



MicroRNAs in lymphoproliferative disease with a focus on Hodgkin lymphoma

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HL origin is GC-B

Malignancy	SHM	Ongoing SHM	GC B-cell expression profile ^{27, 71, 99, 130}	Putative cell of origin
Mantle-cell lymphoma	No (except for a small percentage ¹³¹)	No	No	Pre-GC B cell
Chronic lymphocytic leukaemia (CLL) [‡]	Yes and no	No	No	Antigen-experienced B cell (pre- or post-GC)
Burkitt lymphoma	Yes	No	Yes	GC B cell
Follicular lymphoma	Yes	Yes	Yes	GC B cell
Marginal-zone lymphoma — nodal, extranodal (MALT) and splenic	Yes (except for some splenic variants ¹³²)	Yes (prevalent in MALT lymphomas ¹³³)	No§	GC B cell or post-GC B cell
GC B-cell-like DLBCL	Yes	Yes	Yes	GC B cell
Activated B-cell-like DLBCL	Yes	No	No	GC B-cell subset or extra-GC mutated B cell ^{23,25}
Lymphoplasmacytic lymphoma (LPL)	Yes	Yes	No ¹	Post-GC B cell
Multiple myeloma	Yes	No	No	Post-GC B cell
Hodgkin lymphoma (classical type)	Yes	No	No	GC or post-GC B cell
Hodgkin lymphoma (nodular lymphocyte pre-dominant type)	Yes	Yes	Yes	GC B cell

L Di Lisio et al. 2012

Germinal-centre B cells.



Nature Reviews | Immunology

1) GC-B cells mutate their immunoglobulin genes (w/ AID)

2) GC-Bs acquire mutations to maintain/ improve the affinity of the B-cell receptor (BCR) for antigen

3) leading to a rescue from programmed cell death and differentiation.

Mechanisms of malignant transformation of GC-B cells.



Nature Reviews | Immunology

1) **c-MYC overexpression** is a result of translocation by Burkitt lymphoma cells

2) **nuclear factor- B (NF- B) pathway** activation blocks apoptosis in diffuse large B-cell lymphomas (DLBCLs), marginalzone lymphomas, Hodgkin lymphomas and Epstein–Barr virus-related lymphomas.

3) **BCL2 gene** translocation, amplification or transcriptional activation blocks apoptosis and stimulates GC-B proliferation in various non-Hodgkin lymphomas.

4) **Translocation of PAX5** (paired box gene 5) in lymphoplasmacytic lymphomas is also likely to block plasmacytic differentiation..

microRNAs

- class of small RNA molecules (~ 22 nts)
- highly conserved
- regulate gene expression at posttranscriptional level
- members of a RISC complex
- binding to 3 'UTR of target mRNA leads to translational repression or degradation of the mRNA
- implicated in number of cellular processes – metabolism, development, differentiation
- involved in solid tumors, leukemias, lymphomas (rev. in Dalmay 2008, Croce 2008)



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Stage-specific microRNAs involved in B-cell differentiation

	Naive B cells	Germinal center B cells	Memory B cells	Plasma cells
♠	miR-181 ³¹	miR-17-5p ^{16,32}	miR-223 ^{16,32}	
	mi-34a ²⁴	miR-181b ^{25,32}		
	miR-223 ^{16,31,32}	miR-125b 31,33		
		miR-155 ²⁶		
$\mathbf{\Psi}$		miR-223 ³¹⁻³³	miR-181b ³¹⁻³³	miR-181b ^{16,32}
		miR-150 ^{22,31,33}	miR-17-5p ^{16,32}	miR-17-5p ³²
				miR-30 ^{16,32}

Interactions between genes and microRNAs in GC differentiation



miR-9 inhibits Blimp1 (*PRDM1*) in Hodgkin/Reed-Sternberg cells



Nie et al. 2008

microRNA-mediated *PRDM1* inactivation by miR-9 in Hodgkin/Reed-Sternberg cells



Interactions between genes and microRNAs in GC differentiation





0.0

neg.ctrl 40nM100nM

neg.ctrl 40nM 100nM

Vargova et al. 2011, Fig 5

miR-155

PU.1

0.00

BIC (miR-155) RNA-ISH in HL

Tissue	BIC⁻	BIC ⁺
FL*	15	0
BL*	8	
MCL	6	0
MZL	0	2
DLBCL	6	12
PMBL	0	8
HL*	5	53
TCRBCL [†]	16	
ALCL*	7	0
TCL	0	3



Hodgkin and Reed-Sternberg cells

Cytoplasmatic expression in Hodgkin and Reed-Sternberg cells of miR-21 (A), miR-134 (B), miR-138 (C), and miR-155 (D).



Navarro et al. 2007

Hypothesis

- Lymphomas originate from a block of differentiation.
- miR-155 dependent inhibition of PU.1 involves HL pathogenesis.
- How can we use this in clinical questions (biomarkers)?

Questions

- To compare miR-155 levels across lymphomas?
- In what other lymphomas is miR-155 overexpressed?
- Is PU.1 repressed in that lymphomas?
- relationship btw miR-155 and PU.1 and clinical course of the patients?

miR-155/PU.1 in lymphoma

- RNA isolation from the biopsies of lymph nodes (Trizol)
- RQ-PCR (TaqMan) normalization: RNU44, GAPDH

*** p < 0.0001

- ** p < 0.001
- * p < 0.01
- miR-155 above average
- miR-155 bellow average



Hodgkin lymphoma

Description of patients

N = 16 Male = 8, Female = 8 Age median = 28, min = 20, max = 67

Nodular sclerosis = 8 Mixed cellularity = 7 Lymphocyte rich = 1

New diagnosis = 10 Relaps = 6



NS - nodular sclerosis, MC - mixed cellularity, LR - leukocyte rich



Hodgkin lymphoma

and response to first line of therapy



- response to first line of therapy is a valuable prognostic marker in HL
- miR-155 is upregulated in lymph nodes of patients that did not achieve remission or relapsed very early



Diffuse large B-cell lymphoma

and its subtypes



- ABC-DLBCL subtype is more aggressive than GCB-DLBCL
- miR-155 is upregulated in lymph nodes of patients with ABC-DLBCL compared to GCB-DLBCL (Eis et al. 2005)





-Arrows 🔺 indicate HRS cells of lacunar type, some in regression 🔶

-Eosinophilic intercellular staining of fibrous tissue . Accessory cells on the backgound may represent inflamatory lymphocytes (indicated by dashed line). Macrophages are possibly also present.

PU.1 protein - Immuno

Č. 12607/11

79 year female, Hodgkin Lymphoma, nodular sclerosis, dg.11/2011, (1000x). White arrow marks HRS cells, positive nuclear staining (FITC, indirect labeling, green) may represent inflamatory lymphocytes.



79 year female, Hodgkin Lymphoma, nodular sclerosis, dg.11/2011

Conclusions

- miR-155 is upregulated in HL and B cell malignancies from GCs incl. DLBCL, B-CLL/SLL, FL, MZL.
- miR-155 expression is reflected by downregulation of its target: major hematopoietic transcription factor PU.1
- in B cell malignancies (incl. HL), miR-155 upregulation may reflect aggressiveness exemplified by patients that did not achieve complete remission or relapsed early.

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