Role of microenvironment in tumor progression

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Non-small-cell lung carcinoma (NSCLC)

- The leading cause of cancer death in France and Worldwide
- Poor survival
- Late diagnosis
- Ineffective treatments
- Relapse : 40 % early stages I-II

Prone to metastasize



Aran D, et al. Nat Commun. 2015















miRNA-223 effets in cancer cells **FOXO1A** invalidation of the second second miR-223-3p A549 FOXO1 α -TUBULIN



miR-223-3p promotes EMT phenotype







miRNA-223 is protumoral and associated with poor survial !





miR-223 is efficiently transferred in epithelial cells



miR-223 is efficiently transferred in epithelial cells



miR-223 is efficiently transferred in epithelial cells



How stable is an ex-miRNA?



Ex-miRNA are unstable !



ex-miRNA targets are quickly restored



ex-miRNA induced phenotypes are transient



ex-miRNA degradation



ex-miRNA is degradated by XRN1



XRN1 invalidation delays ex-miR-223 phenotype



XRN1 deletion is associated with poorer prognosis



Disease Free Survival	XRN1_HETLOSS	XRN1 CNA≥2	
Median survival (months)	25.36	41	



First evidence of rapid decay of ex-miRNA
miRNA-dependent rapid shift of phenotype
Involvement of XRN1 in miRNA decay
Increased diffusion of cell depending of neutrophil proximity

Role of neutrophils in cancer and metastasis Zangari et al. 2017





Is it possible to isolate individual signatures from a single pattern?

- Math aspects: define the best model
- Biological aspects: reduce number of variables => meaningfull
- Clinical aspects: stratification, survival

Deconvolution of signals



Cancer Patients

Kuner R, et al. Lung Cancer 2009

Affymetrix microarrays





Microarray

Signals expressed in 65536 levels of grey



Distribution of expression



Distribution of expression



Mathematical model= Optimization

	Fibro	B-Lympho	Monocytes	CD4-Lympho	CD8-Lympho	Eosino	NK	Neutro	Vessel
Fibro	1.00	0.65	0.72	0.65	0.64	0.47	0.59	0.28	0.90
B-Lympho	0.65	1.00	0.86	0.94	0.95	0.66	0.85	0.47	0.63
Monocytes	0.72	0.86	1.00	0.84	0.86	0.78	0.84	0.67	0.70
CD4-Lympho	0.65	0.94	0.84	1.00	0.98	0.64	0.89	0.49	0.63
CD8-Lympho	0.64	0.95	0.86	0.98	1.00	0.70	0.93	0.55	0.62
Eosino	0.47	0.66	0.78	0.64	0.70	1.00	0.78	0.84	0.48
NK	0.59	0.85	0.84	0.89	0.93	0.78	1.00	0.67	0.57
Neutro	0.28	0.47	0.67	0.49	0.55	0.84	0.67	1.00	0.30
Vessel	0.90	0.63	0.70	0.63	0.62	0.48	0.57	0.30	1.00

partial least squares, least squares, manual...others?

Reconstitution of signature in patients (calc vs obs)





Clinical Data

Tumor subtype (ADC, SCC) Staging (I, II, III) **TNM-T (Tumor size) TNM-N (Lymph node) Time until relapse in month** Relapse (0/1) **Survival time in month** Died (0/1)**censored: follow-up < 3 years** Age (39-83y) Sex (14F/44M)



Neutrophils are associated with progression



Neutrophil to Lymphocyte Ratio

Survival proportions: Survival of KM plot relapse INTR





Neutrophil to Lymphocyte Ratio



Original Article

Predictive Clinical Outcome of the Intratumoral CD66b-Positive Neutrophilto-CD8-Positive T-Cell Ratio in Patients With Resectable Nonsmall Cell Lung Cancer

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Étude de la procédure PLS1 Sélection d'estimateurs ridge Sélection d'estimateurs ridge « classiques » Sélection d'estimateurs en kernel ridge Modélisation de la signature génique du cancer du poumon

Le contexte d'étude Notre méthodologie

Élaboration des bases de données

Phase 2 : Traitements des bases de données



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miR-223 is efficently transferred in epithelial cells (I)



miR-223 is efficently transferred in epithelial cells (I)



miR-223 is efficently transfered in epithelial cells (II)

Nanoparticle tracking analysis









miR-223 is efficently transfered in epithelial cells (III)

A549

+ MV

à

A549

800 700

600 500

0

SE .

miR-223 expression in A549 (FC, linear)



+ UC

Is extracellular miR-223 functional once engulfed by recipient cells?

