Supplementary Methods

In the present study we observe seven haplotypes HYPA, LYPA, LYQA, LXPA, HYPD, LYPB and LYQC from the six SNPs H/L, X/Y, P/Q, A/D, A/B and A/C. We will refer to these six SNPs by their rare allele: H, X, Q, D, B and C, respectively. The latter three are positioned in *MBL2* exon 1 and never occurs in the same chromosome, i.e. these can be seen as one 4-allelic marker and explains why the haplotypes can be represented by 4 alleles. Formally these would be HYPAAA, LYPAAA, LYQAAA, LXPAAA, HYPDAA, LYPABA and LYQAAC. We will code genotypes and multilocus genotypes by the number of rare alleles, i.e. 0 (C/C), 1 (C/R) and 2 (R/R) where C and R denotes the common and rare allele, respectively. Obviously, each individual carry exactly two of these haplotypes: 0, 1 or 2 of each. Thus, with the 0/1/2 coding the sum of the seven possible haplotypes will be two for each individual. Clearly, the following set of seven equations is therefore true:

$$
\begin{aligned}
H &= HYPA + HYPD = 2 - (LYPA + LYQA + LXPA + LYPB + LYQC) = 2 - L \\
X &= LXPA \\
Q &= LYQA + LYQC \\
D &= HYPD \\
B &= LYPB \\
C &= LYQC \\
2 &= HYPA + LYPA + LYQA + LXPA + HYPD + LYPB + LYQC
\end{aligned}
$$

A direct calculation now gives that the model for multiple SNPs with a trend parameter for each of the six single markers, $\text{logit}(p) = \alpha_0 + \alpha_1 H + \alpha_2 X + \alpha_3 Q + \alpha_4 D + \alpha_5 B + \alpha_6 C$, can be re-parameterised to the model containing a trend parameter for each of the seven haplotypes, $\text{logit}(p) = \beta_0 + \beta_1 LYPA + \beta_2 LYQA + \beta_3 LXPA + \beta_4 HYPD + \beta_5 LYPB + \beta_6 LYQC$, with $\beta_0 = \alpha_0 + 2\alpha_1$, $\beta_1 = -\alpha_1$, $\beta_2 = \alpha_3 - \alpha_1$, $\beta_3 = \alpha_2 - \alpha_1$, $\beta_4 = \alpha_4$, $\beta_5 = \alpha_5 - \alpha_1$, and $\beta_6 = \alpha_6 + \alpha_3 - \alpha_1$.

https://doi.org/10.1111/j.1601-5215.2012.00607.x Published online by Cambridge University Press

Supplementary Tables

Supplementary table legends

Supplementary Table 1. Estimated median MBL concentration in serum.

Median MBL concentration in serum (ng/ml) estimated from Tobit regressions (on log-transformed data) with patients and controls specific means and an additive effect of haplotypes (Table 3 model 4). The 95% confidence intervals in the parentheses were estimated by use of the normal approximation on results from ordinary bootstrapping with 10000 replicates (Davison, A.C., Hinkley, D.V., Canty, A.J., Bootstrap methods and their application, Cambridge University Press, Cambridge, 1997). Results from using only the two markers X/Y and A/O (Table 3 model 3) are given before the corresponding four-marker multilocus genotype groups (e.g. YA/YA corresponds to YA=2, XA=YO=0). The results in the first row (Any) are from the model with only patient/control status as a factor (Table 3 model 1).

Supplementary Table 2. Estimated median MASP-2 concentration in serum.

Median MASP-2 concentration in serum (ng/ml) estimated from regressions analysis (on log-transformed data) with patients, controls and *MASP2* genotype specific means (interaction effect) and a linear effect of the O variant (A/O) in *MBL2* exon 1 (Table 4 model 4). The 95% confidence intervals (in the parentheses) were estimated by use of the normal approximation on results from ordinary bootstrapping with 10000 replicates. Results obtained from Table 4 model 3 (patient/control; *MASP2* genotype and the interaction effect) are given before the corresponding combination with *MBL2* genotype (*MASP2* A/A and *MASP2* A/G rows)). The results in the first row (Any) are from Table 4 model 1 which only includes the patient/control factor (i.e. any genotype combination).

https://doi.org/10.1111/j.1601-5215.2012.00607.x Published online by Cambridge University Press

Supplementary Table 1. Estimated median MBL concentration in serum.

