LETTER TO THE EDITOR

Insights into clonal and complete blood count changes at disease evolution among patients with clonal cytopenia of undetermined significance

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Table s1: Differences in CBC and karyotype between diagnosis and follow-up BMB (section 1); and NGS and scores between diagnosis and follow-up for patients with follow-up NGS (section 2)

Section 1				
	Overall (n= 109)	Did not progress (N=46)	progress (N=63)	p value
Delta cytogenetics				0.42
Normal to abnormal	4 (3.7%)	0 (0.0%)	4 (6.4%)	
Remained normal	74 (69.2%)	33 (71.7%)	41 (66.1)	
Abnormal to normal	4 (3.7%)	3 (6.5%)	1 (1.6%)	
Remained abnormal	25 (23.4%)	9 (19.6%)	16 (25.8%)	
Delta Hg				0.43
Decrease	66 (61.1%)	26 (56.5%)	40 (64.5%)	
Increase	42 (38.9%)	20 (43.5%)	22 (35.5%)	
Delta Plt				0.18
Decrease	80 (74.1%)	31 (67.4%)	49 (79%)	
Increase	28 (25.9%)	15 (32.6%)	13 (21%)	
Delta WBC				0.03*
Decrease	67 (62%)	23 (50.0%)	44 (71%)	
Increase	41 (38%)	23 (50.0%)	18 (29%)	

Section 2				
	Overall (N=74)	Did not progress(N=34)	Progress (N=40)	p value
Pathogenic mutations				0.622
Gain of new pathogenic mutations, n (%)	22 (31.4%)	9 (28.1%)	13 (34.2%)	
Gain and loss of pathogenic mutations, n (%)	1 (1.4%)	1 (3.1%)	0 (0.0%)	
Loss of pathogenic mutations, n (%)	7 (10.0%)	4 (12.5%)	3 (7.9%)	
Same, n (%)	40 (57.1%)	18 (56.2%)	22 (57.9%)	
VAF variation (5%)				0.002*
Expansion, n (%)	37 (53.6%)	10 (31.2%)	27 (73.0%)	
Reduction, n (%)	8 (11.6%)	4 (12.5%)	4 (10.8%)	
Same, n (%)	17 (24.6%)	14 (43.8%)	3 (8.1%)	
Expansion and reduction, n (%)	7 (10.1%)	4 (12.5%)	3 (8.1%)	
Expansion in clones (>5%), n (%)	37 (53.6%)	10 (31.2%)	27 (73.0%)	< 0.001*
VAF variation (10%)				0.154
Expansion, n (%)	13 (18.8%)	3 (9.4%)	10 (27.0%)	
Reduction, n (%)	5 (7.2%)	4 (12.5%)	1 (2.7%)	
Same, n (%)	49 (71.0%	24 (75.0%)	25 (67.6%)	
Expansion and reduction, n (%)	2 (2.9%)	1 (3.1%)	1 (2.7%)	
Expansion in clones (>10%), n (%)	13 (18.8%)	3 (9.4%)	10 (27.0%)	0.0344*

VUS				0.235
New, n (%)	11 (16.2%)	6 (18.8%)	5 (13.9%)	
Loss, n (%)	5 (7.4%)	4 (12.5%)	1 (2.8%)	
Same, n (%)	52 (76.5%)	22 (68.8%)	30 (83.3%)	
Delta CHRS class				0.926
Step up, n (%)	9 (16.1%)	4 (18.2%)	5 (14.7%)	
Step down, n (%)	3 (5.4%)	1 (4.5%)	2 (5.9%)	
Same, n (%)	44 (78.6%)	17 (77.3%)	27 (79.4%)	
Delta CCRS score				0.589
Step up, n (%)	16 (28.6%)	6 (27.3%)	10 (29.4%)	
Step down, n (%)	11 (19.6%)	3 (13.6%)	8 (23.5%)	
Same, n (%)	29 (51.8%)	13 (59.1%)	16 (47.1%)	
Delta CCRS class				0.478
Step up, n (%)	13 (19.1%)	6 (20.0%)	7 (18.4%)	
Step down, n (%)	6 (8.8%)	4 (13.3%)	2 (5.3%)	
Same, n (%)	49 (72.1%)	20 (66.7%)	29 (76.3%)	
Delta CCRS score				0.416
Step up, n (%)	19 (27.9%)	6 (20.0%)	13 (34.2%)	
Step down, n (%)	11 (16.2%)	5 (16.7%)	6 (15.8%)	

