

## **ASPEN Biomarker Analysis: Response to Bruton Tyrosine Kinase Inhibitor (BTKi) Treatment in Patients with Waldenström Macroglobulinemia (WM) Harboring *CXCR4*, *TP53*, and *TERT* Mutations**

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**Background:** *MYD88*, *CXCR4*, and *ARID1A* are the most frequently mutated genes in WM (*Blood* 2014;123[11]:1637-1646), and the mutational status of *MYD88* and *CXCR4* impacts BTKi ibrutinib efficacy in WM (*N Engl J Med* 2015;372(15):1430-1440; *Blood* 2020;136(18):2038-2050). ASPEN is a randomized, phase 3 study comparing zanubrutinib with ibrutinib in patients with *MYD88*<sup>MUT</sup> WM; patients with *MYD88*<sup>WT</sup> WM received zanubrutinib.

**Aims:** To evaluate low frequency genetic alterations in patients with WM and their association with efficacy of ibrutinib and zanubrutinib (separately and pooled) in different subpopulations.

**Methods:** 190 patients with *MYD88*<sup>MUT</sup> (98 zanubrutinib; 92 ibrutinib) and 20 patients with *MYD88*<sup>WT</sup> (all zanubrutinib) had evaluable NGS results. NGS was performed on pretreatment bone marrow aspirates

using a 152-gene panel with 0.25% sensitivity. Correlation between genetic alterations and treatment responses was analyzed by multivariate analyses.

**Results:** *CXCR4* (25.7%), *TP53* (24.8%), *ARID1A* (15.2%), and *TERT* (9.1%) were the most frequently mutated genes identified. *TP53*<sup>MUT</sup> rates were similar between patients with *MYD88*<sup>MUT</sup> and *MYD88*<sup>WT</sup>. *TERT*<sup>MUT</sup> was detected only in patients with *MYD88*<sup>MUT</sup> (10% [19/190] mutation rate). *ARID1A*<sup>MUT</sup> and *TERT*<sup>MUT</sup> were associated with a higher rate of *CXCR4*<sup>MUT</sup> and were more often detected in patients with *MYD88*<sup>MUT</sup>.

In the pooled analysis of patients with *MYD88*<sup>MUT</sup> WM, patients with *CXCR4*<sup>MUT</sup>, *TP53*<sup>MUT</sup>, and *TERT*<sup>MUT</sup> trended toward a lower very good partial response (VGPR) + complete response (CR) rate and a less favorable progression-free survival (PFS) than patients with the respective WT alleles (HR=1.32, 2.15, and 1.79, respectively) (Figure 1). The median time to response (VGPR+CR) also appeared longer in patients with mutant alleles.

As shown in Table 1, among *CXCR4*<sup>MUT</sup> subgroups, a lower major response rate (MRR) was observed in patients with *CXCR4* nonsense (*CXCR4*<sup>NS</sup>; 53.8%; *P* = 0.135) compared with *CXCR4* frameshift (*CXCR4*<sup>FS</sup>; 85.7%; *P* = 0.958) and *CXCR4*<sup>WT</sup> (84.7%) receiving ibrutinib, whereas comparable MRR was observed across all subpopulations receiving zanubrutinib (85.7%, 73.7%, and 83.1%, respectively). The median PFS (months) in patients receiving ibrutinib by *CXCR4*<sup>NS</sup>, *CXCR4*<sup>FS</sup>, and *CXCR4*<sup>WT</sup> mutational statuses was 39.8, 44.2, and not reached (NR), respectively, and NR in all subpopulations receiving zanubrutinib.

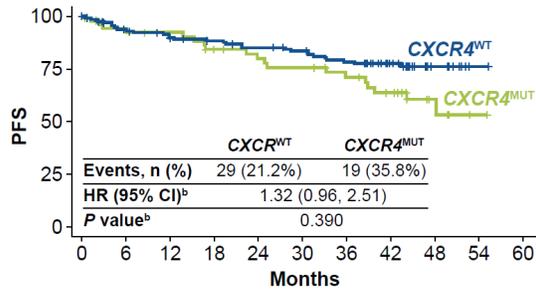
The VGPR+CR rate (13.6% vs 30.0%; *P*=0.202) and MRR (63.6% vs 85.7%; *P*=0.040) were lower in patients with *TP53*<sup>MUT</sup> than *TP53*<sup>WT</sup> with ibrutinib; VGPR+CR rate (34.6% vs 37.5%; *P*=0.636) and MRR (80.8% vs 81.9%; *P*=0.978) were similar between *TP53*<sup>MUT</sup> and *TP53*<sup>WT</sup> subgroups with zanubrutinib.

