

Investigation of microRNA expression profiles related to morphological heterogeneity in triple-negative breast cancer

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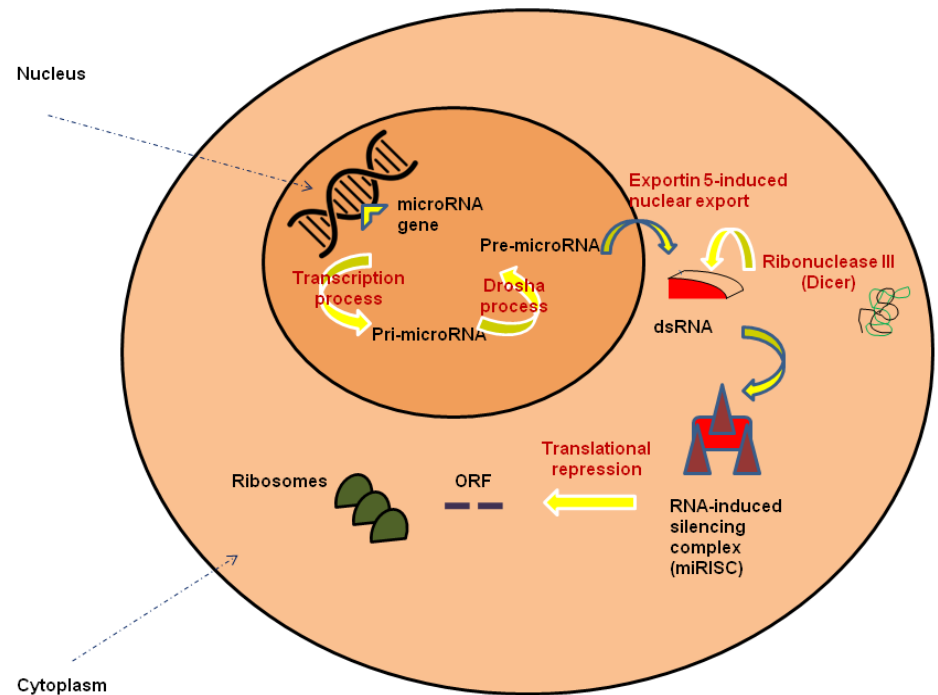
Introduction

- **Triple-negative breast cancers (TNBCs)**
 - morphologically heterogeneous group of breast cancers characterized by absent or minimal hormone receptor and HER2/neu/ERBB2 protein expression or gene amplification with specific response to therapy
- **Molecular subtypes of TNBCs (Lehmann B. D. et al., 2011)**
 - Luminal androgen receptor (**LAR**); Basal –like 1 (**BL-1**); Basal - like 2 (**BL-2**); Immunomodulatory (**IM**); Mesenchymal – like (**M**); Mesenchymal – stem like (**MSL-L**)
- **Potential TNBC molecular targets**
 - AR, PARP, EGFR, VEGF, lncRNA, **microRNA**, siRNA, p53, CD95, PD-1/PD-L1