Same, n (%)	38 (55.9%)	19 (63.3%)	19 (50.0%)	
Delta IPSSM class				0.054
Step up, n (%)	32 (47.8%)	9 (31.0%)	23 (60.5%)	
Step down, n (%)	3 (4.5%)	2 (6.9%)	1 (2.6%)	
Same, n (%)	32 (47.8%)	18 (62.1%)	14 (36.8%)	
Delta IPSSM score				0.134
Step up, n (%)	50 (74.6%)	19 (65.5%)	31 (81.6%)	
Step down, n (%)	17 (25.4%)	10 (34.5%)	7 (18.4%)	
Delta IPSSR class				0.415
Step up, n (%)	26 (39.4%)	12 (41.4%)	14 (37.8%)	
Step down, n (%)	6 (9.1%)	4 (13.8%)	2 (5.4%)	
Same, n (%)	34 (51.5%)	13 (44.8%)	21 (56.8%)	
Delta IPSSR score				0.113
Step up, n (%)	38 (57.6%)	15 (51.7%)	23 (62.2%)	
Step down, n (%)	13 (19.7%)	9 (31.0%)	4 (10.8%)	
Same, n (%)	15 (22.7%)	5 (17.2%)	10 (27.0%)	

Table s2: abnormal karyotypes

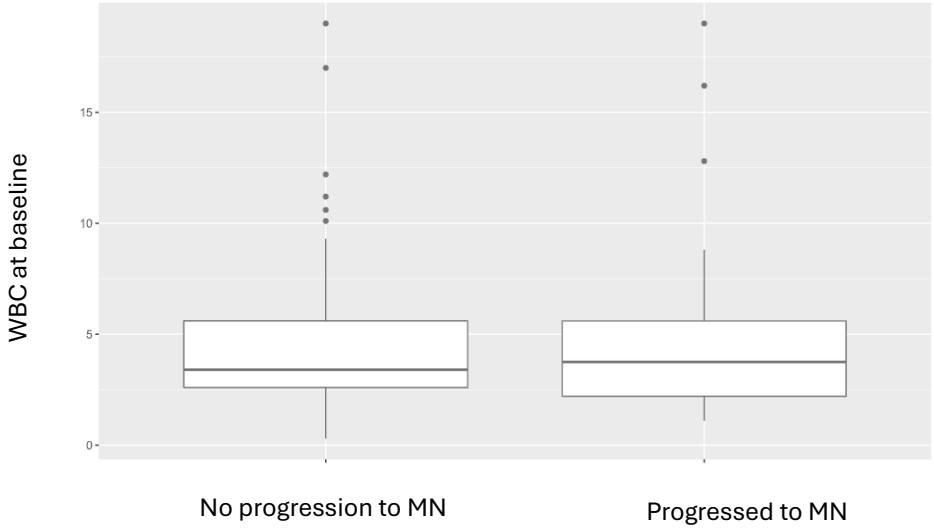
45,X,-Y,del(4)(q21q25)[20]/46,XY[1]
46,XY,del(20)(q11.2q13.3)[10]/56-65,sl,+1,+5,del(7)(q11.2q22),+9,+10,+11,+15,+22[cp2]/46,XY,del(7)(p11.2p15)[2]/46,XY[6]
47,XY,+8[11]/46,XY[9]
47,XX,+12,add(14)(q22)[8]/46,XX[2]
48,XX,+6,+8[4]/46,XX[16]
47,XY,+8[14]/46,XY[6]
46,XX,add(10)(q22)[4]/46,XX[16]
46,XX,del(20)(q11.2q13.3)[20]
46,X,t(X;12)(p11.4;p13.1)[20]
47,XX,+21[18]/46,XX[2
20q del
47,XY,+Y[6]/46,XY[14]
47,XY,+8[20]
47,XY,+8[20]
47,XX,+13[4]/46,XX[16]
46,XX,del(13)(q12q22)[5]/46,XX[15]
46,XY, der(6)t(1;6)(q21; p25)[17]/46,XY[3]
45,X,-Y[3]/46,XY[17]
47,XY,+8[7]/46,XY[13]
47,XX,+9[1]/46,XX[19]
47,XY,+8[16]/46,XY[4] Abnormal
47,XY,+8[15]/46,XY[5]
46,XX,add(9)(p13),del(20)(q11.2q13.3)[19]/46,XX[1]
46,XY,del(9)(q13q22)[20]
47,XY,+8[20]
46,XX,+1,der(1;21)(q10;q10)[20]
46,XX,del(5)(q13q33),t(10;13)(p10;q10)[3]/46,XX[17]
46,XY,del(20)(q11.2q13.1)[5]/46,XY[15]

