

1 Short Communication

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Proteomic profiling of antigens in circulating immune complexes

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associated with each of seven autoimmune diseases

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6 Kaname Ohyama^{1,2}, Miyako Baba¹, Mami Tamai³, Nozomi Aibara¹, Kunihiro Ichinose³,

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Naoya Kishikawa¹, Atsushi Kawakami³ and Naotaka Kuroda^{1*}

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9 ¹Course of Pharmaceutical Sciences, Graduate School of Biomedical Sciences, Nagasaki University,

10 Nagasaki, Japan

11 ² Nagasaki University Research Centre for Genomic Instability and Carcinogenesis (NRGIC)

12 ³ Unit of Translational Medicine, Department of Immunology and Rheumatology, Graduate School of

13 Biomedical Sciences, Nagasaki University, Nagasaki, Japan

14

15 *Address correspondence to this author: Course of Pharmaceutical Sciences, Graduate School of

16 Biomedical Sciences, Nagasaki University, 1-14 Bunkyo-machi, Nagasaki 852-8521, Japan. Tel:

17 +81-95-819-2894; Fax: +81-95-819-2444; E-mail: n-kuro@nagasaki-u.ac.jp

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19 Keywords: autoimmune disease; immune complexome analysis; immune complex; tandem
20 mass spectrometry

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22 Nonstandard abbreviations: AAV, anti-neutrophil cytoplasmic antibody-associated vasculitis;
23 CICs, circulating immune complexes; DM, dermatomyositis; ICs, immune complexes;
24 MCTD, mixed connective tissue disease; nano-LC-MS/MS, nano-liquid
25 chromatography-tandem mass spectrometry; RA, rheumatoid arthritis; SLE, systemic lupus
26 erythematosus; SS, Sjögren's syndrome; SSc, systemic scleroderma; TA, Takayasu's arteritis

27

28 **Abstract**

29 **Objective:** Immune complexes (ICs) trigger humoral immune responses. Therefore, the
30 identification of constituent antigens within ICs would have very different clinical
31 significance than identification of free antigens.

32 **Design and Methods:** Here, we applied immune complexome analysis of serum to the study
33 of seven major autoimmune diseases—anti-neutrophil cytoplasmic antibody-associated
34 vasculitis, Takayasu’s arteritis, mixed connective tissue disease, dermatomyositis, Sjögren’s
35 syndrome, systemic scleroderma, and systemic lupus erythematosus— and healthy donors to
36 comprehensively identify antigens incorporated into circulating ICs and to find
37 disease-specific antigens.

38 **Results:** We identified 468 distinct IC- associated antigens using this method. Importantly,
39 62 of those antigens were disease-specific antigens, and there were at least three
40 disease-specific antigens for each of the seven autoimmune diseases. Of the disease-specific
41 antigens identified, coiled-coil domain-containing protein 158 and spectrin were identified as
42 potential autoantigens important to SSc and SS pathogenesis, respectively; notable titin and
43 spectrin autoantibodies are reportedly found in SSc and SS patients, respectively.

44 **Conclusion:** Immune complexome analysis may be generally applicable to the study of the
45 relationship between ICs and autoimmune diseases in animals and humans.

46

47 **Introduction**

48 For a long time, immune complexes (ICs) assembly was thought to represent a common
49 pathogenic pathway for several diseases (infections, vasculitis, and connective tissue
50 autoimmune disorders). Actually, concentrations of circulating ICs (CICs) in sera from
51 patients with rheumatoid arthritis (RA), systemic lupus erythematosus (SLE), or systemic
52 scleroderma (SSc) were significantly higher than those in sera from healthy controls [1, 2].
53 Many researchers have investigated the mechanisms by which ICs could underlie
54 pathogenicity [3]. An autoimmune response is directed against several autoantigens [4, 5];
55 therefore, comprehensive profiling of the autoantigens that actually assemble into ICs may
56 provide insight into the pathophysiology of specific autoimmune diseases, and such profiling
57 could form the basis for novel diagnosis and treatment strategies for these diseases.
58 However, such comprehensive profiling studies for CICs are limited because tools screening
59 of ICs are lacking.

60 We developed a proteomic strategy, designated immune complexome analysis, in which
61 ICs are separated from whole serum and then subjected to direct tryptic digestion and
62 nano-liquid chromatography-tandem mass spectrometry (nano-LC-MS/MS) to
63 comprehensively identify and profile constituent antigens in CICs [6]. We used this method
64 to identify CIC-associated antigens in sera from patients with RA, and found that
65 thrombospondin-1 is a constituent of CICs and is more highly specific and sensitive for
66 established and early RA than other conventional diagnostic markers such as rheumatoid

67 factor or anti-citrulline-containing protein/peptide antibody [6, 7].

