

GENETIC MARKERS IN LYMPHOMA

a practical overview

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- **B and T cell monoclonalities**

Rearrangement of immunoglobulin and TCR genes

→ may help to establish the malignant nature of a lymphoproliferative lesion

- **Identification of non-random chromosomal abnormalities**

t(14;18) or t(11;14) translocations in FL and MCL respectively

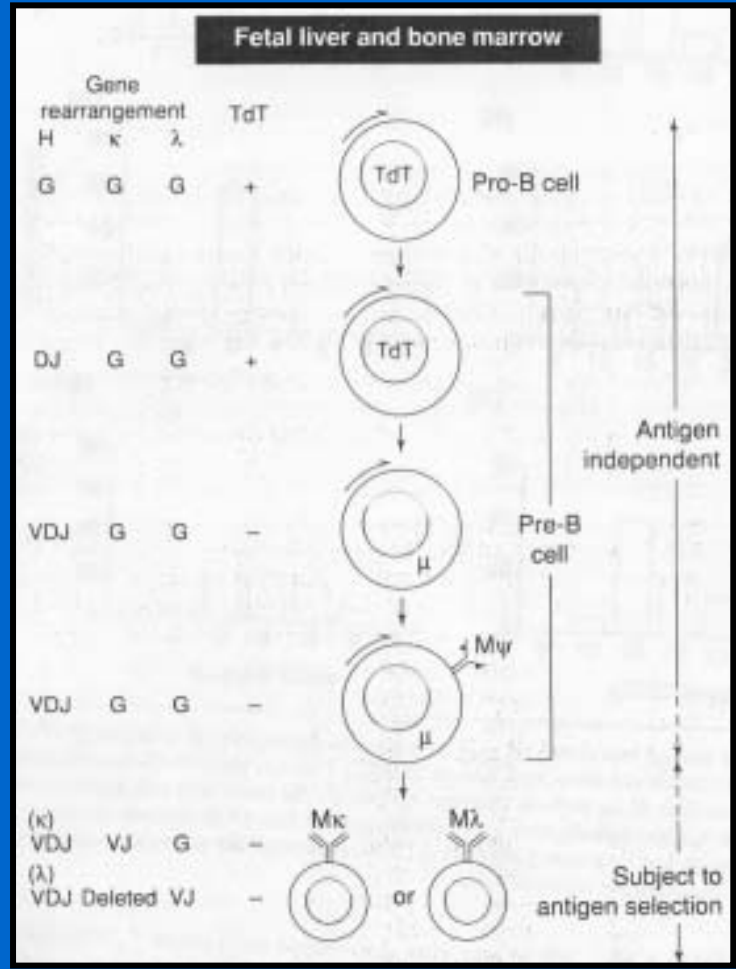
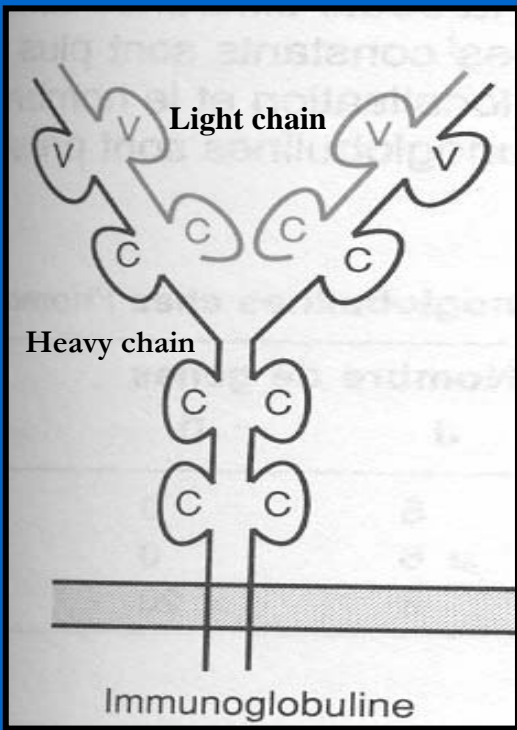
→ allow lymphoma subtype classification

B and T cell monoclonality

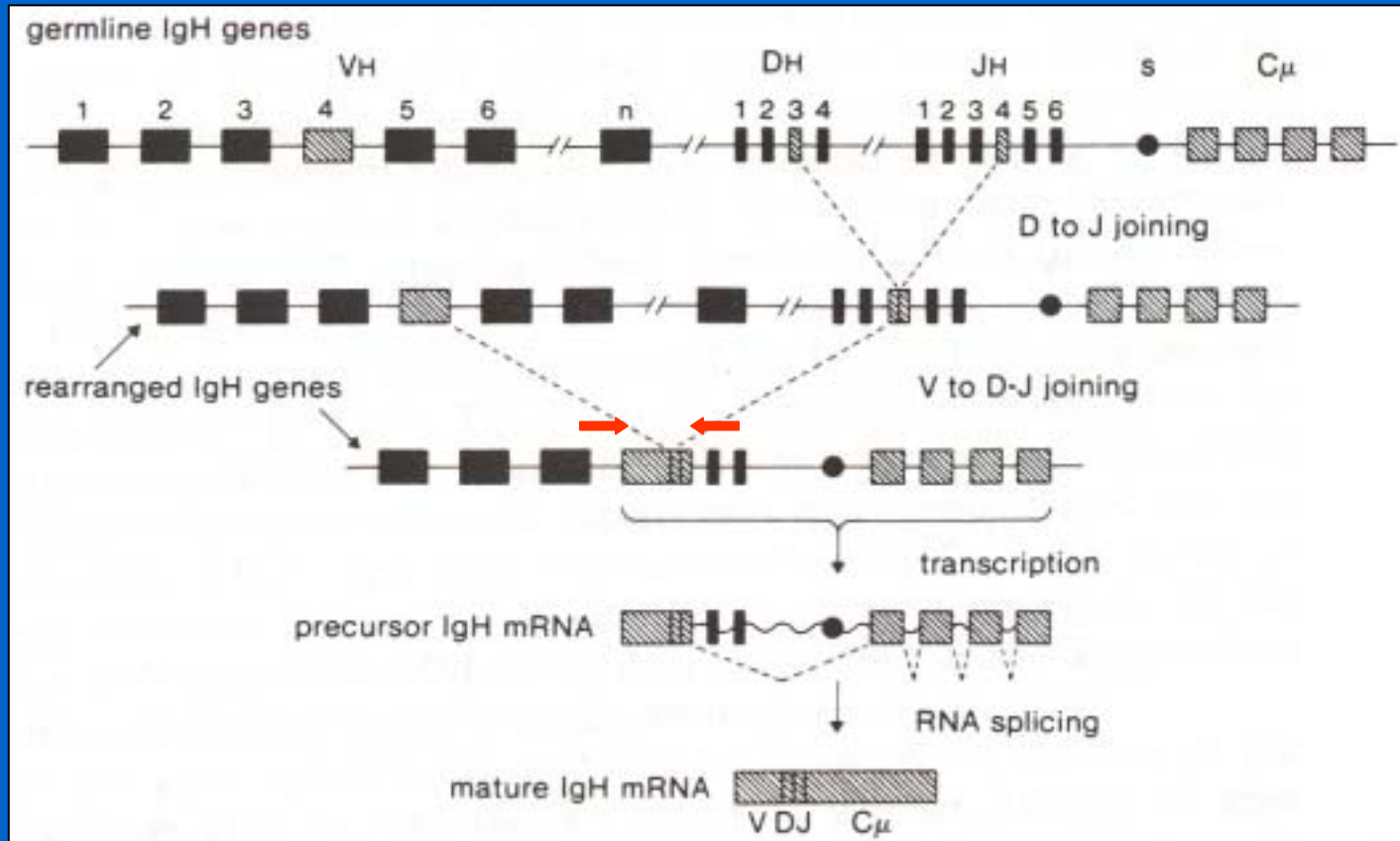
what does that mean?

