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

Isabella Piga1, Giulia Capitol2, Francesca Clerici1, Allia Mahajneh1, Virginia Brambilla3, Vanna Denti1, Andrew Smith1, Stefania Galimberti2, Fulvio Magni1, Fabio Pagni3

1University of Milano - Bicocca, Proteomics and Metabolomics platform, School of Medicine and Surgery, Vredaio al Lombard, Italy.
2University of Milano - Bicocca, Center of Biostatistics for Clinical Epidemiology, School of Medicine and Surgery, Vredaio al Lombard, Italy.
3University of Milano - Bicocca, School of Medicine and Surgery, Pathology Section, San Gerardo Hospital, ASST Monza, Italy.

INTRODUCTION

THYROID FINE NEEDLE ASPIRATION (FNA) BIOPSY

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

TOTAL THYROIDECTOMY
25% FNA (THY3)

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THY2: Benign lesions
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PUBLIC HEALTH COST
Surgical stress/complications
Lifelong hormone therapy

CLINICAL PROBLEM

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

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 (75 ROIs)
4 groups of ROIs for THY5 (75 ROIs)

RESULTS

20 discriminant features

VALIDATION
n=4 THY2; n=1 THY3; n=1 THY4; n=4 THY5; n=1 metastatic lymph node

PROCESSING PARAMETERS

• TIC Normalization
• S/N ≥ 6 and intensity threshold ≥ 0.0003
• Inter-Patient Filter (Only features common in at least 25% of the ROIs)

CLASSIFICATION

20% 80%

REFERENCES:

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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.

CONCLUSIONS

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