Among the 20 patients with *MYD88*<sup>WT</sup>, 4 had *TP53*<sup>MUT</sup>, with a lower MRR (50%), and none achieved VGPR or CR, compared with *TP53*<sup>WT</sup> (63% MRR and 25% VGPR+CR).

**Conclusion:** In addition to *CXCR4*<sup>MUT</sup> and *ARID1A*<sup>MUT</sup>, *TP53*<sup>MUT</sup> and *TERT*<sup>MUT</sup> were detected at a high rate in the ASPEN study. *CXCR4*<sup>MUT</sup>, *TP53*<sup>MUT</sup>, and *TERT*<sup>MUT</sup> were correlated with inferior response to BTKi therapy, and more patients with *CXCR4*<sup>MUT</sup> were present in the zanubrutinib arm. Consistent with more potent inhibition of BTK, zanubrutinib demonstrated deeper responses in patients with *CXCR4*<sup>MUT</sup> or *TP53*<sup>MUT</sup> WM compared with ibrutinib, with more favorable response regardless of the mutational status.

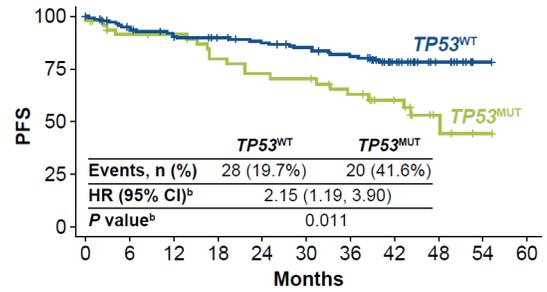
Figure 1. Progression-Free Survivals in patients with *MYD88*<sup>MUT</sup> WM by (A) *CXCR4* and (B) *TP53* Mutational Status

A. PFS by *CXCR4* Mutational Status<sup>a</sup>



<i>CXCR4</i> <sup>MUT</sup>	53	49	46	40	37	35	31	24	8	1	0
<i>CXCR4</i> <sup>WT</sup>	137	122	116	110	105	101	94	60	18	2	0

B. PFS by *TP53* Mutational Status<sup>a</sup>



<i>TP53</i> <sup>MUT</sup>	48	41	40	34	31	30	25	19	6	1	0
<i>TP53</i> <sup>WT</sup>	142	130	122	116	111	106	100	65	20	2	0

Data cutoff: October 31, 2021.

<sup>a</sup>Pooled analysis of patients with *MYD88*<sup>MUT</sup> WM from cohort 1 including 98 treated by zanubrutinib and 92 treated by ibrutinib.

<sup>b</sup>HR and P values were estimated using a Cox regression model with *CXCR4* (WT, FS, NS), *TP53* (WT, MUT), and *TERT* (WT, MUT) mutational statuses as covariates. WT is the reference group.

FS, frameshift; HR, hazard ratio; NS, nonsense; PFS, progression-free survival; WT, wild type.

**Table 1.** Response Assessment by *CXCR4* and *TP53* Mutational Statuses in Patients With *MYD88*<sup>MUT</sup> WM<sup>a</sup>

