

Single nucleotide polymorphism in the *IL17A* gene is associated with interstitial lung disease positive to anti-Jo1 antisynthetase autoantibodies

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Supplementary information

Immunoblot test principle

In the immunoblot, antigens coated on membranes are used as a solid phase to detect specific antibodies in patient samples. The test performance is either manual, semi-, or fully automated. If a sample contains specific antibodies, these bind to the membrane-bound antigens. In the next step, an alkaline phosphatase (AP) labeled antibody (conjugate) is added, which binds to the specific antibodies. The alkaline phosphatase catalyzes a color reaction with the subsequently added nitro blue tetrazolium chloride/5-Bromo-4-Chloro-3-indolyl phosphate (NBT/BCIP). If specific antibodies are present in the patient sample, a dark line appears at the respective antigen position. The intensity of the resulting staining is proportional to the antibody concentration in the sample.

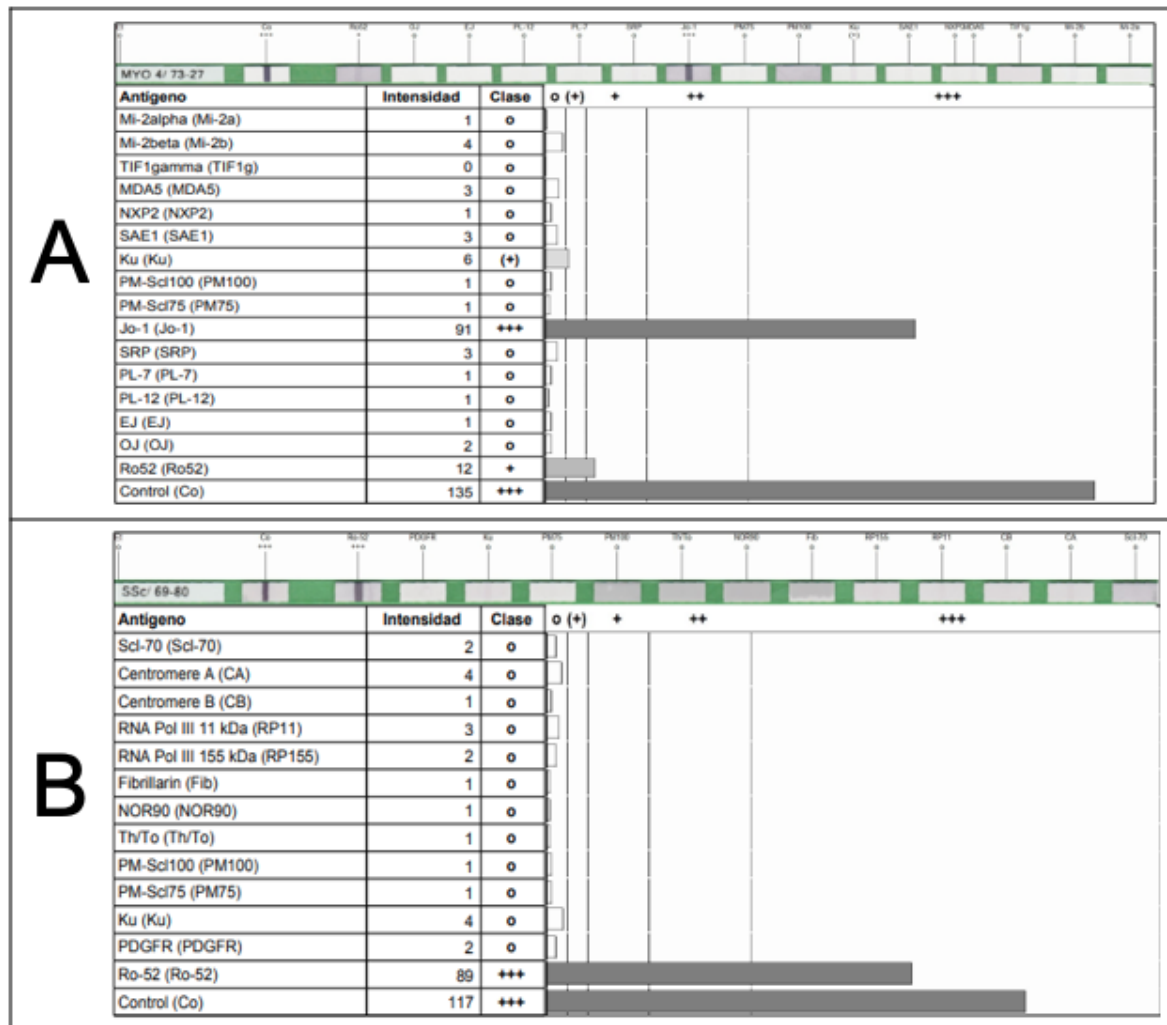


Figure S1. Two examples of the immunoblots. (A) Immunoblot showing the Jo1 positive autoantibody. (B) Immunoblot showing the Ro52 positive autoantibody.

Table S1. Allele and genotype frequencies of *IL17A* SNPs evaluated in anti-Ro52+ and anti-Ro52- ASSD patients.

Model	Anti-Ro52+		Anti-Ro52-		p-value
	n= 61	F (%)	n= 59	F (%)	
rs2275913					
Full-Genotypes					
GG	43	70.49	38	64.41	0.76
GA	16	26.23	18	30.51	0.60
