human prostate cancer using a simple String Identifier (SID1.0). *J Biomed Inform* 44: 615-620.
61. Mo W, Zhang J, Li X, Meng D, Gao Y, et al. (2013) Identification of novel AR-targeted microRNAs mediating androgen signalling through critical pathways to regulate cell viability in prostate cancer. *PLoS One* 8: e56592.