

**48<sup>th</sup> General Assembly of ERIC Members  
ASH 2019  
Orlando December 8<sup>th</sup>, 2019**

**PREVALENCE OF *BTK* AND *PLCG2* GENE MUTATIONS IN  
CHRONIC LYMPHOCYTIC LEUKEMIA PATIENTS RELAPSING  
ON IBRUTINIB: A EUROPEAN RESEARCH INITIATIVE ON  
CLL (ERIC) REAL-WORLD STUDY**

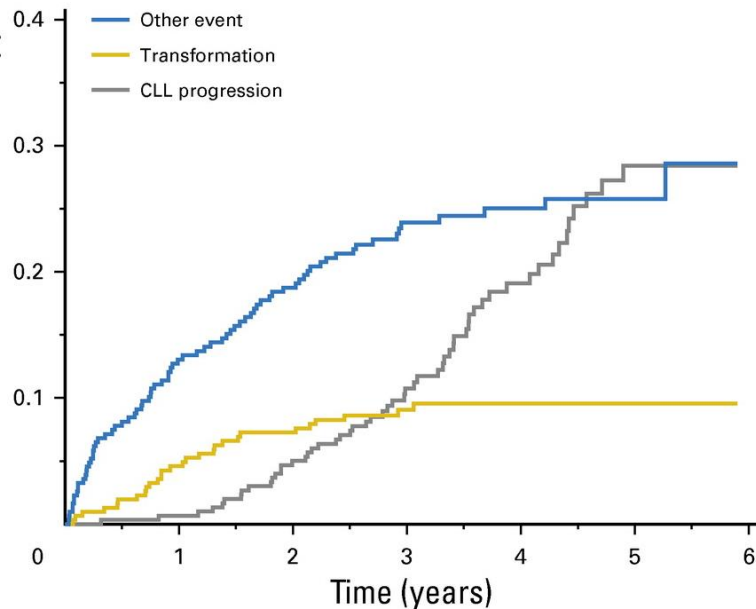
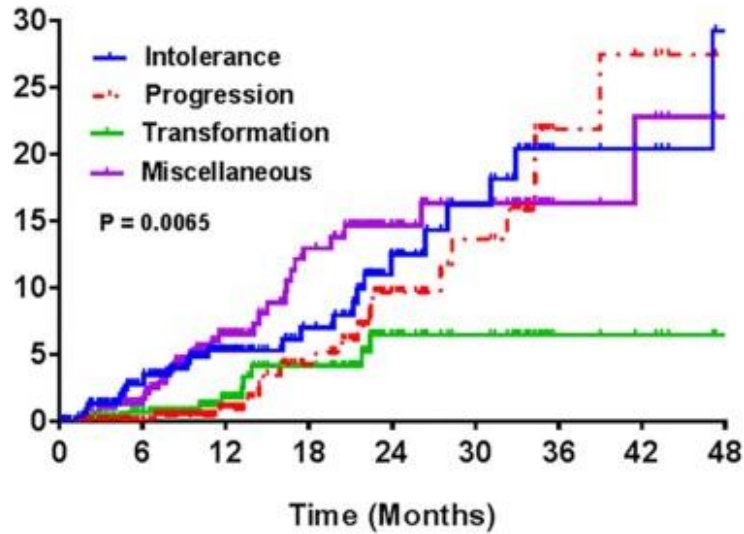
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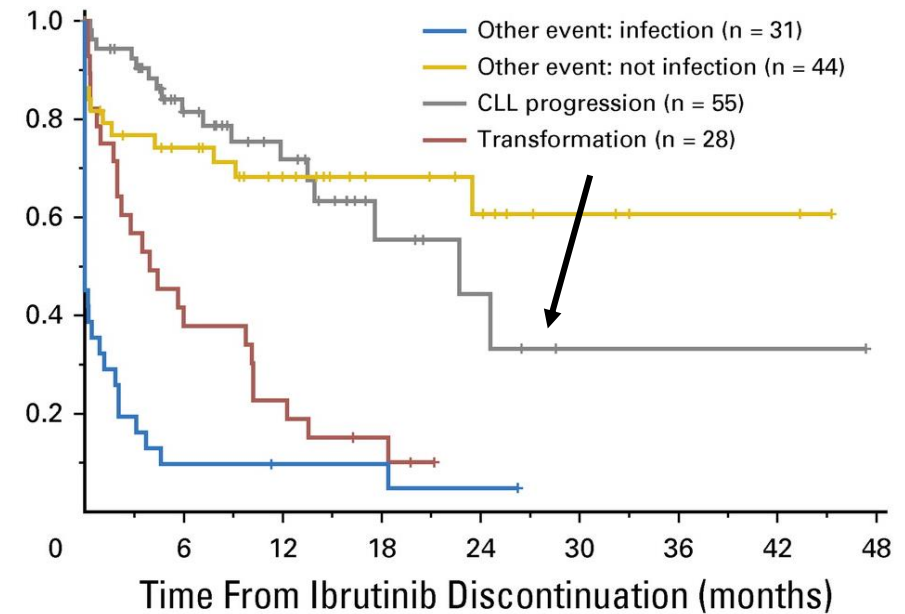
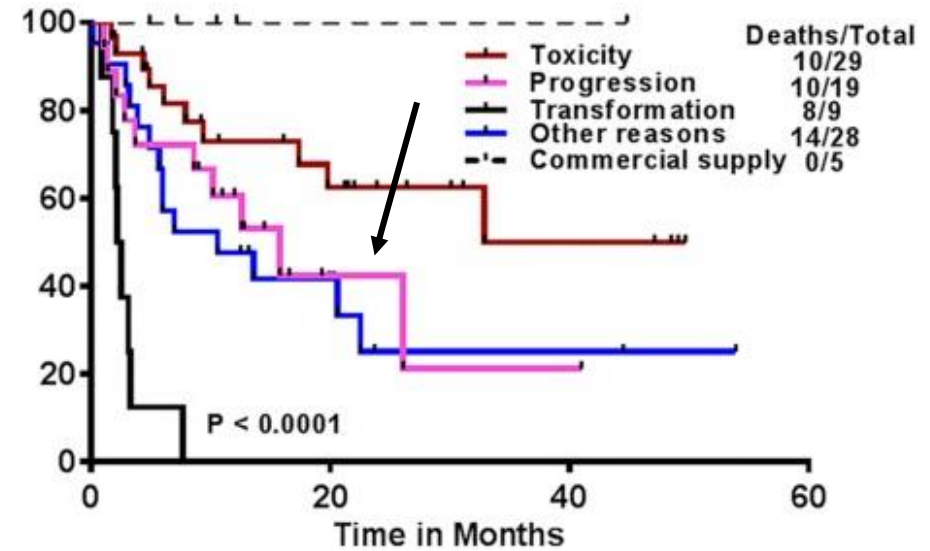
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# Ibrutinib discontinuation and outcome

