

T(14;18) translocation
as a candidate marker
of high-grade transformation
in HCV-associated
Malt lymphomas

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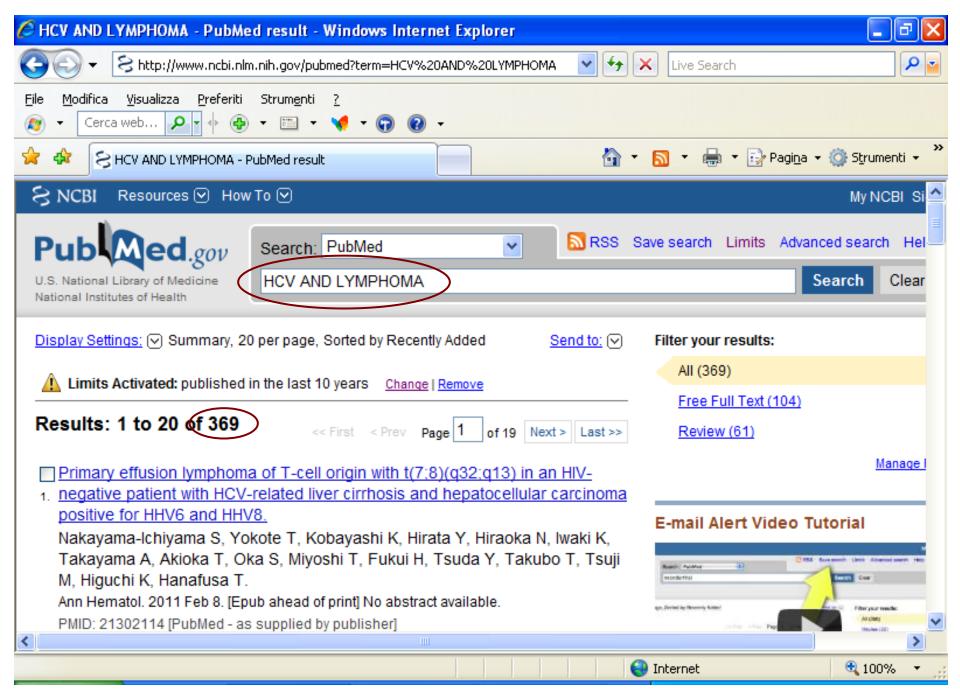
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Table I. Prevalence of anti-HCV antibodies (Abs) and/or HCV-RNA among Italian case-control studies and case-series of non-Hodgkin's lymphoma patients.

			NHL cases ^a	Anti-HC	V Abs positivity	HCV RNA positivity		
Authors/refs.	Location	All NHL cases		NHL	% (95% CI)	NHL	% (95% CI) ^b	
All studies		2810	2736	539	19.7 (18.2-21.2)	206	14.7 (12.8-16.6	
Case-control studies		1195	1168	272	23.3 (20.9-25.7)	124	21.6 (18.2-24.9)	
Talamini et al (10)	Pordenone/Naples	225	202	40	19.8 (14.3-25.3)			
Mele et al (6)	9 Italian towns	400	400	70	17.5 (13.8-21.2)	60	15.0 (11.5-18.5	
Guida et al (86)	Bari	60	56	12	21.4 (10.7-32.2)			
Montella et al (87)	Naples	101	101	25	24.8 (16.3-33.2)			
Vallisa et al (88)	Piacenza	175	175	65	37.1 (30.0-44.3)	64	36.6 (29.4-43.7	
De Vita et al (89)	Aviano/Pordenone	84	84	20	23.8 (14.7-32.9)			
Musto et al (90)	Foggia	150	150	40	26.7 (19.6-33.7)			
Case series		1615	1568	267	17.0 (15.2-18.9)	82	9.9 (7.9-12.0)	
De Renzo et al (91)	Naples	61	61	12	19.7 (9.7-29.6)			
Pioltelli et al (92)	Northern Italy	300	300	48	160 (11.9-20.1)	41	13.7 (9.8-17.6	
Luppi et al (93)	Modena	157	157	35	22.3 (15.8-28.8)			
Catassi et al (94)	8 Italian towns	143	104	15	14.4 (7.7-21.2)			
Silvestri et al (17)	Udine	470	470	42	8.9 (6.4-11.5)	31	6.6 (4.4-8.8)	
Pivetti et al (95)	Turin	47	47	7	14.9 (4.7-25.1)			
Pioltelli et al (96)	Milan	126	126	26	20.6 (13.6-27.7)			
Musolino et al (97)	Messina	24	24	2	8.3 (0.0-19.4)	5	20.8 (4.6-37.1	
Mazzaro et al (5)	NorthEast Italy	199	197	55	27.9 (21.7-34.2)		92	
Andriani et al (98)	Rome	38	32	8	25.0 (10.0-40.0)	5	15.6 (3.0-28.2	
Ferri et al (99)	Pisa	50	50	17	34.0 (20.9-47.1)		STATE STATESTICAL	