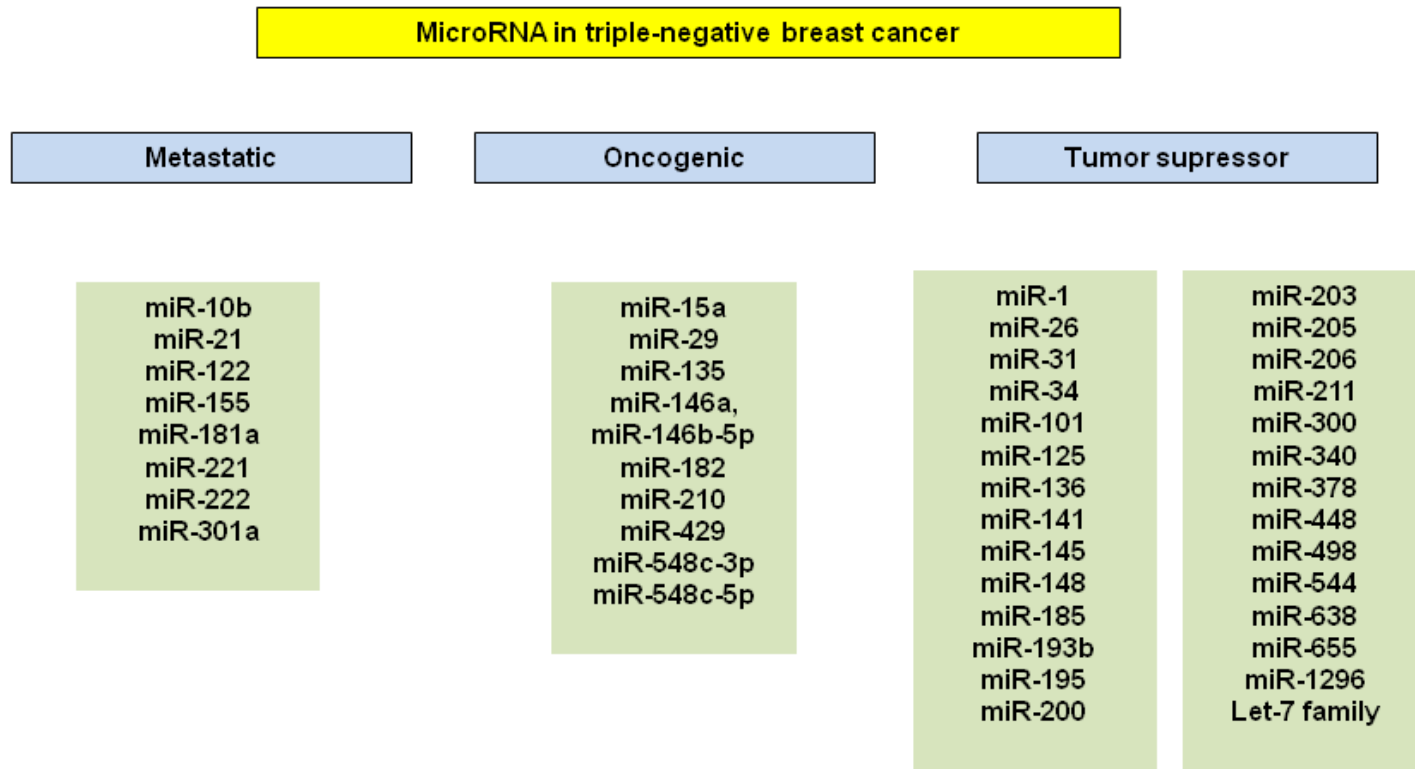
Introduction

- **microRNA (miR)** - regulation of more than 50% human genes
 - non-coding RNA molecules, differing in length from 18 to 25 nucleotides
 - carcinogenesis; epithelial to mesenchymal transition (EMT); inflammation; angiogenesis; cell proliferation and migration; resistance to chemotherapy

Biosynthesis of microRNAs



Introduction



Objective and methods

- **3 953 female breast cancers** (2007-2018); **460 TNBCs** (11.6%);
- **70 TNBCs (absence of neoadjuvant therapy prior to surgical therapy, complete tumor volume)**
- histological tumor type (WHO classification)
- **Tumor morphology preservation:**
 - central necrosis/fibrosis
 - regions of clear cell/apocrine and/or spindle tumor cell transformation; cribriform-like pattern; small rounded neoplastic acini; monstrous tumor cells; medullary features; ductal carcinoma in situ (DCIS)
- non-neoplastic mammary gland tissue
- tumor-infiltrating lympho/plasmocytes (TILs)