Cumulative incidence of discontinuation of ibrutinib therapy



Survival Probability



# *BTK* and *PLCG2* mutations in CLL patients relapsed on ibrutinib

Ref.	Pts with mut/total	Analytical Method	<i>BTK</i> mutations	VAF %	<i>PLCG2</i> mutations	VAF %
Woyach, 2014	6/6	WES	C481S	17-60	R665W; L845F S707Y	8-38
Ahn, 2017	8/10	High sensitivity NGS; ddPCR	C481S C481R	1.6-78.2 15.8	6nt del; R665W P664S; S707Y; L845F	0.1-18.3
Woyach, 2017	40/46 (retrospective); 8/8 (prospective)	Targeted Deep Sequencing	C481S C481R C481F C481A	0.2-94.8 18.1 1.1-100 45.3	R665W; S707P; S707F; S707Y; L845F; D993Y; L845/846del	3.6-44
Burger, 2016	2/4	WES; ddPCR	C481S	NR	M1141R; S707F; M1141K; D993H	12.0-35.0 (CCF)
Landau, 2017	5/7	Targeted Deep Sequencing	C481S	2.2-78.2	R665W; S707Y; L845F	0.2-4.7
Kadri, 2017	1/3	Targeted Deep Sequencing	C481S C481R	8.5-90.0 2.5	NR	NR
Kanagal-Shamanna, 2019	16/23	Targeted Deep Sequencing	C481S; C481F C481R; C481Y V537I	11(1-91)	None	NA