68 In this report, we used immune complexome analysis of serum to study seven major
69 autoimmune diseases—anti-neutrophil cytoplasmic antibody-associated vasculitis (AAV),
70 Takayasu’s arteritis (TA), mixed connective tissue disease (MCTD), dermatomyositis (DM),
71 Sjögren’s syndrome (SS), SSc, and SLE—to comprehensively identify antigens incorporated
72 into CICs and find disease-specific antigens.

73

74 **Materials and methods**

75 Serum samples were collected from 66 patients; each patient had AAV (n=7; 35-86 years;
76 3 female; 4 patients are Microscopic polyantitis and 3 patients are Granulomatosis with
77 polyantitis), TA (n=7; 28-63 years; 7 female), MCTD (n=9; 43-77 years; 9 female), DM (n=8;
78 30-69 years; 6 female), SS (n=14; 35-78 years; 14 female), SSc (n=7; 55-78 years; 6 female),
79 or SLE (n=14; 16-67 years; 13 female) as diagnosed based on classification criteria from the
80 Ministry of Health, Labour and Welfare, Japan for AAV, MCTD, and DM; classification
81 criteria from the American College of Rheumatology for TA, SSc, and SLE; or the criteria for
82 SS proposed by the American-European Consensus Group. All sample collection and
83 diagnoses were performed at Nagasaki University Hospital and all the patients were newly
84 diagnosed. Also, healthy donors (n=11; 30-65 years; 2 female) are enrolled in this study.
85 Each serum sample was subjected to a single pretreatment process and replicate
86 nano-LC-MS/MS analyses. All experiments were performed in accordance with the
87 Helsinki Declaration and with approval from the institutional ethics committees of the

88 Graduate School of Biomedical Sciences, Nagasaki University. Each patient provided
89 written informed consent for their participation in this study.

90 CICs were purified by magnetic beads with immobilized Protein G or Protein A
91 (PureProteome[®], Millipore, Darmstadt, Germany). The tryptic digestion procedure and
92 nano-LC-MS/MS analysis were performed as previously [6].

93

94 **Results and discussion**

95 Here, we present the first comprehensive identification of the constituent antigens
96 assembled into CICs from patients with AAV, TA, MCTD, DM, SS, SSc, or SLE (Table S1).
97 We identified 341 and 264 human antigens via immune complexome analysis with Protein G
98 or Protein A beads, respectively; 468 distinct antigens were identified in all, and each of these
99 was found in independent samples from two or more patients (Table S2). Notably, only 29%
100 (137) of these 468 distinct antigens were recovered with both Protein G and Protein A beads;
101 204 antigens were recovered only when using Protein G beads, and 127 antigens were
102 recovered only when using Protein A beads. This indicates that the parallel use of Protein G
103 and Protein A beads recovered a wider range of antigens than the use of either bead type alone.
104 Furthermore, among 341 and 264 antigens identified with Protein G or Protein A, 127 and 92
105 antigens were also found in healthy donors, respectively; therefore, these antigens were
106 thought to form common CICs in human bodies (Table S2). It is interesting that much more
107 antigens identified with Protein G than Protein A and there is a little overlap between Protein
108 G and Protein A immune complexome. The association constant between IgG and Protein G

109 was reported to be 4-times higher than that between IgG and Protein A [8]. It is known that
110 IgG3 is captured on Protein G (but not Protein A) and IgM, IgA, IgD and IgE are captured on
111 Protein A (but not Protein G). High association constant and binding to IgG3 of Protein G
112 and distinct affinity of Protein A to IgM, IgA, IgD and IgE may contribute to more antigens
113 identified with Protein G than Protein A and a little overlap between Protein G and Protein A.

114 Of the 468 distinct antigens identified, 62 were detected in only one disease group and not
115 in any other disease groups by using Protein G or Protein A (Table 1). Also, these antigens
116 were not found in healthy donors. Although there is the possibility that a protein
117 nonspecifically binds to Protein G or Protein A beads, those disease-specific antigens are not
118 thought to directly bind to the beads because nonspecifically binding proteins should be found
119 in multiple diseases. Also, in this study, many disease-specific antigens are identified;
120 therefore, it is difficult to determine if each protein nonspecifically binds to the beads by
121 using a recombinant or natural protein as our previous study [6].

