

MicroRNA Profiling Discriminates Nodular Hyperplasia versus Follicular Adenoma

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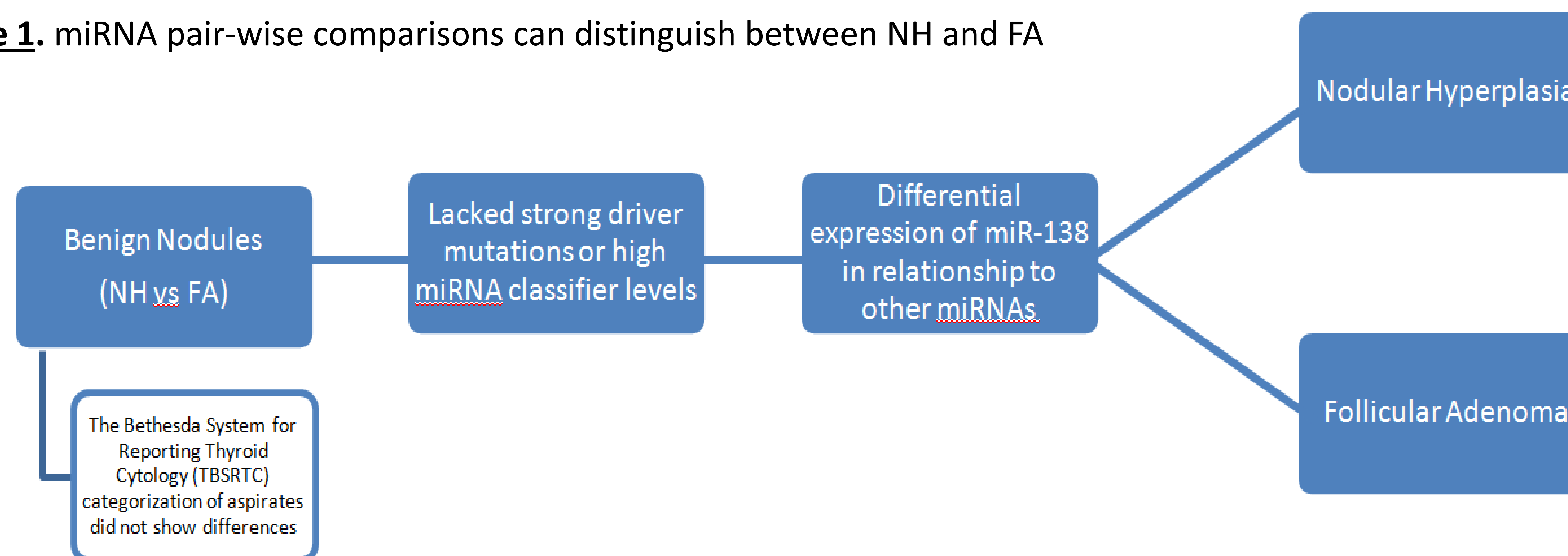
INTRODUCTION:

- A variety of benign entities produce thyroid nodular disease, the two most common being nodular hyperplasia (NH) and follicular adenoma (FA).
- NH is non-neoplastic, not requiring surgical excision unless symptomatic.
- FA, considered neoplastic, can justify local resection when viewed as a precursor for progression to cancer.
- Current molecular testing based solely on mutational analysis or RNA classifier does not differentiate between these or other benign states limiting surgery decision-making.
- We show that microRNA (miRNA) profiling can discriminate NH from FA with high accuracy for more informed molecular assessment of cytology indeterminate nodular disease.

METHODS:

- Cytologically indeterminate thyroid nodules underwent molecular testing (oncogene point mutation/fusion detection [ThyGenX] and miRNA profiling using a 10 marker panel algorithmic classifier determination as well as pair-wise analysis of individual miRNA expression differences [ThyraMIR]), performed either directly on the needle aspirates or via microdissection of cytology slides.
- Histopathology review of combined testing outcome yielded 24 cases of NH and 20 cases of FA.

Figure 1. miRNA pair-wise comparisons can distinguish between NH and FA



- While the miRNA classifier can discriminate between benign vs malignant states with high accuracy, it cannot differentiate between NH and FA
- Multiple pair-wise differences among specific miRNA panel markers were capable of distinguishing between NH and FA with high accuracy ($p < .0001$)
- Differential expression of miR-138 in relationship to other miRNAs was most discriminating

CONCLUSIONS:

- A major objective of molecular testing of thyroid nodules is accurate preoperative diagnosis of thyroid nodule states, both benign and malignant.
- Benign entities are diverse and cannot be discriminated based solely by lack of detectable mutational change.
- We show that the two most common benign lesions are associated with objective miRNA profiling differences enabling the separation of NH and FA preoperatively optimizing individual patient care.

Table 1. microRNA classifier panel

10 MicroRNA (MiR) Classifier Panel	
Down-regulated	miR-204-5p, miR-139-5p, miR-29b-1-5p, miR-155-5p, miR-138-1-3p
Up-regulated	miR-375, miR-551-b-3p, miR-146b-5p, miR-31-5p, miR-222-3p