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Metabolic profiling of renal cell carcinoma tissue using gas chromatography metabolomics

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Abstract

Background: Renal cell carcinoma (RCC) is marked by dysregulation of angiogenesis, energy metabolism, and nutrient sensing pathways [1]. This diversity is an obstacle to achieving long-term responses to treatment, notwithstanding progress in targeted and immunotherapeutic drugs. Objective: This study aimed to characterise the metabolic dysregulations that occur in RCC tissue using a metabolomics approach. Methods: Tumour and non-tumour kidney tissues were collected from 18 patients who underwent nephrectomy at the Portuguese Oncology Institute of Porto (IPO-Porto). Ethical approval (238/2018) and written consent were obtained. Tissues were homogenised, and metabolites were extracted using a methanol-water technique. Metabolites were then analysed by gas chromatography-mass spectrometry (GC-MS) analysis. Statistical methods and pathway analysis were used to interpret potential dysregulations associated with RCC. Results: RCC tissue showed a significant reduction in amino acid levels (including alanine, asparagine, aspartate, serine, tyrosine, among others), except for β -alanine and glutamate, which exhibited significant elevated levels. Perturbations in organic acids were observed, with a significant decrease in fumarate and gluconate levels and an increase in 3-aminobutyrate, citrate, and lactate. Increased levels of glucose and maltose were also found in RCC tissue, whereas sugar derivatives such as myoinositol and scyllo-inositol showed decreased levels. Pathway analysis suggested dysregulation in amino acid, energy (TCA cycle, pyruvate metabolism), sugar, and glutathione metabolism pathways in RCC tissue. Conclusions: These results reveal the metabolic reprogramming related with the development and progression of RCC. Understanding these alterations provides important insights for improving RCC treatment strategies.

Keywords: renal cell carcinoma; tissue; metabolic reprogramming; metabolomics

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References

1. Zhu, H.; Wang, X.; Lu, S.; Ou, K. Metabolic reprogramming of clear cell renal cell carcinoma. Front Endocrinol (Lausanne) (2023), 14, 1195500.



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