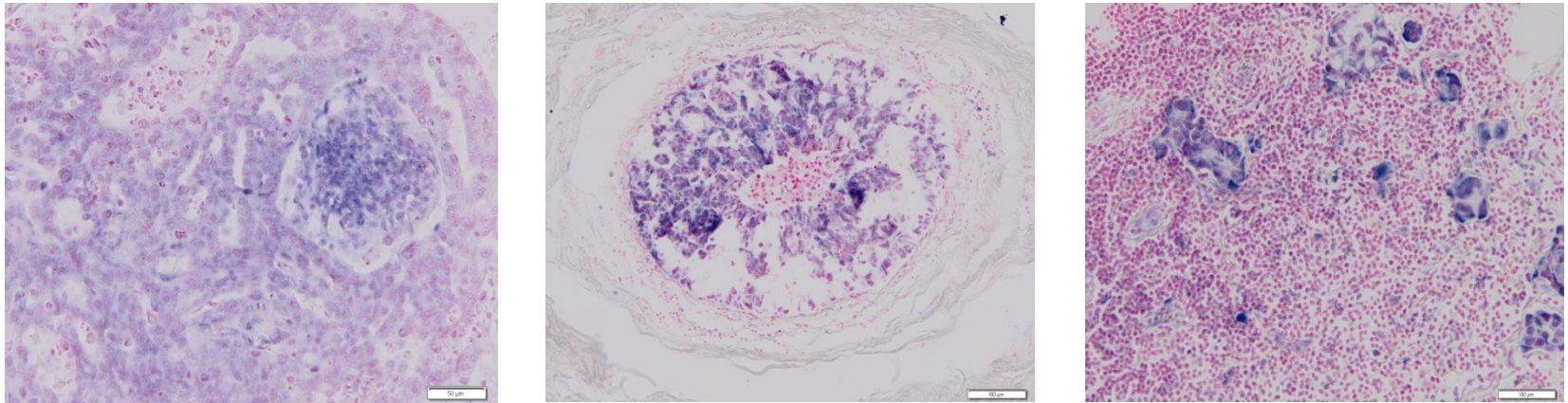
Objective and methods

- 70 TNBCs FFPE tissues
 - **PALM MicroBeamlaser capture microdissection (LCM)**
PALM RoboSoftware version 4.6 (Carl Zeiss Microscopy GmbH, Germany)
 - 10 μm breast cancer sections (6 slides); RNase-free conditions; Cresyl Violet
 - 2 extra breast cancer sections; hematoxylin-eosin
 - **Total RNA including small RNA purification**
AllPrep DNA/RNA FFPE kit, Qiagen, Germany
 - **Microarray analysis; Biostatistical analysis**
MiRNA 4.0 Array and FlashTag™ Biotin HSR RNA Labeling Kit,
Applied Biosystems, CA, USA ; R Core Team, ver. 3.5.0 (2018-04-23)

Objective and methods

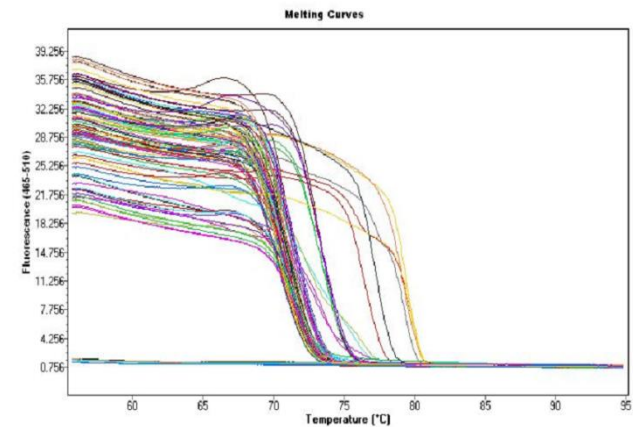
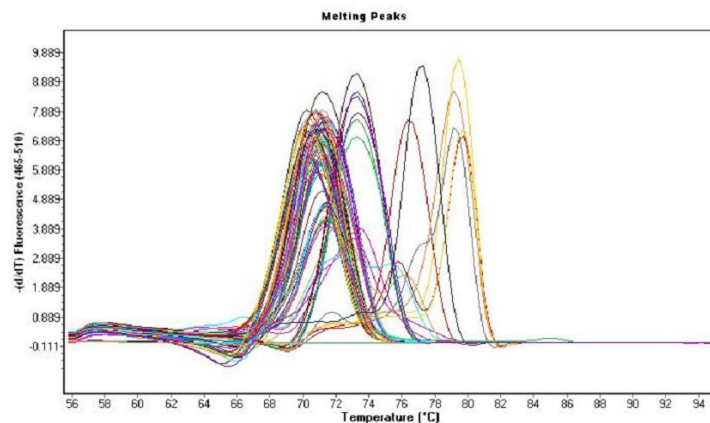
■ In-situ hybridisation

miRCURY™ LNA™ microRNA ISH Detection Probes & Kit (Exiqon/Qiagen, Germany)