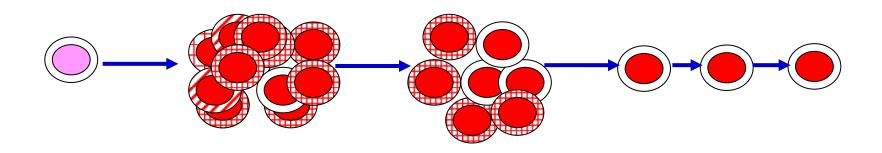


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NATURAL HISTORY OF B-CELL LYMPHOMA

NORMAL B LYMPHOCYTE

POLICLONAL HYPERPLASIA OLIGOCLONAL HYPERPLASIA MONOCLONAL LYMPHOMA



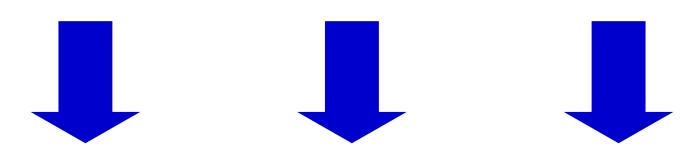
ANTIGENIC STIMULATION

GENETIC ALTERATIONS

Chronic inflammation and antigenic stimulation may be caused by infection of:

- Helicobacter pylori
- Chlamydia psittaci
- Epstein-Barr Virus
- Human Immunodeficiency Virus
- Hepatitis C Virus

In the context of genetic alterations, previous studies have suggested a role for t(14;18) translocation in the development of lymphoproliferative disorders of HCV-infected individuals

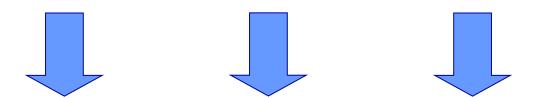


Zignego <i>et al</i> Hepatology, 2000			go <i>et al</i> M ed., 2002	Libra <i>et al</i> Leukemia, 2003		
Patient	t(14;18)	Patient	t(14;18)	Patient	t(14;18)	
HCV + MC	5/7 (71%)	HCV + MC	28/37 (76%)	HCV + NHL	8/39 (20%)	
HCV	13/50 (26%)	HCV	30/101 (38%)	NHL/HCV-	3/101 (3%)	

MALT Lymphoma

- MALT lymphomas are extra-nodal lymphomas and are typically indolent.
- The most common site of the disease is the stomach. Gastric MALT lymphoma is caused frequently by Helicobacter pylori infection.
- MALT lymphomas can be cured in many cases by antibiotics against H. pylori.
- However, approximately 15-20% of MALT lymphomas may develop into high-grade lymphomas.

We recently show for the first time that t(14;18) clusters in HCV-associated Malt lymphomas (Libra *et al*, J Hepatol. 2008)



It has been demonstrated that t(14;18) occurs in high-grade lymphomas derived from low-grade including Malt lymphomas (Capello *et al*, Blood 2000)



Therefore we hypothesized that t(14;18) may play a role in the high-grade transformation of Malt lymphomas, especially in those occurred among HCV+ patients

Cases

- ·58 DLBCL samples derived from MALT lymphoma were included for the analysis
- · A series of 124 de novo DLBCL were included as control group
- •DLBLC samples derived from FL were excluded

Frequency of t(14;18) in 58 transformed DLBCL patients with and without HCV infection

