# The interplay between BcR signalling and the p53 pathway upon DNA damage in primary CLL cells

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# Background

- Constitutively activated pro-proliferative B cell receptor (BcR) signalling and deregulated DNA damage response are major drivers in CLL.
- Inhibitors targeting the BcR signalling were considered to act independently of the p53 pathway that is part of DNA damage response in cells.
- Different frequencies of TP53 gene defects in different BCR stereotyped subsets and subgroups based on IGVH usage (PMID: 24725250) suggested a potential interplay between p53 and BcR signalling.

# Objective

To investigate whether a therapeutical inhibition of BcR level, phosphorylation and its signalling alters p53 transcriptional activity.

# Materials and methods

- In-silico analysis of publicly available data (PMID: 33833385) was used to track transcription programmes after BcR activation in primary CLL cells.
- Patients cohort: primary CLL cells with wild-type TP53 gene,
- pilot cohort: n=13 for combination with ibrutinib and n=12 for combination with idelalisib,
- validation cohort: n=24.
- Treatment of primary CLL cells for 24 hours:
- 1.5 μM doxorubicin or 15 μM fludarabine DNA damaging agents stabilizing p53 in cells,
- 10 μM ibrutinib or idelalisib tyrosine kinase inhibitors targeting BcR signalling,
- treatment combinations are indicated in the results section.
- Analysis of p53 level and phospho-patterns by SDS-PAGE and Zn(II)Phos-Tag method followed by western blots using anti-p53 antibody.
- qRT-PCR of p53 target genes BAX, BBC3, CDKN1A, GADD45A.

# **1. Activated BcR signalling changes** expression of p53 targets

*In-silico* analysis of transcriptomic data from 3 proliferative primary CLL samples with unmutated IGHV and wt-TP53 (PMID: 33833385).

■ Focus on significant changes (FDR<0.05; logFC≥|2|) in the expression</p> of typical p53 targets (list of targets – PMID: 28288132).

After 24 hours, activation of BcR signalling led to significant changes in the expression of 13 out of 116 typical p53 targets.

Genes listed in the table are mostly involved in regulating cell proliferation, cell death and stress response, including DNA-damage response.

Differentially expressed p53 targets after BcR activation					
3 targets	logFC	FDR	p53 targets	logFC	FDR
FAS	4.475785	2.10E-18	SESN2	2.749924	5.16E-05
CSF1	5.483876	1.81E-14	EPS8L2	-3.52068	7.05E-05
ENC1	-7.80791	3.44E-12	NINJ1	3.598083	0.000152
RIM22	-3.69048	4.10E-11	SLC12A4	2.415349	0.000236
ATF3	5.025042	8.54E-08	PTP4A1	-2.27854	0.000321
BTG2	-2.75325	1.27E-07	PLK2	-3.0477	0.001079
APTM5	-3.28526	9.97E-07			

### 4. Decrease in p53 level is not mirrored in the expression of its target genes



#### **RIGHT PANEL**

#### **BOTTOM PANEL**



# Results

# 2. Ibrutinib, but not idelalisib, decreases p53 level under DNA-damaging conditions

Graph shows changes in the p53 level where combinatorial treatment with tyrosine kinase inhibitors and DNA damaging agents was compared to DNA damaging agents used alone.

The grey dashed line represents no change in the p53 level, red lines represent the median, whiskers 1<sup>st</sup> and 3<sup>rd</sup> quartile. Indicated p-values were calculated by Wilcoxon Signed Rank Test.

Ibrutinib, but not idelalisib, treatment led to a significant decrease in the level of p53 protein with a more homogeneous effect in the doxorubicin group.

Validation of ibrutinib effect on p53 protein stabilized by doxorubicin.

Representative western blots and a graph show a **34% median decrease** in p53 level.



- The relative expression of four p53 downstream effectors did not decrease after adding ibrutinib to doxorubicine compared to doxorubicin alone.
- We hypothesize that p53 targets are either activated by **p53-independent mechanism** or potential effect of ibrutinib on p53 transcriptional function is masked by persisting DNA damaging conditions.
- p<0.05, \*\*p<0.01, n.s. non-significant, Wilcoxon</p> test. Red lines represent median, whiskers 1st and 3rd quartile.

# 3. Ibrutinib decreases p53 level but doesn't change p53 phosphorylation pattern

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Stability and function of p53 are highly dependent on p53 phosphorylations that are tightly regulated.

Zn(II)Phos-Tag method (representative) western blots shown) revealed that ibrutinib does not change the p53 phosphorylation pattern, only the level of total p53 protein.



+P/-P with/without phosphatase treatment.

Each band in -P lines represents differentially phosphorylated p53 protein creating specific phospho-pattern.

A band in +P samples represents the total p53 level.

# Conclusion

We documented the interplay between p53 and BcR signalling in primary CLL cells.

Ibrutinib decreases the level of p53 in cells without a detectable effect on p53 transcriptional activity.