46,XX,del(20)(q11.2q13.3)[20]
46,XY,del(20)(q11.2q13.1)[20]
46,XY,del(20)(q11.2q13.1)[20]
46,XY,del(20)(q11.2q13.3)[11]/45,X,-Y[4]/46,XY[5]
46,XY,t(1;3)(p36;q21)[3]/46,XY[17]
45,XY,del(5)(q13q33),psu dic(17;20)(p11.2;q11.2)[10]/46,XY[10]
46,XY,del(20)(q11.2q13.3)[12]/46,XY[8]
46,XY,del(20)(q11.2q13.3)[1]/46,XY[19]
47,XY,+8[14]/46,XY[6]
45,X,-Y[20]
45,X,-Y[20]
46,XY,del(20)(q11.2q13.3)[4]/46,XY[16].
46,XY,del(9)(q12q34)[11]/46,XY[9].
46,XX,del(20)(q11.2q13.3)[7]/46,XX[13] 46,XX,del(20)(q11.2q13.3)[7]/46,XX[13]
48,XX,+8,+9[2]/46,XX[18]
46,XX,del(20)(q11.2q13.3)[20]
47,XX,+6[3]/46,XX[17].
47,XXYc[20]
46,XY,del(20)(q11.2q13.3)[17]/46,XY[3]
45,X,-Y[20]
45,X,-Y[20]
46,XX,del(20)(q11.2q13.1)[1]/46,XX[19]
46,XY,del(20)(q11.2q13.1)[18]/46,XY[2]
45,X,-X[17]/46,XX[3]
45,X,-Y[11]/46,XY[9]
46,XY[17] with non-clonal chromosomal rearrangements and breakage
45,X,-Y[7]/46,XY[13]
45,X,-Y[13]/46,XY[7]
45,X,-X[18]/46,XX[2]
46,XX,add(8)(p11.2),add(17)(q11.2)[16]/46,XX[4]
47,XX,inv(3)(p11q29),+r?c[2]/47,XX,+r?c[18]

46,XY,del(13)(q12q22)[3]/46,XY[17]
47,XX,+8[16]/46,XX[4]
45,X,-Y[5]/46,XY[15]
47,XY,+8[20]
del 1q - del 20
46,XY,inv(2)(p11.2q13)?c[20]

Figure s1: Box plot for WBCs at time of CCUS diagnosis and at time of follow up (1st plot for baseline WBCs and 2nd plot for WBCs at follow up). We can see how the median WBC count was higher at baseline among patients who eventually progressed (3.7 vs 3, p=0.6), and at time of progression, the median WBC count was lower among patients who progressed compared to those who did not progress (2.7 vs 3.3, p=0.6)

1. At CCUS diagnosis:



2. At follow up:

