Assessment of Skeletal Muscle Strength, Fatigue and Respiratory Efficiency in Young Healthy Females during Different Phases of Menstrual Cycle

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Background. Fluctuating levels of sex steroids across the menstrual cycle not only produce physiological changes in the reproductive system but also affect skeletal muscle strength and the respiratory efficiency. Increasing participation of women in competitive sports has drawn attention of the scientists to understanding of the effect of the menstrual cycle on athletic performance. Physical work capacity depends on respiratory efficiency and skeletal muscle strength.

Objectives. To evaluate skeletal muscle performance and respiratory efficiency during different phases of menstrual cycle in non-athletic eumenorrheic women.

Materials & methods. Fifty non-athletic healthy female subjects aged between 20-30 years of age with normal BMI and history of regular menstrual cycle have been selected. Muscle strength and time of fatigue has been determined using hand grip dynamometer. Respiratory efficiency has been assessed using respiratory blast test and respiratory endurance test during premenstrual and proliferative phase of menstrual cycle. Student’s paired test has been used for analyzing of the data. P < 0.05 has been considered to be statistically significant.

Result. Muscle strength, respiratory blast test and respiratory endurance tests are not statistically significant during different phases of menstrual cycle. Time of fatigue is significantly higher (p < 0.05) during the proliferative phase compared to the premenstrual phase.

Conclusion. In females, muscles undergo easy fatigability during premenstrual phase hence it has to be considered during athletic training and selection program.

Key words. follicular phase, luteal phase, respiratory blast test, respiratory endurance, skeletal muscle performance.

Radiogenomics of Renal Cell Carcinoma: Our Clinical Experience

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Renal cell carcinoma (RCC) is relatively common pathology that is found roughly in 3% of all cases of malignant neoplasia in adults and approximately in 90% of malignant tumors arising because of a kidney [10]. Associations
between imaging features and genomic landscape of RCC have been recently
investigated in order to characterize better tumor, diagnosing more precisely,
staging and establishing more accurate prognosis comparing to classic histo-
pathologic approach. Such integration of imaging and molecular biomarkers
has led to novel concept of “radiogenomics” or “radiogenetics” [4, 5, 7]. A great
number of investigators have assessed a role of certain microRNAs (miR) in
context of RCC radiogenomics, however the quantity of such works is quite
small [3, 4, 9].

In our previous work we have already described usefulness of expression of
mi-R-15a measured in urine during RCC diagnostics [1]. Moreover, high miR-15a
expression values have been significantly associated with poor survival rates
in patients with RCC [2].

The purpose. The goal of the study is investigation of associations between
cross-sectional imaging features of RCC and urine expression levels of miR-15a.

Materials and methods. Conducting of the research has been approved
by Ethical Committee of Danylo Halytsky Lviv National Medical University,
Ukraine (protocol № 5, 05.25.2015), and has been carried out in accordance
with ethical standards formulated in the Declaration of Helsinki 1975. Our
study has been conducted at Urology Department of this institution and at
General and Molecular Pathophysiology Department of Bogomoletz Institute of
Physiology of National Academy of Sciences of Ukraine during 2015-2017 years.

52 adult patients with RCC according to clinical and imaging data have
been engaged in the study. The size of the tumors have ranged from 2,08 to
12,7 sm and average size of 7,01 ± 2,08 cm. Percutaneous kidney biopsy or
previous kidney tumor treatment has been performed in all patients. In all
patients’ multiphase CT or MRI imaging with contrast enhancement has been
performed prior to surgical treatment using standard abdominal protocols [6].
In all cases urine collecting and miR-15a expression measuring has been per-
formed according to earlier described method, using quantitative polymerase
chain reaction [1]. Associations between miR-15a expression and such RCC
imaging features as necrosis, renal vein invasion, presence of intratumoral cal-
cifications, definition of tumor margin and architecture, presence of collecting
system invasion, intratumoral hypervascularity, homogeneous or nodular tu-
mor enhancement pattern on nephrographic phase images have been assessed.
All patients have been treated surgically with following pathologic analysis.

Microsoft Excel 2016 and SPSS v.22 software packages have been used for
the statistical data processing.

Results and discussion. RCC cases have been classified concordantly
to 7th edition of AJCC cancer staging manual: T1aN0M0 (n = 13, 25,0 %),
T1bN0M0 (n = 15, 28,85 %), T2aN0M0 (n = 12, 23,08 %), T2bN0M0 (n = 5,
9,62 %), T3aN0M0 (n = 4, 7,69 %), T3aN1M0 (n = 3, 5,77 %). Based on
pathologic analysis all RCCs have been classified according to histologic sub-
types – clear cell RCC (n = 22), papillary RCC (n = 16), chromophobe RCC
(n = 14). Simplified two-tiered Fuhrman grading system has been used, in
which grades I and II (low grade, n = 12) and grades III and IV (high grade,
n = 10) have been combined for the clear cell RCC grading.

As a result of our investigation we have found significant evidences of as-
sociations between miR-15a expression levels and RCC imaging features. The
expression values of miR-15a in urine of patients with RCC have varied from
91,35 to 5,52 relative fluorescence units (RFU), average has been – 54,58 ± 37,76
RFU. High expression levels of miR-15a (> 25 RFU) in patients with RCC have
been common in presence of such tumor imaging features as necrosis (p < 0,05),
ill-defined margins of the lesion (p < 0,05) and intratumoral hypervascularity
(p < 0,01). Lower miR-15a expression levels (< 25 RFU) have been associated
with imaging evidence of renal vein (p < 0,05) and collecting system (p < 0,05)
invasion, nodular tumor enhancement pattern on nephrographic phase images
(p < 0,05) and multicystic tumor architecture (p < 0,05). However, there has
not been significant association between miR-15a expression and presence of intratumoral calcifications on cross-sectional images (p > 0.05). The mean values of miR-15a expression for each of RCC imaging characteristics as well their frequency are presented on figure 1.

**Conclusions.** Radiogenomic analysis may provide valuable information for predicting of miR-15a expression levels in urine of patients with RCC. In clinical conditions under which there is no possibility to perform genetic assay, imaging features of RCC can be used as surrogates of miR-15a expression to perform prognostication of disease biologic behavior.

![Figure 1. Associations between RCC imaging features and mean miR-15 expression levels in urine](image-url)

**REFERENCES**


RESEARCH ARTICLES

Radiogenomics of Renal Cell Carcinoma: Our Clinical Experience

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Renal cell carcinoma (RCC) is relatively common pathology that is found roughly in 3 % of all cases of malignant neoplasia in adults and approximately in 90 % of malignant tumors arising because of a kidney. Associations between imaging features and genomic landscape of RCC have been recently investigated in order to characterize better tumor diagnosting more precisely, staging and establishing more accurate prognosis comparing to classic histopathologic approach. Such integration of imaging and molecular biomarkers has led to novel concept of “radiogenomics”. In our previous work we have already described usefulness of expression of mi-R-15a measured in urine during RCC diagnostics. Moreover, high miR-15a expression values have been significantly associated with poor survival rates in patients with RCC.

The purpose. The goal of the study is investigation of the associations between cross-sectional imaging features of RCC and urine expression levels of miR-15a.

Materials and methods. 52 adult patients with RCC according to clinical and imaging data have been engaged into study. In all patients’ multiphase CT or MRI imaging with contrast enhancement has been performed prior to surgical treatment using standard abdominal protocols. Urine collecting and miR-15a expression measuring has been performed using quantitative polymerase chain reaction. Associations between miR-15a expression and such RCC imaging features as necrosis, renal vein invasion, presence of intratumoral calcifications, definition of tumor margin and architecture, presence of collecting system invasion, intratumoral hypervascularity, homogeneous or nodular tumor enhancement pattern on nephrographic phase images have been assessed. All patients have been treated surgically with the following pathologic analysis.

Results. RCC cases have been classified concordantly to AJCC cancer staging manual: T1aN0M0 (n = 13, 25,0 %), T1bN0M0 (n = 15, 28,85 %), T2aN0M0 (n = 12, 23,08 %), T2bN0M0 (n = 5, 9,62 %), T3aN0M0 (n = 4, 7,69 %), T3aN1M0 (n = 3, 5,77 %). RCCs have been classified according to histologic subtypes – clear cell RCC (n = 22), papillary RCC (n = 16), chromophobe RCC (n = 14). Simplified two-tiered Fuhrman grading system has been used, in which grades I and II (low grade, n = 12) and grades III and IV (high grade, n = 10) have been combined. The expression values of miR-15a in urine of patients with RCC have varied from 91,35 to 5,52 relative fluorescence units (RFU), mean – 54,58 \( \pm \) 37,76 RFU. High expression levels of miR-15a (> 25 RFU) in patients with RCC have been associated with necrosis (p < 0,05), ill-defined margins of the lesion (p < 0,05) and intratumoral hypervascularity (p < 0,01). Lower miR-15a expression levels (< 25 RFU) have been associated with imaging evidence of renal vein (p < 0,05) and collecting system (p < 0,05) invasion, nodular tumor enhancement pattern (p < 0,05) and multicystic tumor architecture (p < 0,05). There has been no significant association between miR-15a expression and presence of intratumoral calcifications on cross-sectional images (p>0,05).

Conclusions. Radiogenomic analysis may provide valuable information for predicting of emiR-15a expression levels in urine of patients with RCC. In clinical conditions under which there is no possibility to perform genetic assay, imaging features of RCC can be used as surrogates of miR-15a expression to perform prognostication of disease biologic behavior.

Key words: renal cell carcinoma, radiogenomics, microRNA, imaging, biomarker.