Expression levels of genes implicated in the working mechanism of lenalidomide predict treatment response in lower risk myelodysplastic syndrome patients

Authors

Florentien E.M. in't Hout,[1,2] Thessa N. Scheele,[1+] Theresia M. Westers,[3+] Canan Alhan,[3] Carolien Duetz,[3] Eline M.P. Cremers,[3] Heleen A. Visser-Wisselaar,[4] Annelies Verbrugge,[4] Dana A. Chitu,[4] Bert A. van der Reijden,[1] Aniek O. de Graaf,[1] Arjan A. van de Loosdrecht[3+] and Joop H. Jansen;[1+] on behalf of the HOVON89 Study Group

[1]Department of Laboratory Medicine, Laboratory of Hematology, Radboud University Medical Centre, Nijmegen; [2]Department of Hematology, Radboud University Medical Centre, Nijmegen; [3]Department of Hematology, Cancer Center Amsterdam, Amsterdam UMC, Vrije Universiteit Amsterdam, Amsterdam and [4]HOVON Data Center, Department of Hematology, Erasmus MC Cancer Institute, Rotterdam, The Netherlands

[+]TNS, TMW, AAvdL and JHJ contributed equally.

Correspondence:
J.H. JANSEN - Joop.Jansen@Radboudumc.nl

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Supplementary data

Expression levels of genes implicated in lenalidomide's mode of action predict treatment response in lower risk myelodysplastic syndrome patients

Florentien E.M. in 't Hout[1,4], Thessa N. Scheele[1*], Theresia M. Westers[2*], Canan Alhan[2], Carolien Duetz[2], Eline M.P. Cremers[2], Heleen A. Visser-Wisselaar[3], Annelies Verbrugge[3], Dana A. Chitu[3], Bert A. van der Reijden[1], Aniek O. de Graaf[1], Arjan A. van de Loosdrecht[2*], Joop H. Jansen[1*], on behalf of the HOVON89 study group.

[1]*Department of Laboratory medicine, Laboratory of Hematology, Radboud University Medical Centre, Nijmegen, The Netherlands*

[2]*Department of Hematology, Cancer Center Amsterdam, Amsterdam UMC, Vrije Universiteit Amsterdam, The Netherlands*

[3]*HOVON Data Center, Department of Hematology, Erasmus MC Cancer Institute, Rotterdam*

[4]*Department of Hematology, Radboud University Medical Centre, Nijmegen, The Netherlands*

[*] *Equally contributed*

Supplementary Table 1 Clinical characteristics of patients who reached HI-E (responders) and patients who did not reach HI-E upon lenalidomide treatment (non-responders).
SD = standard deviation.
[a]indicates a patient with IPSS score 1.5: this patient was included in the study based on an initial diagnosis of RCMD with int-1 risk; renewed BM analysis > 3 months revealed additional chromosomal abnormalities which could be confirmed in the samples of BM at entry of the study. Patient continued in the study, but was upgraded to IPSS 1.5.

	Responders (n=57)	SD	non-responders (n = 84)	SD
Age (median)	71.2	9.8	71.8	8.3
Sex (male)	31 (54.4%)		50 (59.5%)	
IPSS score				
0	23 (40.3%)		36 (42.9%)	
0,5	24 (42.1%)		32 (38.1%)	
1	9 (15.8%)		16 (19.0%)	
1,5	1 (1.8%)[a]		0 (0.0%)	
Bone marrow blasts (%)	2.4	2.1	2.5	2.4
Hemoglobin (mean, g/dL)	8.64	1.1	8.52	1.0
White blood cell count (mean, × 10^9/L)	4.8	2.7	5.1	2.9
Absolute neutrophil count (mean, × 10^9/L)	2.8	2.2	3.5	3.4
Platelet count (mean, × 10^9/L)	239	130.5	221	157.5

Supplementary Table 2 Primer probe sets used to quantify mRNA expression (applied biosystems).

CSNK1A1	Hs00740463_m1
CRBN	Hs00372266_m1
	Hs00372271_m1
IKZF1	Hs00958474_m1
	Hs00172991_m1
IKZF3	Hs00232635_m1
	Hs00918017_m1
MDM2	Hs01066930_m1
	Hs01066938_m1
CAST	Hs00156280_m1
	Hs00987946_m1
CAPN1	Hs00559804_m1
	Hs01548333_g1

Supplementary Table 3 Spearman correlations of mRNA expression of two independent qPCR primer/probe mixes for multiple genes proposed in the lenalidomide pathway.

Gene	**Spearman r**
CRBN	0.74
IKZF1	0.70
IKZF3	0.93
CAST	0.81
MDM2	0.88
CAPN2	0.92

Supplementary Figure 1 mRNA expression in del(5q) and non-del(5q) MDS patients.