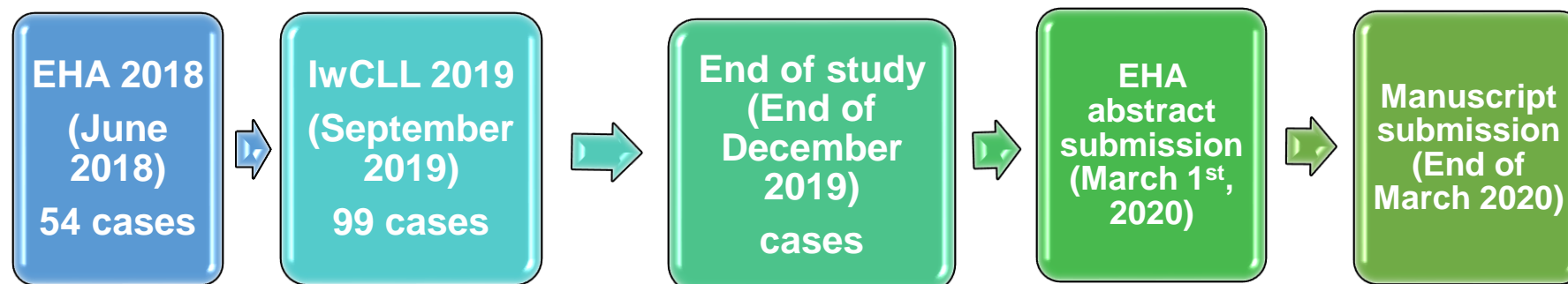
# Participating Sites

## Up to 21 sites

Country	Number of sites (Site IDs)
Italy	7 (OSR MI, Policlinico MI, Torino, UniTo, Padova, Novara, Modena, Niguarda MI)
UK	4 (Southampton, Bournemouth, Cambridge, RMH London)
Greece	2 (Athens, Thessaloniki)
Australia	2 (Melbourne, Sidney)
Sweden	1 (KI Stockholm)
Argentina	1 (Buenos Aires)
Croatia	1 (Zagreb)
Hungary	1 (Budapest)
France	1 (Toulouse)
Russia	1 (Saint Petersburg)

# Update (2Dec2019)

# patients	Batch 1&2	Batch 3	Batch 4	Batch 5	TOTAL
relapsed	22	6	21	(12)	49 + (12)
sensitive (>1y)	32	17	1	0	50
TOTAL	54	23	22	(12)	99-111



# Study Design

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International, retrospective, observational, multicenter study

**20 ERIC participating sites:**

- Italy (7)
- UK (3)
- Greece (2)
- Australia (2)
- Sweden (1)
- Croatia (1)
- Argentina (1)
- Hungary (1)
- France (1)
- Russia (1)

**PRIMARY OBJECTIVE:**

To determine the prevalence of ***BTK*** and ***PLCG2*** mutations in CLL patients **relapsing** or responding to ibrutinib in a real-world setting