FOXO as a bone fide target of miR223



FOXO as a bone fide target of miR223





A dense PMN infiltrate is associated with miR-223-3p expression and decreased FOXO1 expression in lung cancer patients



Microarray analysis

Term	Overlap	Adjusted P- value	Z-score	Combined Score	Genes
ANCHORING JUNCTION (GO:0070161)	34/419	1,15E-05	-2,37	27,00	SCARB2;KRT80;RALA;AHNAK;SDC4;CTNND1;TWF1;CIB2;TENC1;NDRG1;CSRP1; CDH2;EPB41L2;G3BP1;DAG1;FLNB;CD59;RAC1;PDLIM7;TGM2;TNS1;ITGA3;CAV1 ;ITGA1;RRAS2;PLEKHA7;ABI2;DLG5;PKP2;EVL;NF2;AJUBA;LIMS2;ARF6
ADHERENS JUNCTION (GO:0005912)	33/405	1,15E-05	-2,35	26,71	SCARB2;RALA;AHNAK;SDC4;CTNND1;TWF1;CIB2;TENC1;NDRG1;CSRP1;CDH2; EPB41L2;G3BP1;DAG1;FLNB;CD59;RAC1;PDLIM7;TGM2;TNS1;ITGA3;CAV1;ITGA 1;RRAS2;PLEKHA7;ABI2;DLG5;PKP2;EVL;NF2;AJUBA;LIMS2;ARF6
CELL-SUBSTRATE ADHERENS JUNCTION (GO:0005924)	26/358	1,26E-03	-2,35	15,66	SCARB2;RALA;AHNAK;SDC4;CIB2;TWF1;TENC1;CSRP1;CDH2;EPB41L2;G3BP1; DAG1;FLNB;CD59;RAC1;PDLIM7;TGM2;TNS1;ITGA3;CAV1;ITGA1;RRAS2;EVL; AJUBA;LIMS2;ARF6
CELL-SUBSTRATE JUNCTION (GO:0030055)	26/362	1,26E-03	-2,34	15,64	SCARB2;RALA;AHNAK;SDC4;TWF1;CIB2;TENC1;CSRP1;CDH2;EPB41L2;G3BP1; DAG1;FLNB;CD59;RAC1;PDLIM7;TGM2;TNS1;ITGA3;CAV1;ITGA1;RRAS2;EVL; AJUBA;LIMS2;ARF6
FOCAL ADHESION (GO:0005925)	25/352	1,77E-03	-2,29	14,52	SCARB2;RALA;AHNAK;SDC4;TWF1;TENC1;CSRP1;CDH2;EPB41L2;G3BP1;DAG1; FLNB;CD59;RAC1;PDLIM7;TGM2;TNS1;ITGA3;CAV1;ITGA1;RRAS2;EVL;AJUBA; LIMS2;ARF6
CELL-CELL JUNCTION (GO:0005911)	24/335	1,88E-03	-2,25	14,11	KRT80;AHNAK;HEG1;MAGI2;CTNND1;KIAA1462;TWF1;ANK3;MPP5;ATP1B1; CLDN2;NDRG1;PLEKHA7;SIRT2;CLDN4;CDH2;ABI2;PODXL;DLG5;PKP2;DAG1; SYNPO;AJUBA;CGNL1

30

5 -

2

Fold

л

6

EMT/Migration/Invasion ?

miR-223-3p promotes EMT phenotype



Invasion as a bone fide endpoint of phenotypic impact of miR-223



Invasion as a bone fide endpoint of phenotypic impact of miR-223





Invasion as a bone fide endpoint of phenotypic impact of miR-223