During early lymphoid development, the genes encoding antigen receptor undergo rearrangement

example of the Ig heavy chain locus (IgH)

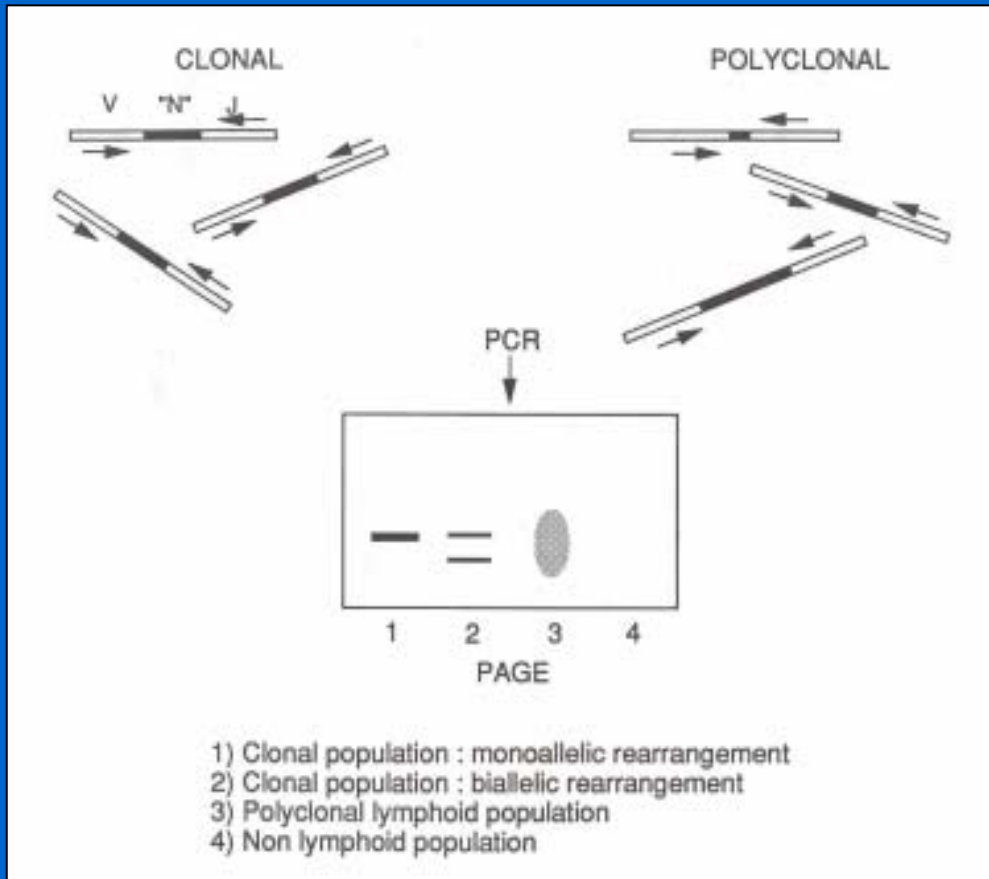


Schematic diagram of IgH gene rearrangements



➔ : indicate the primers location for PCR method

Schematic representation of mono and polyclonal populations detected by PCR.