122 In this study, relatively many disease-specific antigens were found in SSc and SS.
123 Namely, 9 disease-specific antigens were associated with SSc even though only seven SSc
124 patients were enrolled in this study; moreover, SS was associated with 2-fold more
125 disease-specific antigens than was SLE, even though the number of patients with SS was
126 equal to that with SLE. Reportedly, concentrations of CICs are elevated in patients with SSc
127 or SS [9, 10]; thus, these elevated CIC concentrations may contribute to the large number of
128 distinct types of disease-specific antigens associated with each disease. Only 6
129 disease-specific antigens associated with AAV, TA, MCTD, or DM were detected with Protein

130 G beads; however, 19 of the disease-specific antigens associated with AAV, TA, MCTD, or
131 DM were detected with Protein A beads. This finding may indicate that there were more
132 CICs associated with IgA, IgD, IgE, or IgM than those associated with IgG. Conversely,
133 more of the disease-specific antigens associated with SS, SSc, or SLE were recovered only
134 with Protein G beads.

135 To our knowledge, most of the 62 disease-specific antigens have never been reported to be
136 associated with the respective autoimmune disease; however, some do have a recognized
137 association with the respective disease. Some of the autoantibodies previously reported to
138 be associated with SS are known to recognize proteins that contain one or more coiled-coil
139 domains. SS is known to produce autoantibodies that react with a 52-kDa protein
140 component of the SS-A antigen. The antigenic region of this 52 kDa protein is recognized
141 by all SS-A antibody-positive sera and contains a sequence motif reminiscent of a leucine
142 zipper that is predicted to form a coiled-coil region [11]. Similarly, we specifically detected
143 coiled-coil domain-containing protein 158 in SS sera. Spectrin was specifically detected
144 with Protein A beads in serum from patients with SS. Spectrin is a protein that was first
145 characterized in human erythrocytes; the nonerythrocyte spectrin is called fodrin [12].
146 Studies have suggested that 1) the α -subunit of fodrin is cleaved during apoptosis, 2) fodrin
147 plays a role in the development of SS, and 3) fodrin is a candidate autoantigen in primary SS
148 [13, 14]. Although some of our results were consistent with these previous reports, our
149 method did not detect the autoantigens targeted by well-known autoantibodies (e.g. SS-A,
150 SS-B, Jo-1, Scl-70 antibodies) that are associated with SS, DM, SSc, or some combination

151 thereof. Therefore, it is possible that these autoantibodies do not form ICs with their
152 corresponding autoantigens and immune complexome analysis may specifically identify those
153 antigens that actually assemble into ICs.

154 The sensitivity of each disease specific antigens was less than 33%. The sensitivity of
155 individual disease-specific antigens may be improved by developing ELISA methods that ea
156 ch detects a certain IC with high specificity [15]; if such ELISAs were developed, these
157 disease-specific antigens may become promising diagnostic or pathogenic biomarkers.

158

159 **Conflict of interest**

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161

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170 **References**

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Table 1 Summary of disease-specific antigens in CICs isolated from patients with AAV, TA, MCTD, DM, SS, SSc, or SLEProtein G

Accession	Description	AAV (n=7) Frequency/ peptides per hit	TA (n=7) Frequency/ peptides per hit	MCTD (n=9) Frequency/ peptides per hit	DM (n=8) Frequency/ peptides per hit	SS (n=14) Frequency/ peptides per hit	SSc (n=7) Frequency/ peptides per hit	SLE (n=14) Frequency/ peptides per hit
IPI00926948.1	Uncharacterized protein	3/1						
IPI00217511.1	Seven transmembrane helix receptor	2/1						
IPI00555948.1	Androgen-regulated short-chain dehydrogenase/reductase 1 variant (Fragment)			2/1				
IPI01012262.1	Uncharacterized protein			2/1				
IPI00910896.1	cDNA FLJ56556, highly similar to Alpha-1-syntrophin				2/1			
IPI00982295.1	Uncharacterized protein				2/1			
IPI00023711.2	Envoplakin					2/1		
IPI00103630.3	Isoform 2 of Protein phosphatase 1E					3/1		
IPI00249982.4	Isoform 1 of Death-inducer obliterator 1					2/1-9		
IPI00643437.1	Uncharacterized protein					3/1		
IPI00784980.1	Isoform 1 of Coiled-coil domain-containing protein 158					2/1-3		
IPI00796214.1	Isoform 2 of Mediator of RNA polymerase II transcription subunit 12-like protein					2/1		
IPI00796249.1	Uncharacterized protein					4/1		
IPI00796316.5	Uncharacterized protein					7/1-3		
IPI00829812.3	13 kDa protein					2/1		