<i>Patients with MYD88</i> <sup>MUT</sup> <i>treated with ibrutinib</i>					
	<i>CXCR4</i> <sup>WT</sup> (n=72)	<i>CXCR4</i> <sup>FS</sup> (n=7)	<i>CXCR4</i> <sup>NS</sup> (n=13)	<i>TP53</i> <sup>WT</sup> (n=70)	<i>TP53</i> <sup>MUT</sup> (n=22)
<b>VGPR or better, n (%)<sup>b</sup></b>	22 (30.6)	0	2 (15.4)	21 (30.0)	3 (13.6)
OR (95% CI)	-	0.14 (0.00,3.23)	0.64 (0.13,3.08)	-	0.44 (0.12,1.55)
<i>P</i> value	-	0.223	0.579	-	0.202
<b>Major response, n (%)<sup>b</sup></b>	61 (84.7)	6 (85.7)	7 (53.8)	60 (85.7)	14 (63.6)
OR (95% CI)	-	1.06 (0.10, 10.36)	0.33 (0.07,1.41)	-	0.29 (0.09,0.95)
<i>P</i> value	-	0.958	0.135	-	<b>0.040</b>
<b>Time to VGPR or better</b>	11.3	-	31.3	11.4	24.9
Median (min, max), months	(2.0, 49.9)	-	(16.6, 46.0)	(2.0, 49.9)	(5.6, 46.9)
<b>Time to major response</b>	2.8	7.0	2.9	2.9	3.0
Median (min, max), months	(0.9, 49.8)	(2.8, 41.5)	(1.2, 13.6)	(0.9, 49.8)	(1.0, 13.8)
<b>PFS</b>					
Events, n (%)	18 (25.0%)	4 (57.1%)	7 (53.8%)	18 (25.7%)	11 (50.0%)
Median, months <sup>c</sup>	NE	44.2	39.8	NE	44.2
HR (95% CI) <sup>d</sup>	-	2.08 (0.70,6.16)	3.39 (1.23,9.31)	-	2.36 (1.10,5.09)
<i>P</i> value <sup>d</sup>	-	0.185	<b>0.017</b>	-	<b>0.027</b>
<i>Patients with MYD88</i> <sup>MUT</sup> <i>treated with zanubrutinib</i>					
	<i>CXCR4</i> <sup>WT</sup> (n=65)	<i>CXCR4</i> <sup>FS</sup> (n=19)	<i>CXCR4</i> <sup>NS</sup> (n=14)	<i>TP53</i> <sup>WT</sup> (n=72)	<i>TP53</i> <sup>MUT</sup> (n=26)
<b>VGPR or better, n (%)<sup>b</sup></b>	29 (44.6)	5 (26.3)	2 (14.3)	27 (37.5)	9 (34.6)
OR (95% CI)	-	0.51 (0.16,1.66)	0.24 (0.04,1.26)	-	1.27 (0.46,3.52)
<i>P</i> value	-	0.269	0.093	-	0.636
<b>Major response, n (%)<sup>b</sup></b>	54 (83.1)	14 (73.7)	12 (85.7)	59 (81.9)	21 (80.8)
OR (95% CI)	-	0.66 (0.18,2.36)	1.52 (0.25,9.01)	-	1.01 (0.29,3.47)
<i>P</i> value	-	0.524	0.639	-	0.978
<b>Time to VGPR or better</b>	6.5	11.1	10.3	6.5	11.1
Median (min, max), months	(1.9, 42.0)	(2.8, 26.0)	(9.4, 11.1)	(1.9, 42.0)	(3.0, 26.0)
<b>Time to major response</b>	2.8	2.9	4.1	2.8	2.8
Median (min, max), months	(0.9, 28.5)	(1.8, 49.8)	(1.0, 38.7)	(0.9, 49.8)	(1.0, 5.6)
<b>PFS</b>					
Events, n (%)	11 (16.9%)	4 (21.0%)	4 (28.5%)	10 (13.8%)	9 (34.6%)
Median, months <sup>c</sup>	NE	NE	NE	NE	NE
HR (95% CI) <sup>d</sup>	-	0.62 (0.17, 2.25)	0.67 (0.15,2.88)	-	2.20 (0.81, 5.98)
<i>P</i> value <sup>d</sup>	-	0.473	0.598	-	0.120

Data cutoff: October 31, 2021.

<sup>a</sup>Mutation determined by NGS; NGS results were available for 92 patients in the ibrutinib arm and 98 patients in the zanubrutinib arm.

<sup>b</sup>OR and *P* values were estimated using a logistic regression model with *CXCR4* (WT, FS, NS), *TP53* (WT, MUT), and *TERT* (WT, MUT) mutational statuses as covariates. WT is the reference group.

<sup>c</sup>Median PFS was estimated by Kaplan-Meier method.

<sup>d</sup>HR and *P* values were estimated using a Cox regression model with *CXCR4* (WT, FS, NS), *TP53* (WT, MUT), and *TERT* (WT, MUT) mutational statuses as covariates. WT is the reference group.

FS, frameshift; HR, hazard ratio; NE, not estimable; NGS, next-generation sequencing; NS, nonsense; OR, odds ratio; PFS, progression-free survival; VGPR, very good partial response; WM, Waldenström macroglobulinemia; WT, wild type.

**Bold red text** highlights *P* value <0.05.