- monoclonal population implies malignant process

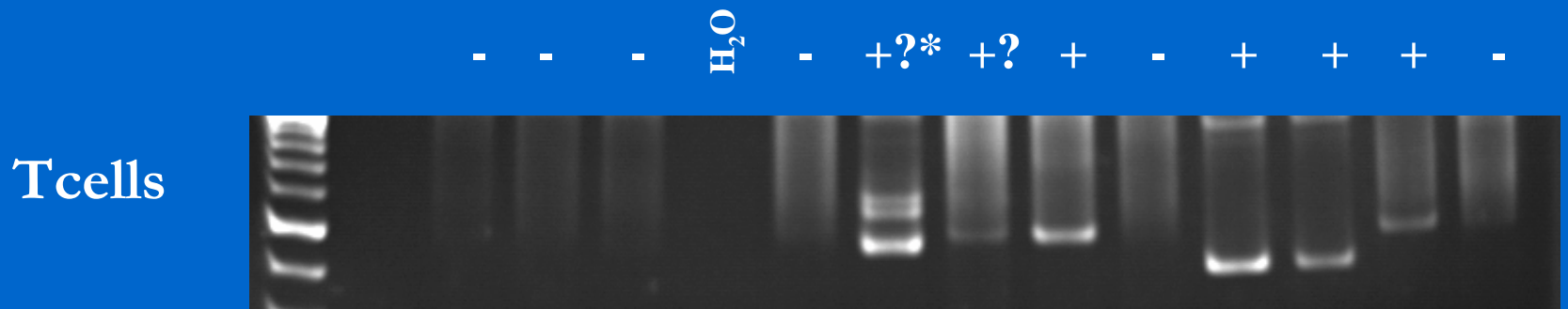
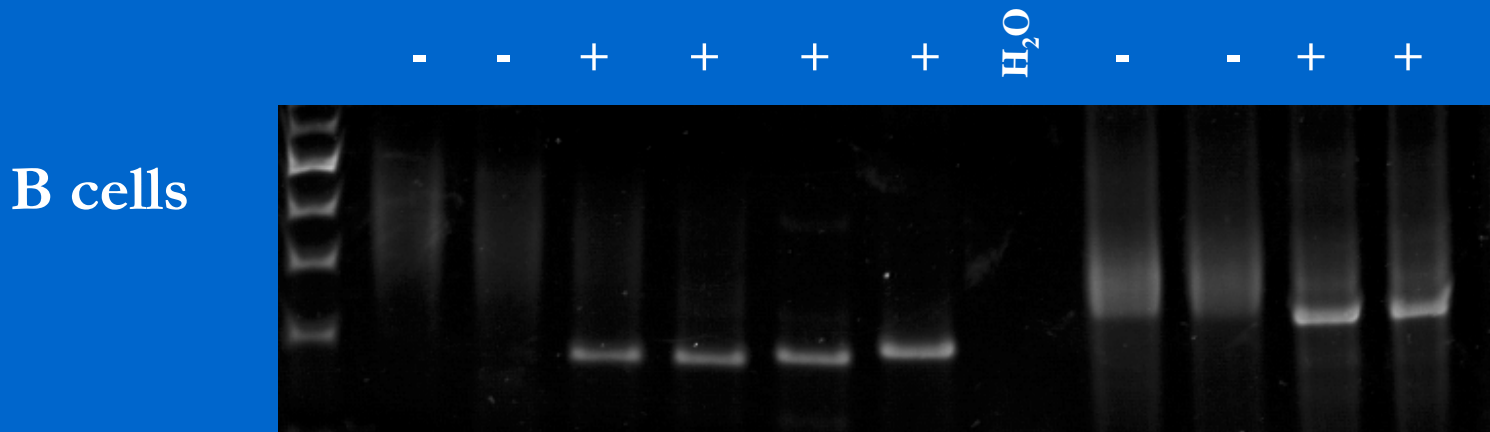
- polyclonal population implies benign lymphoid proliferation

but...

the rule is not absolute

B and T cell monoclonalities - PCR

Illustration on ethidium-bromide-stained gel

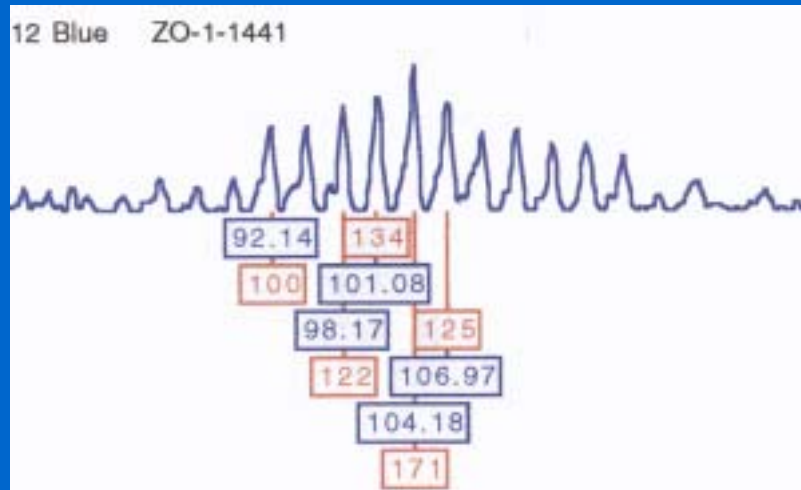


*? oligoclonality

B and T cell monoclonalities - PCR

Illustration on Genescan

polyclonality



monoclonality



PCR

Advantages: (vs Southern Blot)

- simple and faster
- requires much less amounts of pathological material
- greater quantitative sensitivity
- can be applied on DNA paraffin-embedded tissue

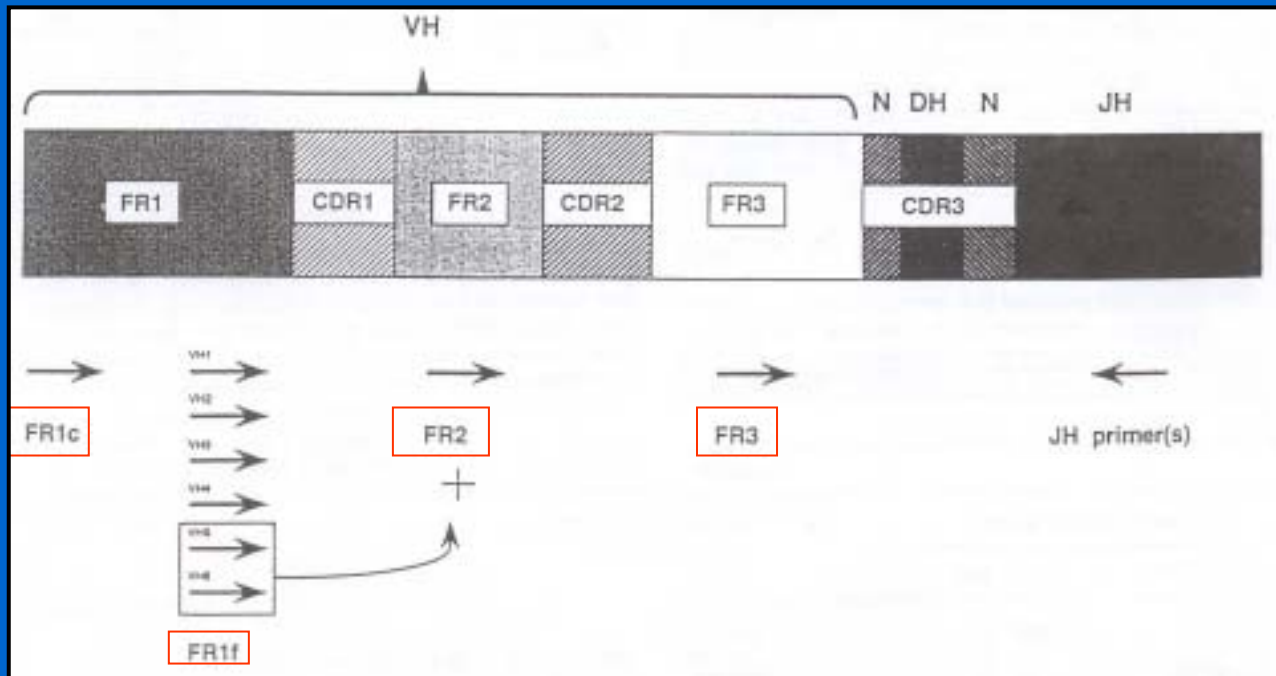
Disadvantages: (vs Southern Blot)

- lower qualitative sensitivity
- need to use several different PCR strategies in order to increase the overall detection rate *

*genomic sequence in a given antigen receptor may vary significantly from one to another and multiple sets of primers may be required

PCR strategies

- Necessity to use several sets of primers in order to increase the overall detection rate (~90 %) of the PCR method: FR3 -JH
FR1c-JH
FR1f-JH,...



