A novel and promising proteomic-based MALDI-MSI thyroid nodule classifier as complementary diagnostic tool in cytopathology

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INTRODUCTION

THYROID FINE NEEDLE ASPIRATION (FNA) BIOPSY

SIAPEC-IAP Classification

THY1: Inadequate sampling
THY2: Benign lesions
THY3: Indeterminate diagnosis
THY4: Suspicious for malignancy
THY5: Malignant lesions

TOTAL THYROIDECTOMY

25% FNA (THY3)

THY: Inadequate sampling
THY2: Benign lesions
THY3: Indeterminate diagnosis
THY4: Suspicious for malignancy
THY5: Malignant lesions

PUBLIC HEALTH COST

CLINICAL PROBLEM

20% 80%

AIMS

• Discriminate Benign and Malignant thyroid nodules
• Classify Indeterminate (THY3) nodules.

SAMPLE PREPARATION METHOD

• Reproducible and Robust
• Specific and sensitive
• Transferable in different clinics

MALDI-MSI PROTEOMICS

IN-VIVO FNA

METHODS

SAMPLE PREPARATION

1. In-vivo FNA
2. CytoStat
3. PreserveCyts

GENERAL WORKFLOW

SIAPPEC IAP

TARGETED PROTEOMICS

MALDI-MSI ANALYSIS

STATISTICAL ANALYSIS

CLASSIFICATION

IN-DETERMINATE

MALDI-MSI PROTEOMIC ANALYSIS

REFERENCES:


RESULTS

TRAINING: ROI

N = 9 hyperplastic patients (THY2)
N = 9 Papillary Thyroid Carcinoma patients (THY5)
Equivalent group of ROIs were generated for each patient:
• 5 groups of ROIs for THY2 (Total: 45 ROIs)
• 4 groups of ROIs for THY5 (Total: 36 ROIs)

VALIDATION SAMPLES

20 discriminant features

CLASSIFICATION

MALDI-MSI PROTEOMIC ANALYSIS

P_308

(THY2)

P_1088

(THY5)

P_1123

(THY5)

P_1187

(THY5)

P_1188 ex vivo

(THY5 – Histological diagnosis: lymph node metastasis)

CONCLUSIONS

We introduce a novel methodological approach to build a proteomic diagnostic tool in thyroid cytopathology by taking advantage of MALDI-MSI technology combined with a biostatistical model.

Reduced number of unnecessary treatments and cost-effectiveness for the healthcare system.