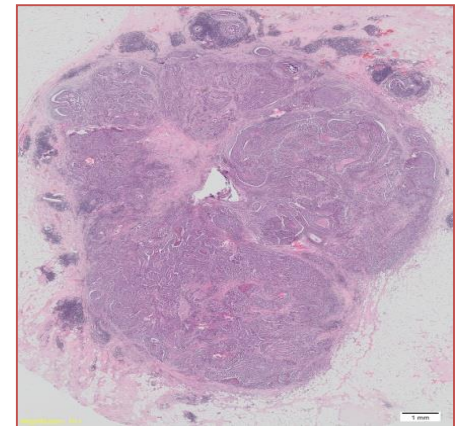
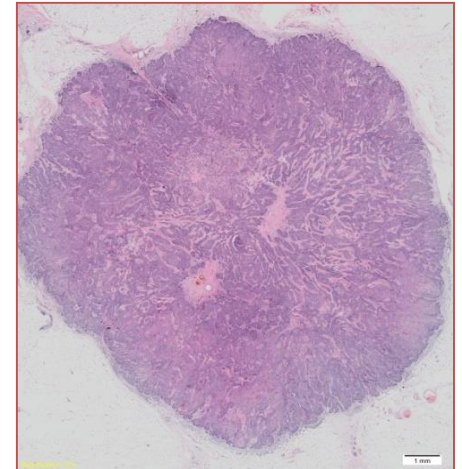
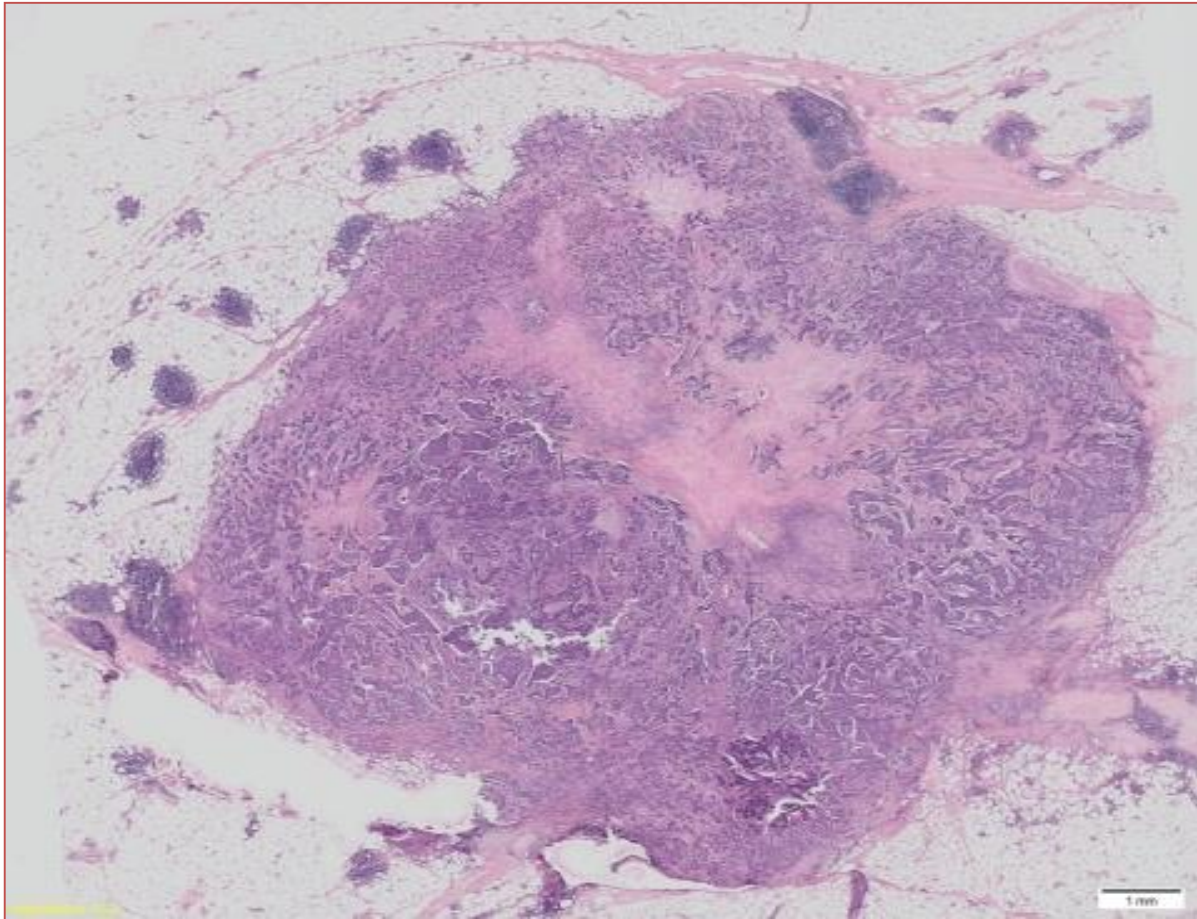