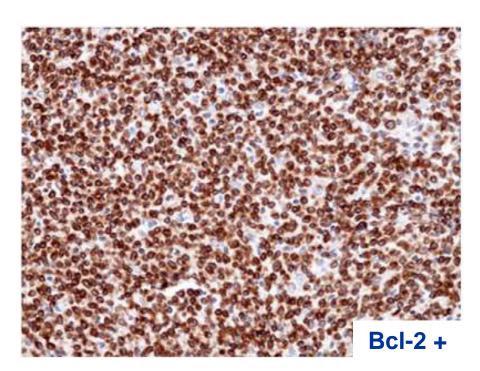
T(14;18)	HCV+	HCV-
+	4	2
-	9	43

P = 0.01; Fisher's Exact Test

Sequencing of the breakpoint in MALT and in the transformed DLBCL

	Bcl-2 3109	N region	$\underline{\mathbf{J}}_{\underline{\mathbf{H}}}6$ 1483		
MALT I diagnosis	tgcagtggtg	tttggttgcat	actactacta		
Transformed DLBCL	tgcagtggtg	tttggttgcat	actactacta		

Immunophenotyping

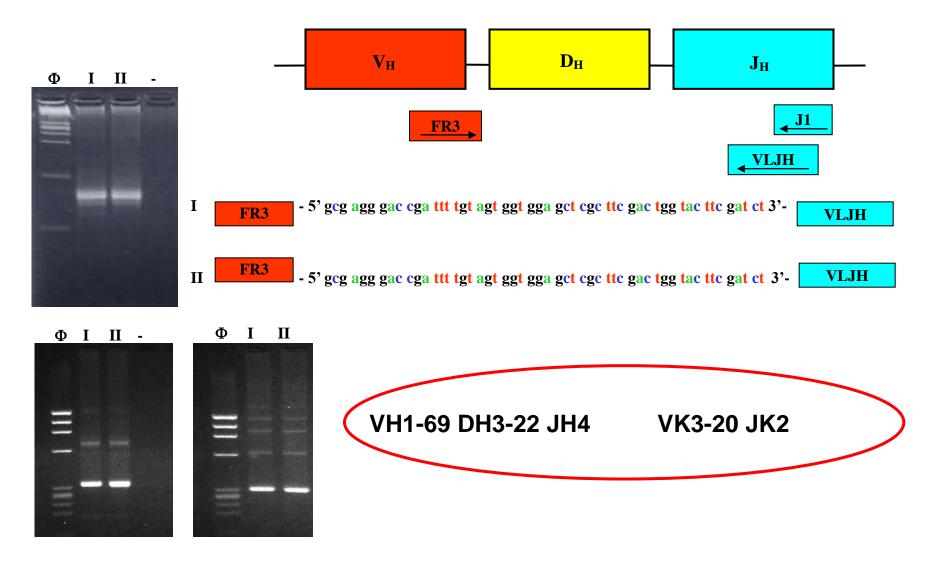


The overexpression of Bcl-2 indicates that this genetic abnormality may sustain survival of B-cells preventing apoptosis

The null expression of <u>CD10</u> and <u>Bcl-6</u> excludes the follicular origin of the tumor samples harboring t(14;18) translocation

To further confirm that the transformed DLBCL originated from the metachronous MALT lymphoma, analysis of B-cell clonality was also performed by VDJ rearrangement

Immunoglobulin gene analysis

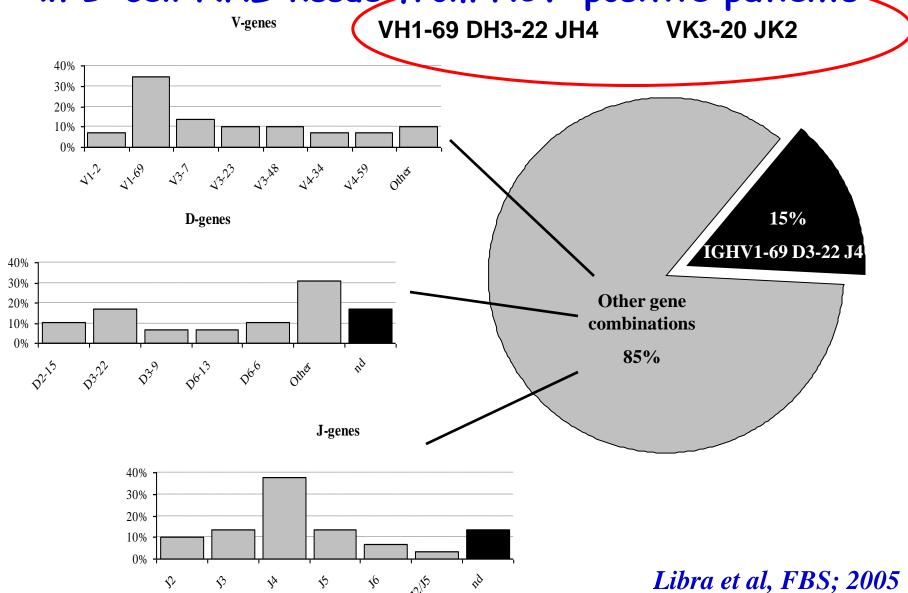


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The results show that these tumors were clonally identical