IPI00844250.2	cDNA FLJ52101					2/1		
IPI00853581.1	Uncharacterized protein					3/1-2		
IPI00917789.1	Uncharacterized protein					2/2		
IPI00979799.1	Similar to VH-7 family (N54P3)D/J protein					2/2		
IPI00968154.1	Uncharacterized protein						2/1	
IPI00946590.1	26 kDa protein						2/1	
IPI00447173.1	Antigen MLAA-39						2/1	
IPI00973260.1	cDNA FLJ55558, highly similar to Regulating synaptic membrane exocytosis protein 1						2/1	
IPI01009738.1	Isoform 3 of Golgin subfamily A member 4						2/1	
IPI00436634.4	Isoform 3 of Nipped-B-like protein						2/1	
IPI00006900.1	Something about silencing protein 10						2/1	
IPI00304557.2	Short palate, lung and nasal epithelium carcinoma-associated protein 2							3/1
IPI00827548.3	cDNA FLJ44825 fis, clone BRACE3046609, highly similar to Homo sapiens inhibitor of Bruton agammaglobulinemia tyrosine kinase (IBTK), mRNA							2/1
IPI00868939.1	Similar to Sarcoma antigen NY-SAR-41							2/1
IPI00908840.1	Isoform 3 of AT-rich interactive domain-containing protein 5B							2/1
IPI00945093.1	Protein							2/1
IPI01011877.1	cDNA FLJ59435, highly similar to Homo sapiens outer dense fiber of sperm tails 2 (ODF2), transcript variant 2, mRNA							2/1

Protein A

Accession	Description	AAV (n=7) Frequency/ peptides per hit	TA (n=7) Frequency/ peptides per hit	MCTD (n=9) Frequency/ peptides per hit	DM (n=8) Frequency/ peptides per hit	SS (n=14) Frequency/ peptides per hit	SSc (n=7) Frequency/ peptides per hit	SLE (n=14) Frequency/ peptides per hit
IPI00552578.2	Serum amyloid A protein	2/1						
IPI00973428.1	Putative uncharacterized protein	2/3						
IPI01025129.1	12 kDa protein	2/1						
IPI00007138.2	Isoform 2 of Disks large-associated protein 4	2/1						
IPI00885166.2	polyadenylate-binding protein 4-like		2/1					
IPI00032931.2	Isoform 2 of Peroxisomal targeting signal 1 receptor		2/1					
IPI00965543.1	collagen alpha-1(XI) chain isoform C preproprotein		2/1					
IPI00827532.1	Anti-folate binding protein (Fragment)			3/1				
IPI00217511.1	Seven transmembrane helix receptor			2/1				
IPI00973424.1	Putative uncharacterized protein			2/3-4				
IPI00645207.2	Uncharacterized protein			2/1				
IPI00917650.2	Protein PIEZO1			2/1				
IPI00432678.1	MRSS6228			2/1				
IPI00977998.1	Uncharacterized protein			2/1				
IPI00007193.7	Isoform 2 of Ankyrin repeat domain-containing protein 26				2/1			
IPI00968154.1	Uncharacterized protein				2/1			
IPI00552943.3	V1-11 protein				2/1			
IPI00470871.6	Uncharacterized protein				2/1			
IPI00023466.2	Protein AF-17				2/1			

IPI00423464.1	Putative uncharacterized protein DKFZp686K03196					5/13-15		
IPI00896471.2	Isoform 2 of Protein SZT2					2/1		
IPI00973032.1	V1-17 protein					2/2		
IPI00022987.3	PRO0483					2/1		
IPI00736625.2	Uncharacterized protein C3orf43					2/1		
IPI00333015.7	Isoform 2 of Spectrin beta chain, brain 1					2/1		
IPI00922213.2	cDNA FLJ53292, highly similar to Homo sapiens fibronectin 1 (FN1), transcript variant 5, mRNA						2/1-9	
IPI00970895.1	Isoform 2 of PR domain-containing protein 11						2/1	
IPI01026317.1	cDNA FLJ55146, highly similar to Complement C4-B							2/1
IPI00165579.6	Isoform 2 of Cytosolic non-specific dipeptidase							2/1
IPI00924585.1	neurabin-1 isoform 5							2/1