# Eligibility Criteria

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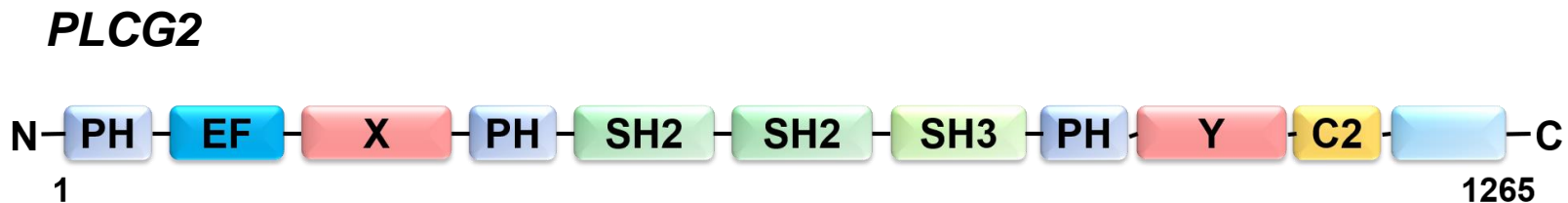
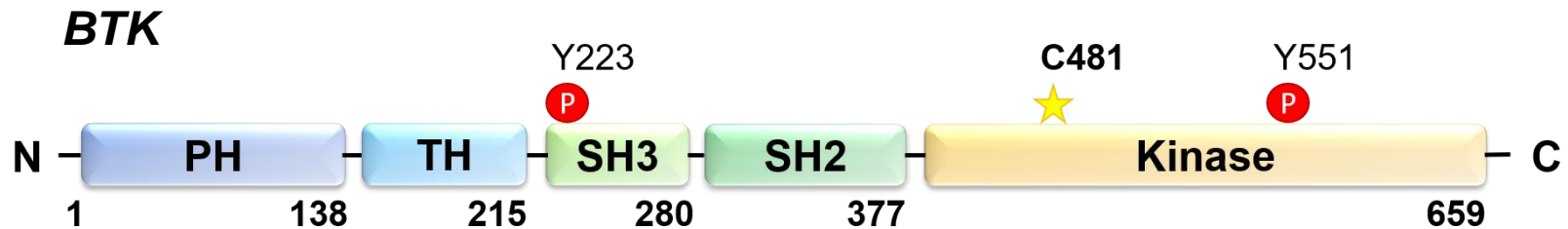
**CLL patients who received ibrutinib treatment at full dose without >14 days interruption**

- **Relapsed cases**: relapse on ibrutinib according to the modified IwCLL 2008 criteria
- **Responders**: responding to ibrutinib according to the modified IwCLL 2008 criteria and have samples collected after at least 1 year of treatment

**Patients with Richter Transformation were excluded**

# Methods

- DNA extraction from purified B cells
- Agilent HaloPlexHS kit (*BTK* and *PLCG2* all exons)
- Paired-end sequencing (NextSeq Illumina)
- Variant allelic frequency (VAF) cutoff of 1% (Targeted deep sequencing)





## Patient cohort (n = 99)

Characteristics	Relapsed n = 49	Responsive n = 50	Overall n = 99
Median age, y (range)	64 (48-86)	71 (46-85)	67 (46-86)
Gender (M:F)	1.87	1.78	1.81
# prior therapies (0/1/≥2)	0/6/37	9/12/29	9/18/66
del(17p) (n= 88)	45.2%	34.8%	39.8%
<i>TP53</i> Mutations	58.2%	48%	53.1%
IGHV Unmutated (n=42)	74.2%	68.3%	70.8%
Duration of ibrutinib treatment (months)	25 (3-57)	35 (8-73)	33 (3-58)
Best Response to ibrutinib CR/PR or nPR	4/34	12/38	16/72

# Concluding Summary

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- We analyzed **49 relapsed** and **50 responding CLL** patients treated with **ibrutinib**
- **Around 50%** of cases **relapsing** on ibrutinib had ***BTK*<sup>C481S/R</sup>** mutations
- ***PLCG2* mutations** were **rare** overall: 6 relapsed cases with ***BTK*<sup>C481S/R</sup>** mutations and only 1 with isolated ***PLCG2*** mutations
- These results indicate the **outgrowth of several resistant clones** during ibrutinib treatment
- It remains to **be established** the **mechanisms** leading to **resistance** in cases **without *BTK/PLCG2* mutations** (ddPCR, WES, RNA-seq)

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