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SALIVA AND URINE METABOLOME IN KIDNEY TRANSPLANT RECIPIENTS.

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INTRODUCTION & AIM

Metabolome represents the collection of low molecular weight compounds that originate from metabolic pathways of the body, drugs, and microorganisms in the oral cavity. Small molecules extracted from tissues or detected in body fluids are measured using mass spectrometry.

Targeted approaches using quantitative assays and validated by LC-MS/MS have indicated that intermediates of the transmethylation pathway, as well as arachidonic acid-derived bioactive metabolites, might be predictive markers for kidney transplant rejection.

Metabolomics analysis of oral cavity samples facilitates differentiation between patients with periodontitis and healthy individuals.

The aim of this study was to evaluate the biofluid metabolome of kidney transplant recipients and their possible association with periodontitis.

METHOD

- ✓ Cross-sectional, analytical, and descriptive study;
- ✓ Four groups;
- ✓ Urine and saliva collections;
- ✓ Gas Chromatography-Mass Spectrometry (GC-MS/MS);
- ✓ Statistical programs: Statistica 12, SPSS 20, Past 3.0, Origin Pro 2019, and MetaboAnalys 5.0

Inclusion criteria: (i) kidney transplantation; (ii) diagnosis of periodontitis; (iii) sites presenting probing pocket depth (PPD) ≥ 4 mm; (iv) those who underwent immunosuppressive therapy; and (v) GC without systemic changes and without the use of medications.

Exclusion criteria: Patients who (i) were pregnant or lactating; (ii) had received a course of periodontal treatment within the last 6 months; (iii) had fever, lower extremity edema, infection, received corticosteroid pulse therapy, uncontrolled hypertension, dyspnea, (iv) total toothless and (v) were not able to provide consent to participate in the study.

61 patients

GT: kidney transplant recipients without periodontal disease (n = 11);

GTDP: kidney transplant recipients with periodontal disease (n = 12);

GCDP: normal renal function with periodontal disease (n = 19)

CG: normal renal function without periodontal disease (n = 19)

CONCLUSION

- ✓ There was no significant difference between the salivary and urinary metabolites when compared among the four groups;
- ✓ It was possible to differentiate the specific metabolites for each group and the relationships between them;
- ✓ The metabolites expressed in groups with periodontal disease were related to bacterial metabolism and anaerobic cell respiration;
- ✓ The most important metabolite for determining the pattern of PCA performed in saliva and urine samples was ornithine-d7-4 and palmitoleic acid, respectively

RESULTS

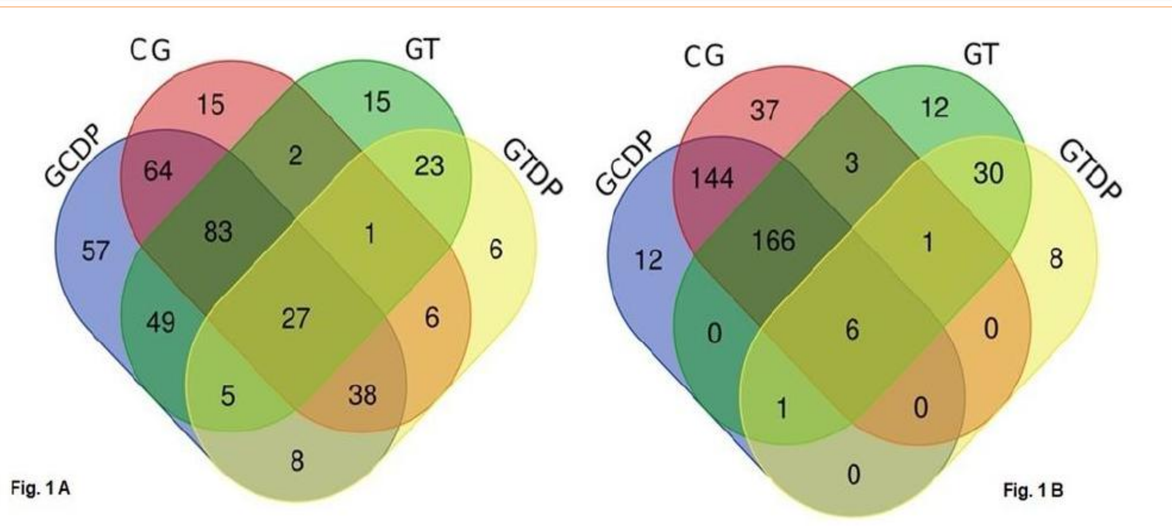

Fig. 1 A and 1 B - Venn diagram representing the number of metabolites in saliva (1 A) and urine (1 B), exclusive for each group and shared among the groups.

