SUPPLEMENTAL MATERIAL

Nordenfelt et al., http://www.jem.org/cgi/content/full/jem.20120325/DC1

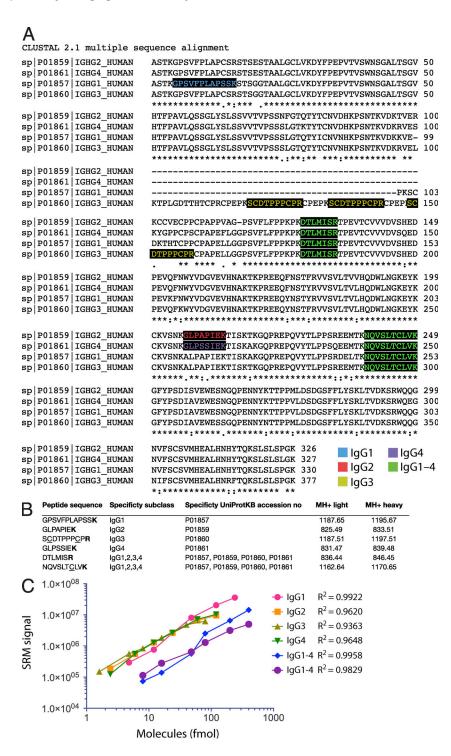


Figure S1. SRM analysis of IgG subclass distribution. (A) Sequence alignment comparing the different human IgG subclasses. Peptides that were selected for identification using SRM analysis are highlighted with the indicated colors. (B) Table of selected peptides for SRM analysis of IgG subclasses. Bold amino acids are isotopically labeled residues of heavy peptides. Cysteines (underlined) are carbamidomethylated. MH+ is the mass of precursor ions of either unlabeled (light) or labeled (heavy) peptides. (C) Signal to dose curve for the selected AQUA-IgG peptides with linear regression values listed in the legend. This information was used in all the SRM-IgG experiments to add the AQUA peptides at a concentration within their linear dynamic range.

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	plasma	saliva	plasma	saliva	plasma	saliva	plasma	saliva
	wt	wt	M-	M-	Н-	H-	M- H-	M- H-
	AVERAGE							
Membrane cofactor protein	2527	1001	2933	1522	4589	1265	2257	994
Complement decay-accelerating factor	724	2518	0	0	0	605	685	1492
CD59 glycoprotein	3359	5770	2817	2227	1797	3612	2715	4321
C4b-binding protein alpha chain	2236211	13551	3619122	976	22088	2178	31162	3826
C4b-binding protein beta chain	814793	3682	882229	722	6554	1951	8688	999
Complement factor H (H factor 1)	697000	97652	871810	26019	463907	24305	348603	20051
Complement factor H-related protein 1 (FHR-1)	15888	2800	7515	1381	40515	1597	34335	2517
Complement factor H-related protein 2 (FHR-2)	3637	2628	1048	1551	4470	2749	10573	0
Complement factor H-related protein 3 (FHR-3)	3787	533	7344	0	3797	0	4647	0
Complement factor H-related protein 4 (FHR-4)	5188	3066	27950	0	17255	0	14416	0
Complement factor H-related protein 5 (FHR-5)	19911	0	12336	0	40261	0	40464	1078
Complement factor I	2504	0	857	0	2148	756	2649	0
Complement C1q subunit A	0	0	0	0	0	0	0	0
Complement C1q subunit B	19716	0	147825	0	8005	4425	16183	618
Complement C1q subunit C	155887	1704	973750	0	101659	0	80529	473
Complement C1r	5018	0	7849	0	1900	0	4411	9
Complement C1s	113221	1114	111615	0	50120	531	41287	676
Mannose-binding protein C	0	1078	2775	1210	0	3005	0	547
Mannan-binding lectin serine protease 1	0	670	809	0	0	3039	0	0
Mannan-binding lectin serine protease 2	0	0	0	0	0	4870	0	0
Ficolin-1	0	1494	0	0	0	2175	0	562
Ficolin-3	0	0	0	0	0	1783	0	51
Complement factor B	25351	3010	16238	1122	100270	2268	91124	2140
Complement factor D	0	1871	0	1327	763	2043	327	1862
Complement C3	568117	2129	301189	991	761947	3543	869422	4696
Properdin	1102256	2213	661483	589	3448146	709	3519376	937
Complement C2	552	795	898	813	0	710	1928	3081
Complement C4-A	147533	4239	85388	0	91382	2300	81421	1492
Complement C5	113786	565	57475	0	352535	1277	300604	1473
Complement C6	58766	0	7998	0	68752	3917	77698	0
Complement C7	124592	0	12820	0	119500	0	127520	0
Complement C8 alpha chain	22771	0	2205	0	21274	0	23694	0
Complement C8 beta chain	75380	910	8377	0	81529	580	77723	0
Complement C8 gamma chain	28166	0	3205	0	17468	0	14944	0
Complement C9	719447	1498	116023	0	886405	1880	809255	1505
C3a anaphylatoxin chemotactic receptor	4945	886	1494	0	800	0	0	0
Integrin beta-2/LFA-1/CR-3	0	0	0	0	0	1464	0	0
Integrin alpha-M/CD11B	0	0	0	0	0	1410	0	0
Integrin alpha-X/CD11C	0	0	676	0	0	2180	0	779
C5a anaphylatoxin chemotactic receptor	0	0	0	0	0	1496	0	0
Complement receptor type 2/CD21	647	563	0	0	0	1870	0	0
Complement receptor type 1/CD35	0	1689	0	765	0	1585	0	0