■ qRT-PCR

miRCURY LNA miRNA PCR System (Qiagen, Germany); Lightcycler 480 System (Roche, Switzerland)



Results



Typical appearance of tumor samples (demarcation, central necrosis/fibrosis, TILs, very often morphological transformation of tumor cells from syncytial to spindle cell or clear cell pattern).

Results

- **2578 hsa-microRNAs analysed, candidate hsa-microRNAs selected**
 - corresponding with the areas of predominantly medullar, clear/apocrine and/or spindle tumor cell transformation, lymphocyte-rich, DCIS and normal mammary gland tissue morphology
 - discriminating specific morphologies

Results

- **hsa-miR-93-5p**; oncogenic and metastatic miRNA
 - discrimination of DCIS and non-neoplastic mammary gland morphology (decreased expression) from invasive tumor areas (increased expression)
- **hsa-miR-106b-5p**; oncogenic and metastatic miRNA
 - discrimination of specific tumor morphologies (increased expression) from TILs (decreased expression)
- **hsa-miR-145-5p**; tumor suppressor miRNA
 - discrimination of specific tumor morphologies and TILs (decreased expression) from non-neoplastic mammary gland morphology
- **hsa-miR-200c-3p**; tumor suppressor miRNA
 - discrimination of TILs

Results

- **hsa-miR-182-5p**; oncogenic miRNA
 - discrimination of specific tumor morphologies (increased expression) from DCIS and TILs (decreased expression)
- **hsa-miR-205-5p**; tumor suppressor miRNA
 - discrimination of aggressive tumor morphologies (spindle tumor cell; increased expression) from TILs (decreased expression) and DCIS or less aggressive tumor morphologies (cribriform-like, small rounded tumor acini)
- **hsa-miR-361-5p**; tumor suppressor miRNA
 - discrimination of less aggressive tumor morphologies (cribriform-like, small rounded tumor acini; increased expression) from others aggressive neoplastic or non-neoplastic morphologies (decreased expression)

Conclusion

- Can miRNA expression reflect the morphological heterogeneity of TNBC?
- Most likely YES
- These morphologies have typical miRNA signature:

Spindle tumor cell morphology: Loss: miRNA-143, miRNA-205;
Gain: miRNA-185, miRNA-155

Clear cell/apocrine tumor morphology: Loss: miRNA-143, miRNA-205;
Gain: miRNA-182

Medullary features: Loss: miRNA-200, miRNA-143, miRNA-205;
Gain: miRNA-155, miRNA-185

TILs: Loss: miRNA-200, miRNA-143, miRNA-205;
Gain: miRNA-150, miRNA-155

Lymph-node metastases: Loss: miRNA-200, miRNA-150;
Gain: miRNA-185

Conclusion

Keep in mind!

Changes of miRNAs can be related to proliferative or metabolic /regressive activity in tumor more than to direct up/down regulation of tumor morphology.



Thank you for your attention

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**"Attitude is a little thing that makes
a big difference."**

W. Churchill