- This detection rate varies according to the underlying disorders

Detection rates by PCR according to the subtype of B-cell neoplasms

- SLL ~ 100 %
- MCL ~ 100 %
- DLBCL ~ 60 %
- FL ~ 50 %

PCR - Pitfalls

False negative:

- chromosomal translocations into the IgH locus (in FL or DLCL)
- Somatic hypermutation (in FL and DLCL)
- partial D-J rearrangements (in immature malignancies)
- no VDJ rearrangement produced (in immature malignancies)
- failure of the IgH primers to recognize the VH segment involved

False positive:

- very weak amount of DNA
- reactive lymphoid populations

Rules to know (1)

- Genotype does not correspond to phenotype !

Lineage infidelity of Ig and TCR gene rearrangements
("Illegitimate rearrangements"):

- 50-60 % of lymphoblastic B cell malignancies.
- 20-30% of lymphoblastic T cell malignancies.
- ~10% of mature B and T cell malignancies.

Therefore, Ig and TCR gene rearrangements should not be systematically used as markers for B and T cell lineages, respectively.

Rules to know (2)

- Monoclonality is not always equivalent to malignancy !
 - Clinically benign lymphoproliferations may consist of clonal cell populations.
 - Although this pitfall is encountered in B cells, it is mainly observed in T cell monoclonality (cf limited combinatorial diversity of TCR- γ and - δ genes)

Rules to know (3)

- Some cases of unequivocal B-cells lymphoma do not generate a clonal signal by PCR despite histological and immunologic evidences of malignancy
- Any result must be interpreted in view of other findings and clinical informations

Chromosomal abnormalities

Chromosomal abnormalities

closely associated with particular morphological subtypes of lymphoma

→ diagnostic markers

prognostic/predictive markers

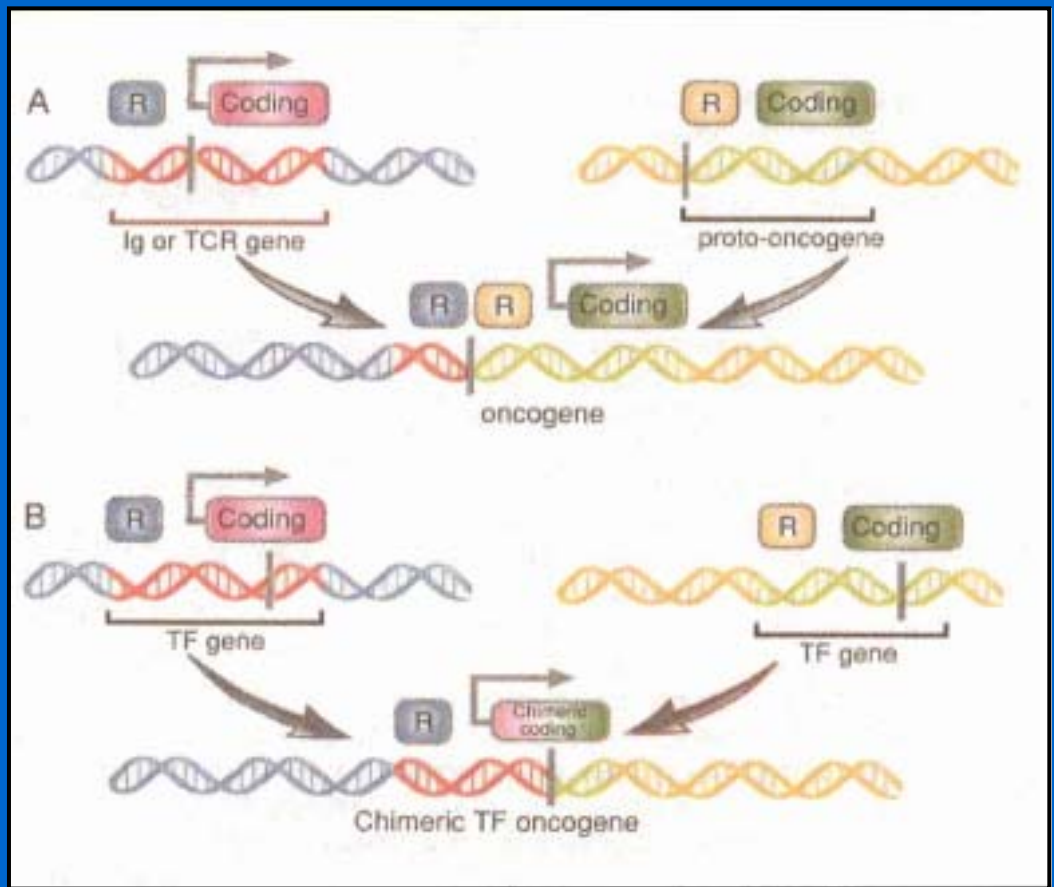
molecular targets for rationale therapies

mainly chromosomal translocations

Two distinct types of chromosomal translocations at molecular level

A. Quantitative changes

BCL2-J_H, BCL1-J_H...



B. Qualitative changes

ALK-NPM, API1-MALT

Recurrent genetic abnormalities in lymphoma

t(14;18) / *BCL2* - J_H

in follicular lymphoma

t(11;14) / *Bcl1* - J_H

in Mantle Zone lymphoma

**t(11;18)/ *API2-MALT1*
del(7q), +3**

in Marginal Zone lymphoma

t(3;14) / *BCL6* - J_H

in Diffuse Large Cell lymphoma

t(8;14) / *cMYC* - J_H

in Burkitt lymphoma

t(2,5) / *ALK-NPM*

in Anaplastic Large Cell Lymphoma

Follicular lymphoma (1)