Figure S2. Heat map over bacteria-bound complement system molecules from SRM adsorption experiments. Data are represented as mean values from eight independent adsorption experiments. The heat map was constructed by comparing values between plasma and saliva conditions for each row. All values <500 was considered to be difficult to separate from background noise and were set to 0. Sample peptides were prepared as described in the Materials and methods.

Table S1. IgG levels in saliva and plasma

	saliva (μg/ml)	Plasma (μg/ml)
lgG1	0.23 (0.05-0.72)	4,470 (1,810-8,030)
lgG2	0.16 (0.03-0.42)	3,130 (1,090-4,970)
lgG3	0.07 (0.02-0.23)	1,770 (380-3,880)
lgG4	0.01 (0.01-0.03)	280 (45-510)
total IgG	0.47 (0.13-1.39)	9.660 (3,790-14,310)

SRM determination of IgG levels in paired saliva and plasma samples from five individuals. Data are represented as mean values including the range of all measurements. Sample peptides were prepared as described in the Materials and methods

Supplemental text

Patient history. A 31-yr-old woman presented at the Department of Infectious Diseases, Skånes University Hospital, Lund, Sweden with a 36-h long history of high fever, chills, and profuse vomiting. She had seropositive rheumatoid arthritis and insulin-dependent diabetes mellitus and medicated with Prednisolone, Methotrexate, and Enbrel (TNF blocker). Her husband and two children had all suffered from milder upper respiratory tract infections in the preceding weeks, but the patient had had no such symptoms. The day before she fell ill she had been working in her garden, and afterward felt pain in her right thigh. At admission she was dehydrated, had a temperature of 39.5°C, pulse of 120 beats/minute, respiratory rate of 22 breaths per minute, and blood pressure of 120/70 mmHg. Routine physical examination was normal except for a tender, well-demarcated 7 × 5-cm erythema on the right ventral thigh. There were no surrounding wounds or hematoma. Strep A test was positive from a throat swab. Laboratory investigation revealed elevated levels of white blood cells (21 × 10°/L), C-reactive protein (CRP; 645 mg/liter), Prothrombin time (INR; 1.4), and Creatinine (157 μmol/liter). Liver function tests, aPTT (activated partial thromboplastin time), and platelet count were normal. After obtaining two aerobic and two anaerobic blood cultures (BacT/Alert; Biomérieux) as well as a throat and urinary culture, the patient received 2 g Cefotaxime (Pc-allergy) and 600 mg Clindamycin intravenously. 5 h later, a blood sample and a tissue scrap from the throat was taken for electron microscopy. The surgeons were contacted, the patient was operated on 12 h after admittance, and the operation showed necrotizing fasciitis in the right thigh. Blood and urine cultures turned out negative. *S. pyogenes* (Emm1) was isolated from the throat culture taken before antibiotics, and in perioperative wound fluid cultures from the necrotic tissue in the thigh collected after two doses of antibiotics. Samples for electron microscopy were also colle

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