

TP53 Network activities

Minor clones, Recommendations' update & Database

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ACTIVITIES OF *TP53* NETWORK

- **Help laboratories keep high standards of *TP53* diagnostics in CLL**
 - ERIC *TP53* Certification (12 Certification rounds, >100 certified laboratories)
 - Cooperation with GenQA/NEQAS (re-certification)
 - Educational workshops
 - *TP53* Helpdesk
 - ERIC Recommendations on *TP53* Analysis in CLL
- **Respond to technical and therapeutical progress**
 - Detection of variants <5-10% VAF – methodical challenges, clinical impact, standardization
- **Transfer knowledge gained in routine *TP53* diagnostics in CLL to wide *TP53* community**
 - ERIC *TP53* database

**ERIC MULTICENTER STUDY ON *TP53* VARIANTS
BELOW 10% VAF**

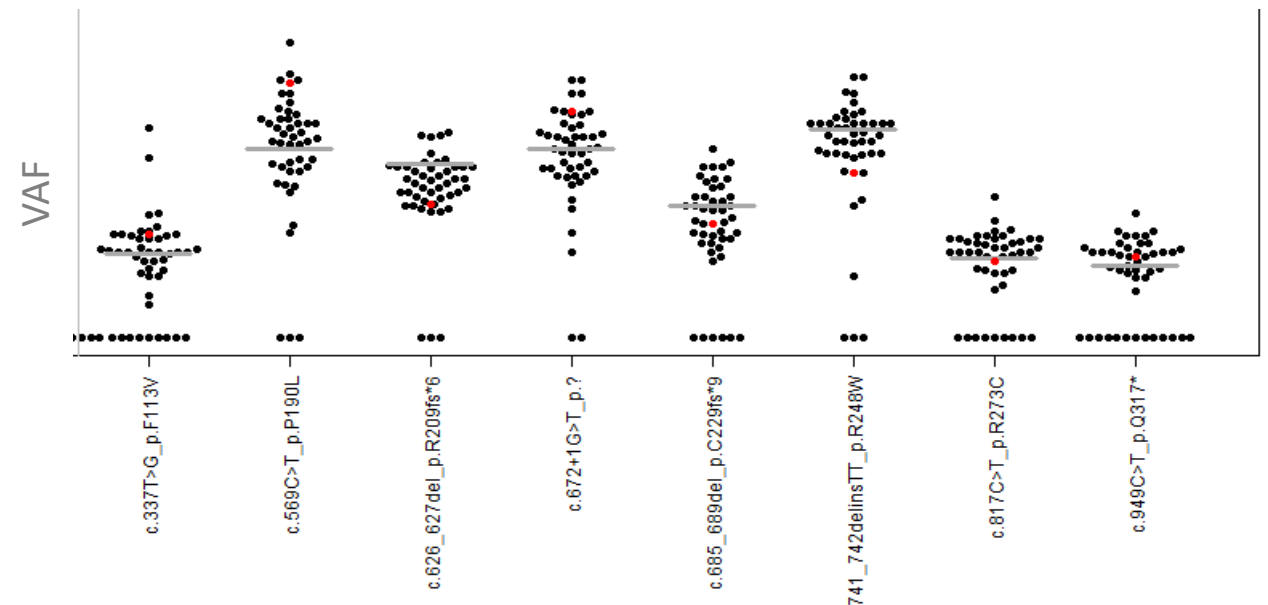
PART1: METHODOICAL HARMONIZATION (41 participants)

Inter-laboratory comparison of NGS results obtained from the set of reference samples

- Invitation to the study by ERIC office – Q3/2018
- 7 samples with 23 variants <10% VAF prepared in Brno and Milan, sent Q2/2019
- Comparison of individual results with results of other groups
 - individual and summary reports Q4/2019
- EHA poster 2020
- **Manuscript preparation – in progress**

✓ 63% laboratories
no false positivity >2% VAF
no false negativity >2% VAF

✗ 17% laboratories
false positivity above their limit of detection





PART 2: DATA COLLECTION (10 participants)

- Patient data collection – since 12/2020
- Data curation – Q4/2021
- **Data analysis – currently running**
- **Manuscript preparation**