The combination of genes in the heavy and light chains was the most common used among HCV-associated lymphomas previously reported

Distribution of VH, DH, and JH genes rearranged in B-cell NHL tissue from HCV-positive patients



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Further molecular characterization of t(14;18) cases

It has been shown that SHM process of multiple oncogens occurs in B-NHL clustering within RGWY motifs (Pasqualucci L, Nature 2001)

Our previous studies show that this phenomenon was not observed in HCV-associated NHL (Libra M, J Pathol 2005)

Similarly, it was observed in t(14;18) cases analyzed in the present study

Further molecular characterization of t(14;18) cases

90 M Libra et al

Table 3. Features of PIM-1, PAX-5, RhoH/TTF, c-MYC, and BCL-6 mutations in HCV-associated NHL

Locus	Mutations/ 100 bp	Deletions or insertions	Single bp substitutions	Transitions/ transversions	G+C	A + T	G + C mutations/ 100 bp [†]	A+T Mutations/ 100 bp*	RGYW [†]
PIM-1	0.19 (0.05-0.28)	I	13	9/4 (2.25)	11	2	0.20	0.079	4 (p = 0.88)
PAX-5	0.17 (0.06-0.58)	0	15	11/4 (2.75)	1.5	0	0.26	0	6 (p = 0.36)
RhoH/TTF	0.22 (0.06-0.89)	1	19	11/8 (1.37)	9	10	0.18	0.26	8 (p = 0.18)
c-MYC exon 1	0.038	0	4	4/0	4	0	0.067	0	2 (p = 0.52)
c-MYC exon 2	0	0	0	0/0	0	0	0	0	0
Total	NA	2	51	35/16 (2.18)	39	12	0.19	0.084	20 (p = 0.08)
BCL-6	0.16 (0.07-0.27)	0	34	19/15 (1.26)	19	15	0.18	0.15	12 ($p = 0.01$)

^{*} Calculated from the number of G + C and A + T nucleotides in the wild-type gene sequences.

Similarly, it was observed in t(14;18) cases analyzed in the present study

[†] The frequency of mutations within RGYW motifs was compared with the frequency of mutations outside RGYW motifs by the χ^2 test.

Further molecular characterization of t(14;18) cases

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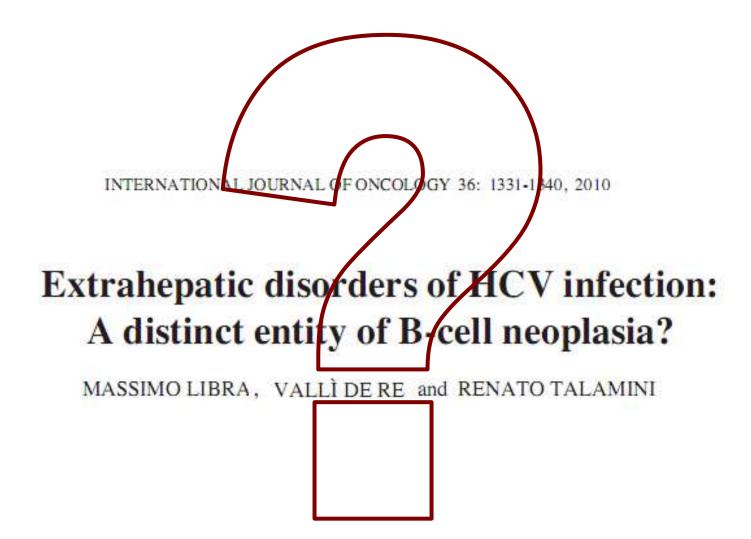
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Taken together these data indicate that t(14;18) may be considered a marker of high-grade transformation in HCV-associated Malt lymphomas

FUTURE DIRECTIONS

- ✓FISH analysis in t(14;18) DLBCL cases
- √ Microarray analysis of this subset of NHL
- ✓ Gene set enrichment analysis (GSEA)



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