t(14;18)(q32;q21) - *BCL2-IgH* oncogene



overexpression of the antiapoptotic Bcl2 protein

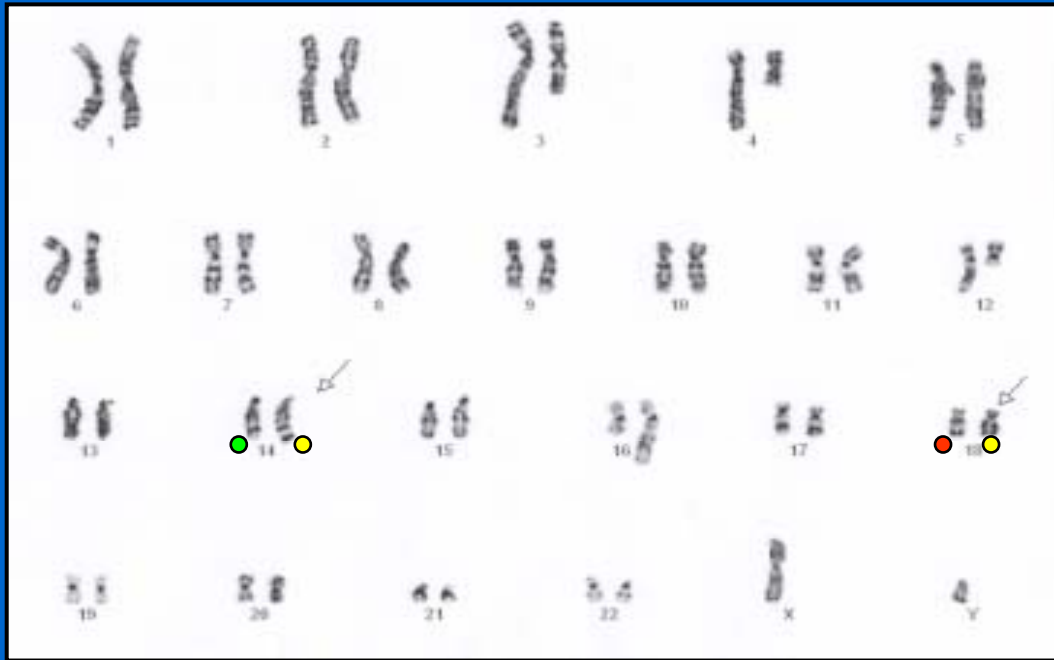


cell survival favoring increased genomic instability

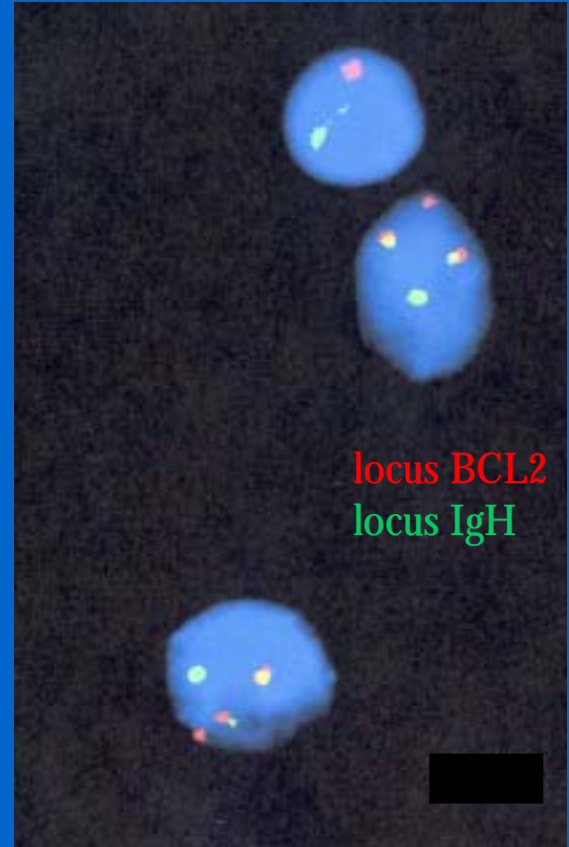


Follicular lymphoma

Follicular lymphoma (2)



$t(14;18)(q32;q21) / BCL2 - IgH$



FISH: « double fusion strategy »

Follicular lymphoma (3)

what to know

grade 1



t(14;18) positive in 80-90% of cases

grade 2

grade 3



t(14;18) positive in $\pm 30\%$ (mainly grade 3a)

t(14;18) negative in $\pm 70\%$ (mainly grade 3b)



BCL2 overexpression

or

no BCL2 overexpression

3q27 / *BCL6* rearrangement

Follicular lymphoma (5)

what to know

Conventional cytogenetic and/or FISH

“golden standard methodologies”

PCR: - four known different breakpoints on *Bcl2* gene

mbr in ~ 45 % of cases

mcr in ~ 7 % of cases

3'UTR in ~ 10 % of cases

icr in ~ 10% of cases

→ several sets of primers required

- some breakpoints are still unknown

Follicular lymphoma (4)