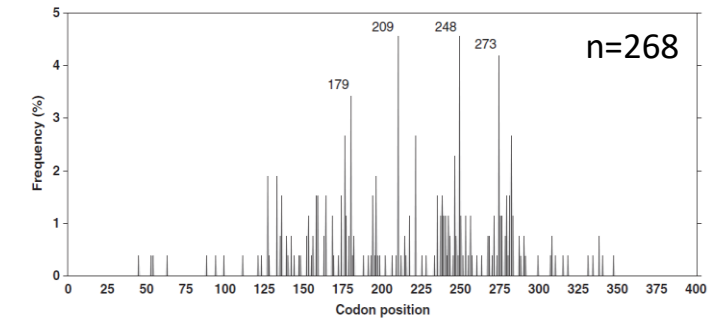
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≈1000 patients

ERIC *TP53* DATABASE

PROJECT AIMS

- To collect a list of *TP53* variants obtained during routine *TP53* screening in CLL
- To create a publicly accessible CLL-specific database of curated *TP53* variants
- Analyze the disease-specific variant profile (update Zenz et al., Leukemia 2010)
- Analyze the association with clinico-biological parameters (treatment, FISH, IGHV,...)
- **Help diagnosticians to assess the clinical impact of detected variants**




WHY?

- Current *TP53* databases – gene specific databases, only published data - risk of redundancies
 - The *TP53* database originally IARC) <https://TP53.isb-cgc.org/>
 - UMD *TP53* database (<http://p53.fr/>)
- CLL is the first malignancy for which testing for the presence of *TP53* defects is fully implemented in the clinics to guide treatment decision-making.

REQUIRED DATA

- **Data on *TP53* variants** (variant description, VAF...)
 - All detected variants irrespective of their functional impact
 - Except for the most common polymorphisms
- **Brief method description** (sample type, sequencing method...)
- **Clinical data – part of ERIC CLL database**
 - Not obligatory but highly welcomed
 - In centers involved in ERIC CLL database – data will be linked based on patient ID

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- Addressing participants Q3-4/2020
 - **Collecting data – Q1-2/2022**
 - Data curation – Q2-Q3/2022
 - Data analysis – since Q4/2022
 - Releasing the database – 2023
 - Preparing a manuscript – 2023

Current state: 45 participants (22 countries)

YOU ARE STILL WELCOMED TO JOIN

HOW TO APPLY:

1) Via application questionnaire (ERIC members received an email with the link):

<https://barcelo.eventsair.com/eric-members-database/database-of-TP53-variants-in-cll/Site/Register>

2) Contact ERIC office or malcikova.jitka@fnbrno.cz

- ERIC TP53 certification required

Project description: <http://www.ericll.org/projects/>

SUB-PROJECT

FUNCTIONAL ANALYSIS OF IN-FRAME VARIANTS

- Deletions and insertions in the *TP53* gene not resulting in frameshift (\approx 5% of *TP53* mutations)
- Pathogenic interpretation is more experience-based than evidence-based
- Very limited solid evidence in literature exists

AIM

- To collect the set of inframe variants within the *TP53* database and analyze their functional impact using Functional analysis in yeast
- REQUIREMENTS: cDNA or RNA of sufficient quality

ERIC RECOMMENDATIONS ON *TP53* ANALYSIS - UPDATE

Do we still need *TP53* analysis in the era of targeted treatment?

- ESMO guidelines recommend targeted treatment for all IGHV unmut patients (*Eischhorst et al., Ann Oncol 2021*)
- **BUT** *TP53* status remains crucial in treatment-decision algorithms in many countries
- Different type of targeted treatment for *TP53*-mut patients?

„Analysis of *TP53* defects - life saving“

Do we need new recommendations?

Current recommendations written in 2017 – what has changed?

- 2022 NGS prevails
 - New technical aspects
 - Detection of minor clones below the detection limit of Sanger sequencing - high risk of clonal selection upon CIT

<i>Malcikova et al., Leukemia 2018</i>	Update
Sanger and NGS equal	NGS preferred (but Sanger better than nothing)
Do not report mutations <5-10% VAF	All variants RELIABLY identified may be reported?
	Extending resources for variant interpretation
	Increasing demands for reporting format

**THANK YOU VERY MUCH
FOR YOUR ATTENTION**

www.ericll.org