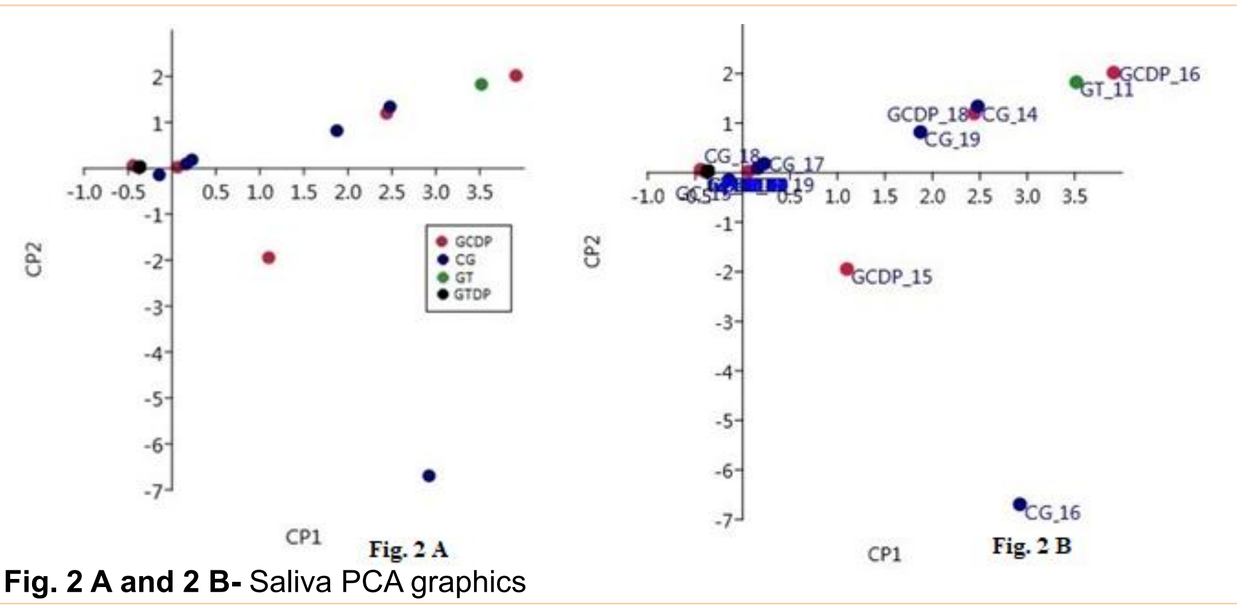

Fig. 2 A and 2 B- Saliva PCA graphics

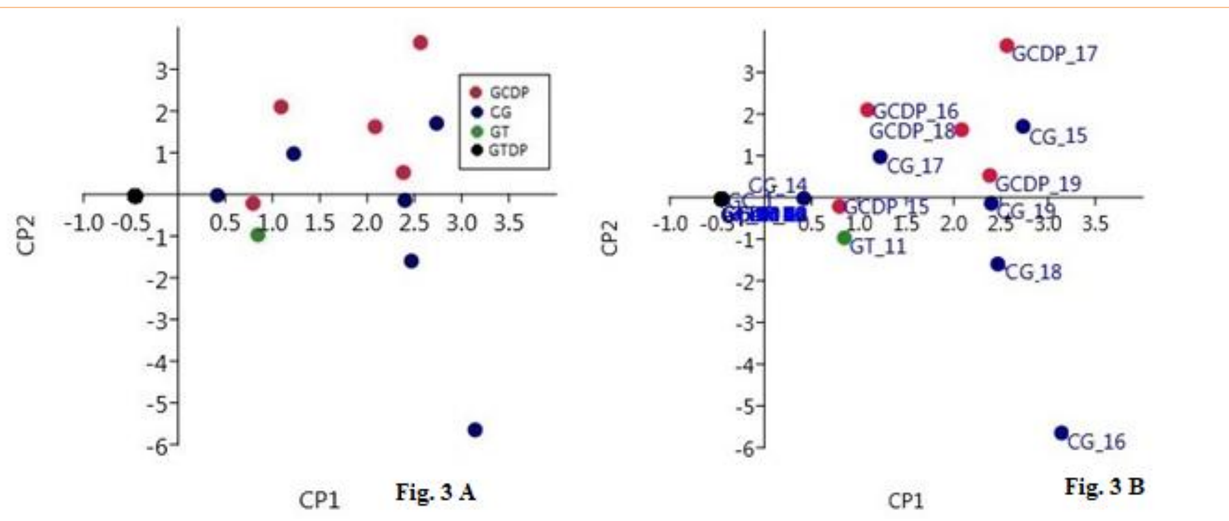

Fig. 3 A and 3 B- Urine PCA graphics

Table 1- Permanova analysis of the four groups for saliva and urine metabolites

PERMANOVA	Saliva	Urine
Permutation N:	9999	9999
Total sum of squares:	1.91×10^{19}	7.82×10^{19}
Within-group sum of squares:	1.84×10^{19}	7.23×10^{19}
F	0.7176	1.574
P	**0.8741**	**0.103**

p <0.05 indicates the significant difference between groups.

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