what to know

Methods : different levels of qualitative sensitivity

FISH

> 95%

Cytogenetics

~ 80-90%

PCR BCL2(mbr)-JH

40-50%

PCR BCL2(mcr)-JH

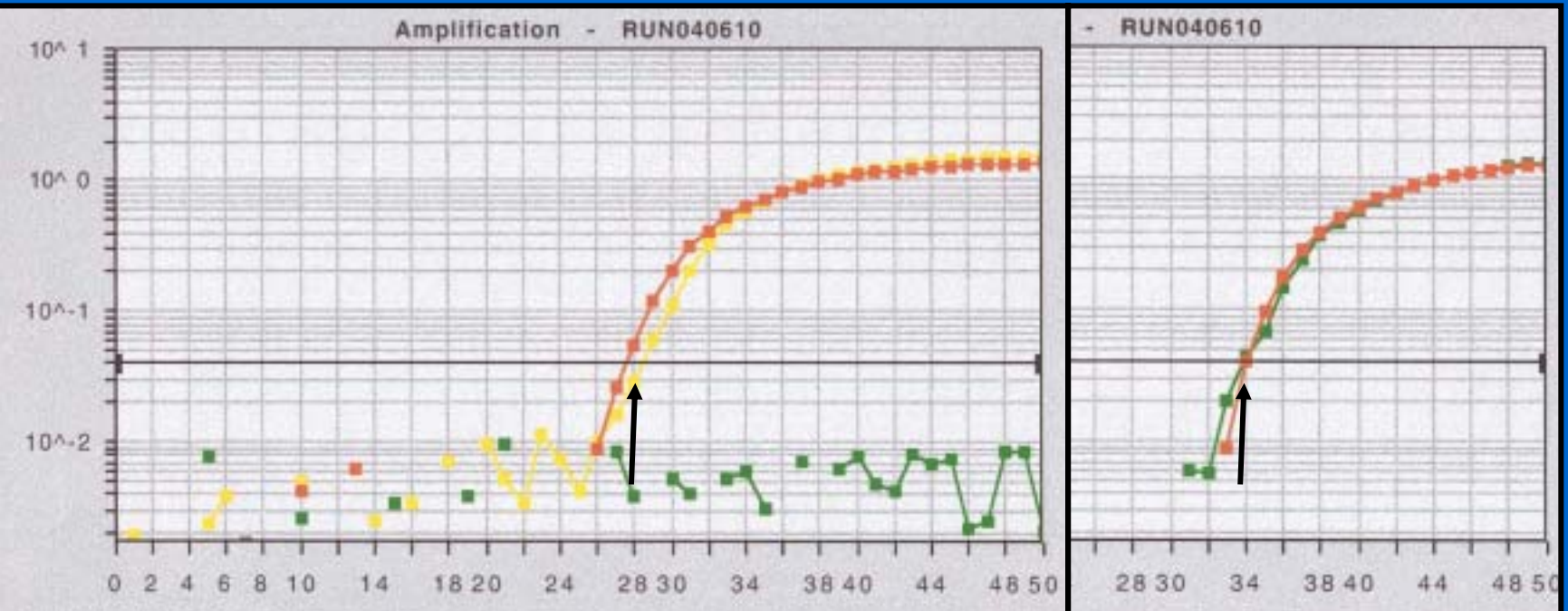
~ 10%

PCR Bcl2-JH in follicular lymphoma

Illustration

at diagnosis

Follow up



the persistence of a positive result or a molecular re-emergence after one year of treatment is highly predictive of a clinical relapse.

Follicular lymphoma (5)

what to know

- At diagnosis: CC and/or FISH *
- Follow up: Quantitative PCR

* FISH can be performed on fresh touch print or paraffin-embedded tissue

Mantle Cell lymphoma

t(11;14)(q13;q32) - *BCL1-IgH* oncogene



overexpression of the Bcl1/cyclin D1 protein



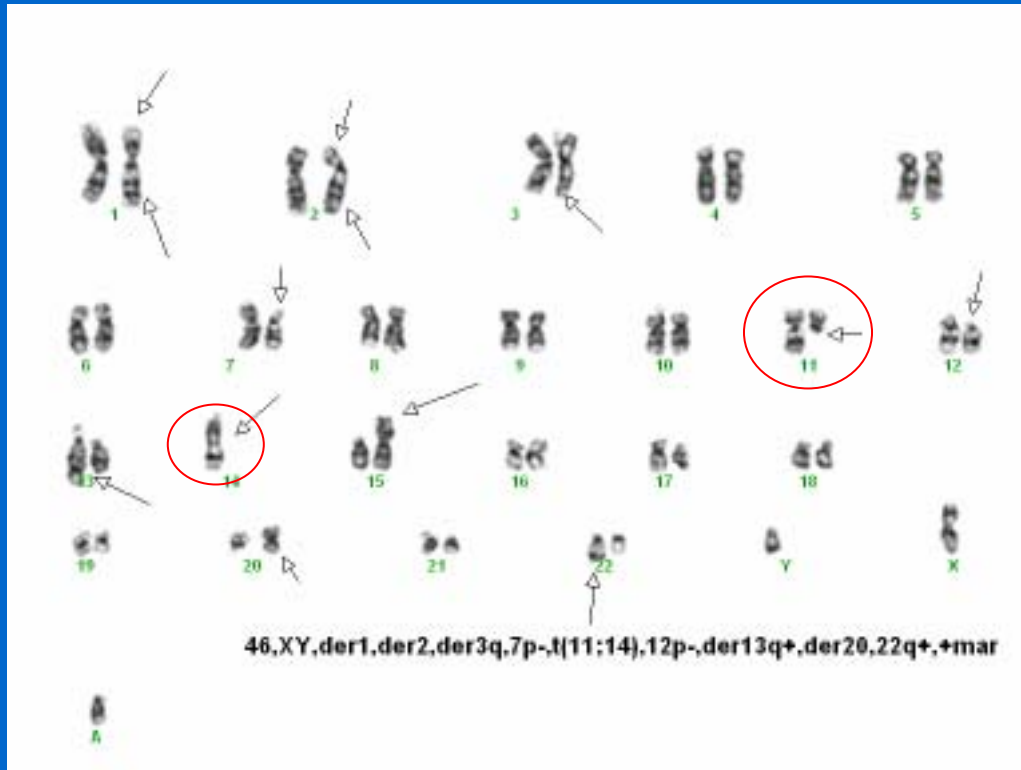
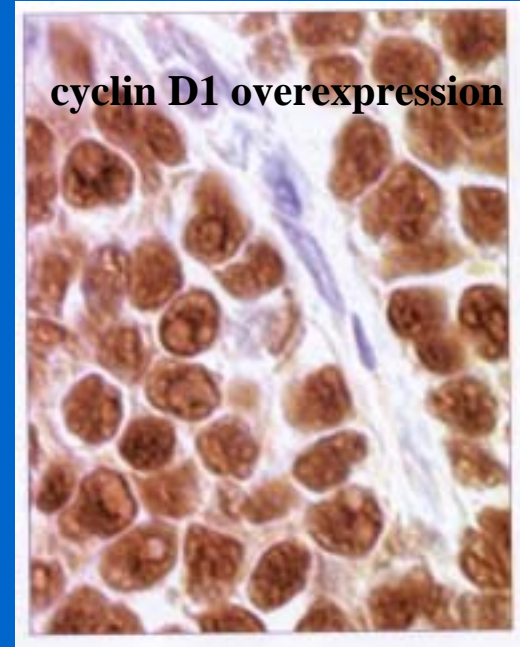
cell cycle activation (G1/S phase)

(+ other genetic alterations involving TSG such as *p16*)

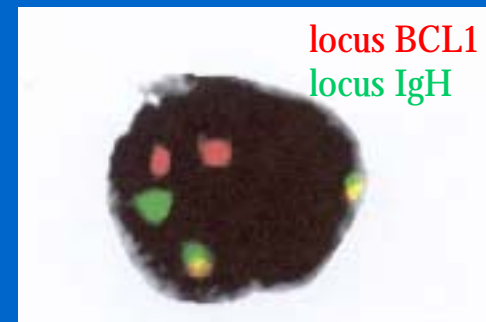


mantle cell lymphoma

Mantle cell lymphoma (2)



$t(11;14)(q13;q32) / BCL1-IgH$



FISH: « double fusion strategy

Mantle cell lymphoma (3)

what to know

Conventional cytogenetic and/or FISH

“golden standard methodologies”

PCR: - one major known breakpoints on *Bcl1* gene
MTC in ~ 50 % of cases
- other breakpoints are heterogeneous
and difficult to detect
(large target region for possible rearrangement breakpoints)

Mantle cell lymphoma (3)

what to know

Methods : different levels of qualitative sensitivity

FISH **> 95%**

Cytogenetics **~ 80%**

PCR BCL1(MTC)-JH **~ 50%**

RT-PCR (CyclinD1 overexpression) **~ 100% ***

* results difficult to interpret

Marginal cell lymphoma (1)

Distribution of chromosomal abnormalities according to the three ≠ subtypes

MZL of MALT type

chromosomal translocations with site-specificity
in terms of their incidence

splenic MZL

numerical abnormalities (mainly trisomies 3, 7, 18)

nodal MZL

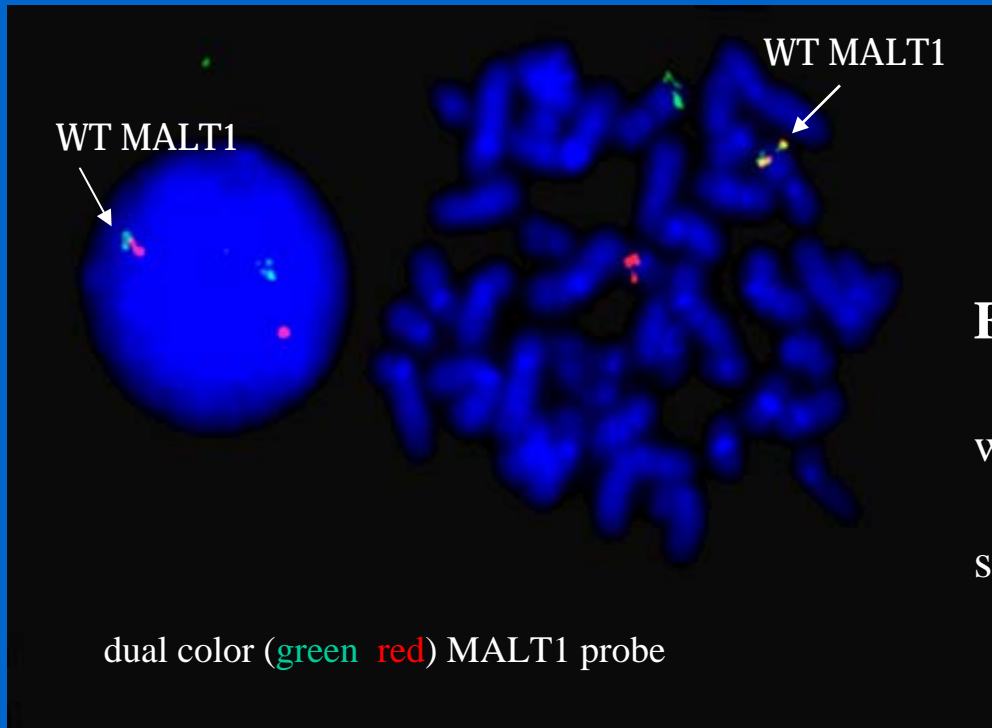
numerical and structural abnormalities: del(7q),+3

Marginal cell lymphoma (2)

MALT type

t(11;18)(q21;q21) <i>API2-MALT1</i>	15 -40%	stomach intestine lung
t(14;18)(q32;q21) <i>MALT1-IgH</i>	20%	salivary gland ocular adnexa skin, liver, lung
t(1;14)(p22;q32) <i>BCL10-IgH</i>	1-2%	stomach, lung
t(3;14)(p14;q32) <i>FOXP1-IgH</i>	5%	thyroid, skin, ocular adnexa

t(11;18)(p21;q21) / *API2-MALT* in gastric MALT lymphoma



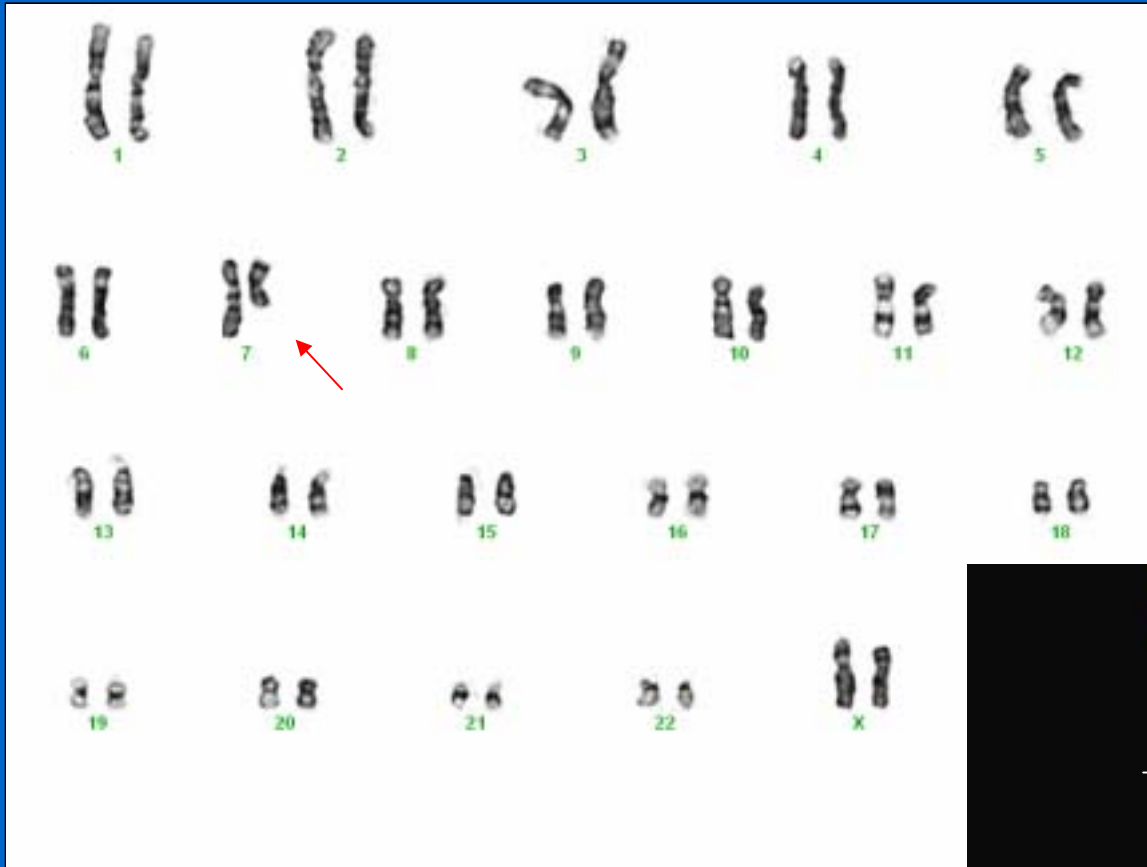
FISH: “break-apart probe strategy”

wild type MALT1: 1 yellow spot

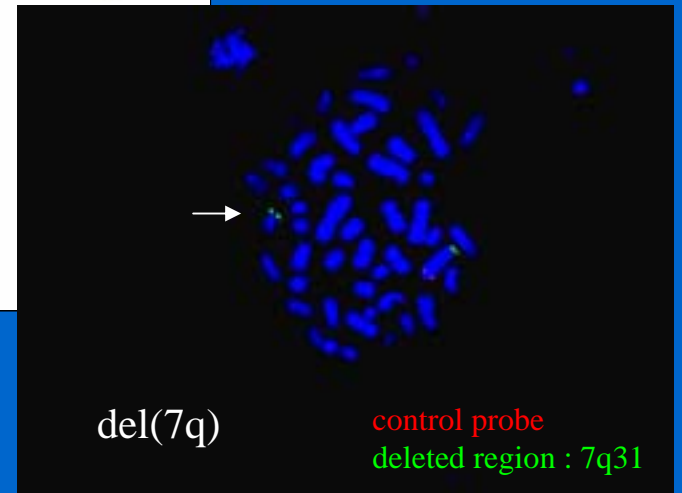
split MALT1: 1 green and 1 red

gastric MALT with t(11;18) do not respond to *Helicobacter pylori* antibiotic

splenic Marginal cell lymphoma (3)



46,XX,del(7)(q22q32)



del(7q)

control probe
deleted region : 7q31

Diffuse Large B cell lymphoma (1)

t(3;14)(q27;q32)

t(3q27;v)

BCL6-IgH oncogene

BCL6-non IgH oncogene

in 30-40% of DLBCL



BCL6 oncogene overexpression*



cell survival and proliferation

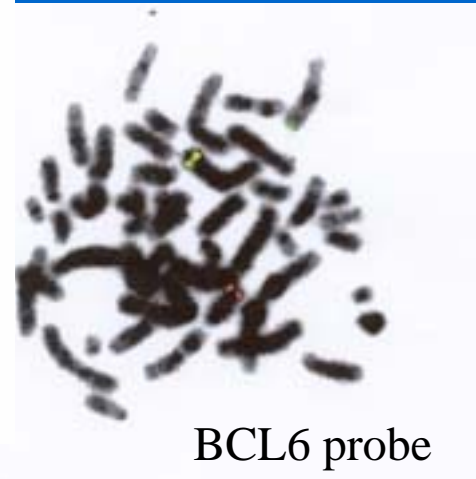
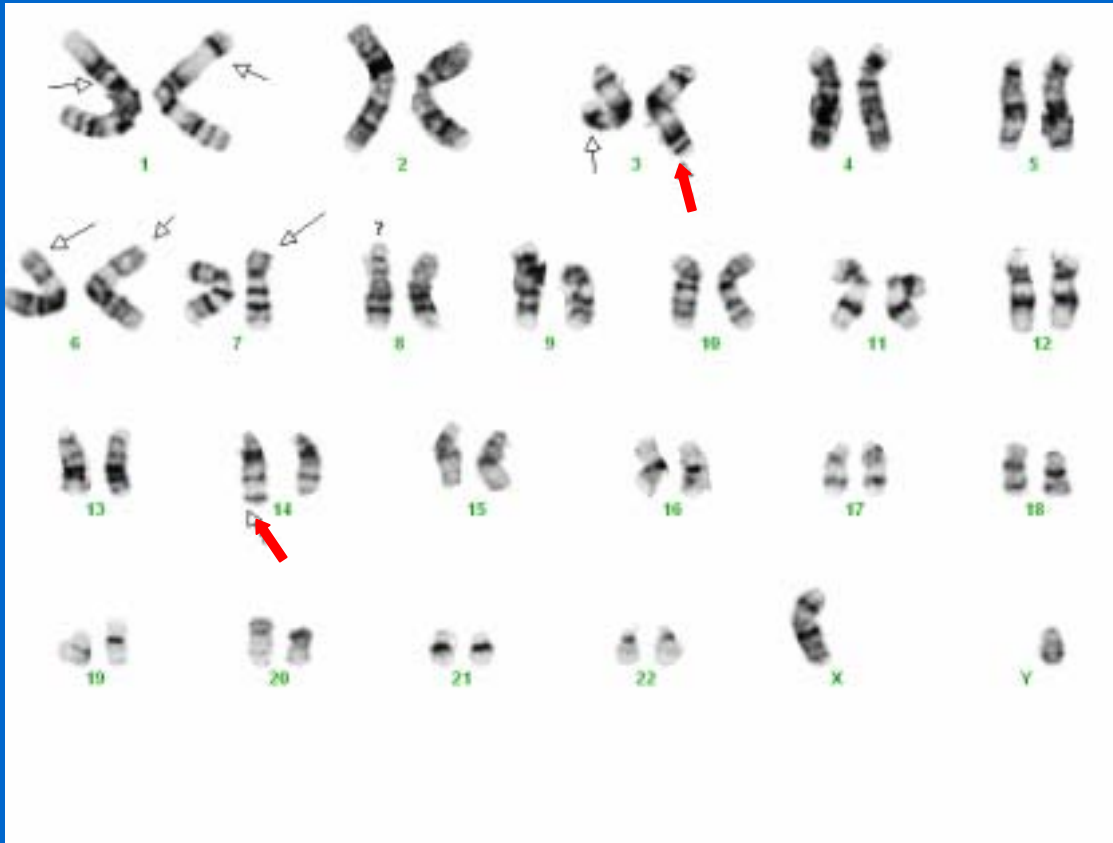


DLBCL

* high *BCL6* overexpression → better outcome

Diffuse Large B cell lymphoma (2)

Illustration



$t(3;14)(q27;q32)$ *BCL6-IgH*

FISH: “break-apart probe strategy”