***MBL2* genotype**	**Controls (N = 349)**	**Patients (N = 98)**
Any	584 (443 - 717)	578 (296 - 831)
YA/YA	4210 (3649 - 4754)	6357 (4907 - 7729)
HYPA/HYPA	4092 (3438 - 4733)	6698 (5017 - 8277)
HYPA/LYPA	2920 (1819 - 3923)	4780 (2897 - 6474)
HYPA/LYQA	4412 (3863 - 4961)	7221 (5514 - 8836)
LYPA/LYPA	2084 (413 - 3485)	3411 (723 - 5658)
LYQA/LYPA	3148 (1965 - 4229)	5153 (3103 - 7000)
LYQA/LYQA	4757 (3553 - 5731)	7785 (5437 - 9979)
YA/XA	1126 (990 - 1261)	1701 (1370 - 2019)
HYPA/LXPA	1116 (974 - 1253)	1826 (1449 - 2179)
LYPA/LXPA	796 (493 - 1069)	1303 (805 - 1749)
LYQA/LXPA	1203 (1 030 - 1370)	1969 (1523 - 2386)
XA/XA	301 (221 - 378)	455 (322 - 580)
LXPA/LXPA	304 (228 - 375)	498 (357 - 627)
YA/YO	188 (156 - 219)	285 (221 - 344)
HYPA/LYPB	138 (109 - 165)	226 (169 - 279)
LYPA/LYPB	99 (56 - 136)	161 (93 - 222)
LYQA/LYPB	149 (117 - 179)	244 (180 - 303)
HYPA/LYQC	136 (31 - 226)	223 (43 - 375)
LYQA/LYQC	147 (35 - 243)	240 (47 - 405)
HYPA/HYPD	385 (259 - 498)	630 (380 - 851)
LYPA /HYPD	275 (139 - 393)	449 (216 - 650)
LYQA /HYPD	415 (278 - 538)	679 (405 - 922)
XA/YO	50 (38 - 62)	76 (56 - 95)
LXPA/HYPD	105 (68 - 138)	172 (102 - 233)
LXPA/LYPB	38 (28 - 47)	62 (44 - 78)
LXPA/LYQC	37 (7 - 63)	61 (10 - 104)
YO/YO	8 (5 - 11)	13 (8 - 17)
HYPD/HYPD	36 (10 - 58)	59 (13 - 97)
HYPD/LYPB	13 (8 - 18)	21 (12 - 29)
HYPD/LYQC	13 (2 - 22)	21 (2 - 37)
LYPB/LYPB	5 (3 - 6)	8 (4 - 10)
LYPB/LYQC	5 (1 - 8)	8 (1 - 13)

https://doi.org/10.1111/j.1601-5215.2012.00607.x Published online by Cambridge University Press

Supplementary Table 2. Estimated median MASP-2 concentration in serum.

***MBL2* genotype**	**Controls (N = 349)**	**Patients (N = 98)**
Any	412 (395 - 428)	442 (394 - 488)
***MASP2* A/A**	431 (415 - 448)	487 (438 - 533)
A/A	409 (390 - 428)	457 (409 - 503)
A/O	459 (437 - 480)	513 (461 - 563)
O/O	515 (466 - 563)	576 (502 - 648)
***MASP2* A/G**	260 (223 - 295)	206 (146 - 261)
A/A	247 (214 - 279)	194 (139 - 245)
A/O	278 (239 - 315)	217 (157 - 274)
O/O	312 (259 - 362)	244 (173 - 309)

https://doi.org/10.1111/j.1601-5215.2012.00607.x Published online by Cambridge University Press