AA	2	3.28	3	5.08	0.62
Alleles					
G	102	83.61	94	79.66	0.43
A	20	16.39	24	20.34	
rs8193036					
Full-Genotypes	n= 60	F (%)	n= 55		
TT	32	53.33	34	61.82	0.36
TC	26	43.33	16	29.09	0.11
CC	2	3.33	5	9.09	0.20
Alleles					
T	90	75	84	76.36	0.81
C	30	25	26	23.64	

The *p*-value <0.05 was considered as significative.

Table S2. Allele and genotype frequencies and genetic models of *IL17A* SNPs evaluated in anti-Ro52+ ASSD patients and HS.

Model	Anti-Ro52+		HS		p-value	OR	CI 95%
	n= 61	F (%)	n = 340	F (%)			
rs2275913							
Full-Genotypes							
GG	43	70.49	243	71.47	0.88	0.95	0.52-1.73
GA	16	26.23	92	27.06	0.89	0.96	0.52-1.78
AA	2	3.28	5	1.47	0.32	2.27	0.43-11.98
Alleles							
G	102	83.61	578	85.00	0.69	0.90	0.53-1.52
A	20	16.39	102	15.00		1.11	0.66-1.88
Dominant							
GG	43	70.49	243	71.47	0.88	0.95	0.52-1.73
GA+AA	18	29.51	97	28.53		1.05	0.58-1.91
Recessive							
GG+GA	59	96.72	335	98.53	0.32	0.44	0.08-2.32
AA	2	3.28	5	1.47		2.27	0.43-11.98
rs8193036							
Full-Genotypes	n= 60	F (%)	n = 343	F (%)			
TT	32	53.33	199	58.02	0.50	0.83	0.48-1.43
TC	26	43.33	125	36.44	0.31	1.33	0.76-2.33
CC	2	3.33	19	5.54	0.48	0.59	0.13-2.59
Alleles							
T	90	75	523	76.24	0.77	0.94	0.60-1.47
C	30	25	163	23.76		1.10	0.68-1.68
Dominant							
TT	32	53.33	199	58.02	0.50	0.83	0.48-1.43
TC+CC	28	46.67	144	41.98		1.21	0.70-2.10
Recessive							
TT+TC	58	96.67	324	94.46	0.48	1.70	0.39-7.50
CC	2	3.33	19	5.54		0.59	0.13-2.59

HS: Healthy subjects; P-value <0.05 was considered as significative.