

PLEKHA1

LOC387715

HTRA1

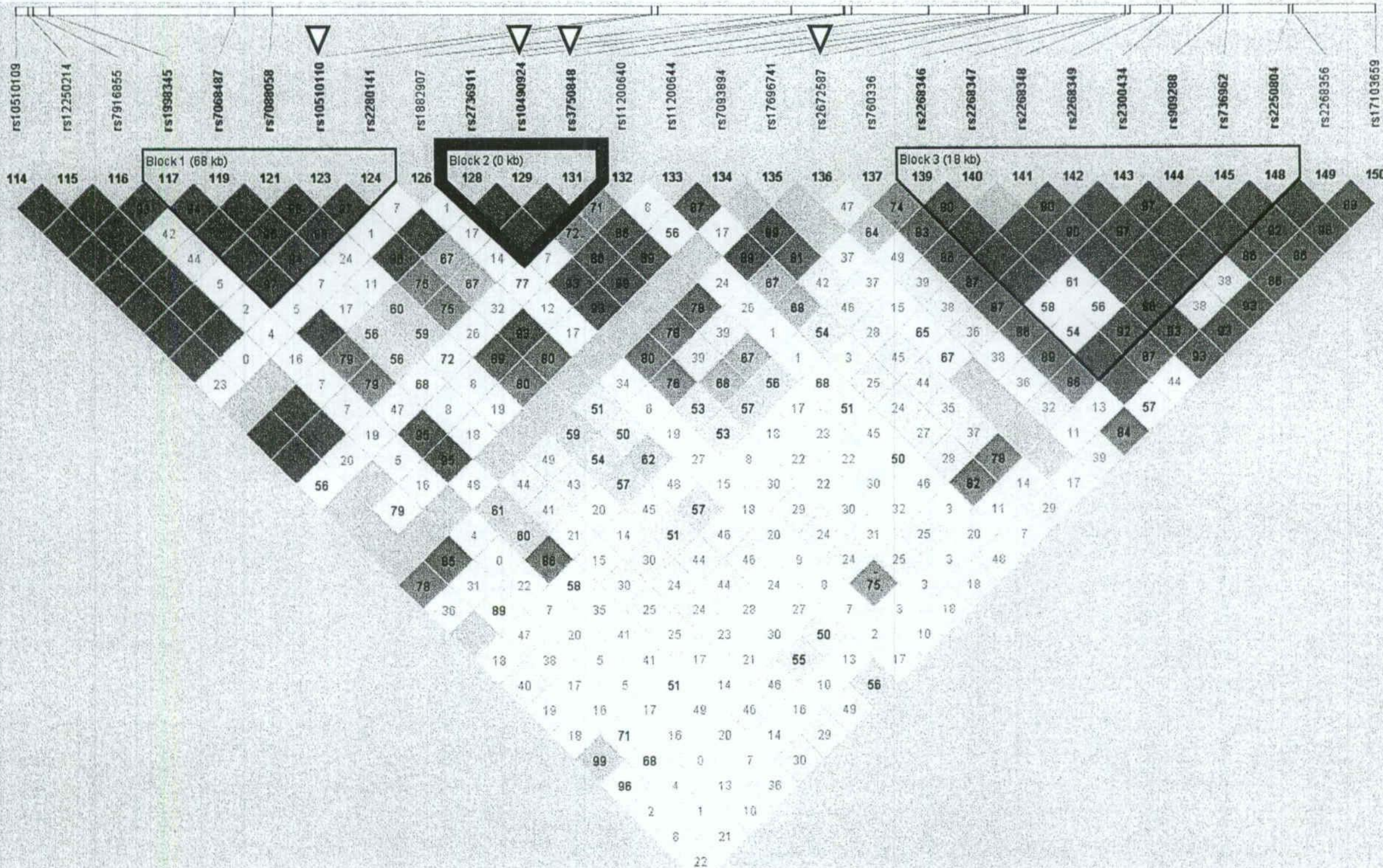


Table 1. Characteristics of AMD cases and control subjects in this study

Characteristic (AMD)					
Sex -no. (%)					
Male	73 (73.00)				
Female	27 (27.00)				
Mean age at recruitment- yr (SE)					
Total	74.56 (0.88)				
Male	73.64 (0.99)				
Female	77.04 (1.83)				
Age distribution - no. (%)					
	50s	60s	70s	80s	90s
Total	7 (7.00)	24 (24.00)	34 (34.00)	34 (34.00)	1 (1.00)
Male	6 (8.22)	17 (23.29)	29 (39.72)	20 (27.40)	1 (1.37)
Female	1 (3.70)	7 (25.93)	5 (18.52)	14 (51.85)	0 (0.00)

Characteristic (Control)

Sex - no. (%)

Male 91 (45.5)

Female 109 (54.5)

Mean age at recruitment - yr (SE)

Total 71.00 (0.75)

Male 71.00 (1.09)

Female 71.00 (1.03)

Age distribution - no. (%)

	30s	40s	50s	60s	70s	80s
Total	3 (1.5))	4 (2.00))	18 (9.00)	43 (21.50)	96 (48.00)	36 (18.00)
Male	0 (0.00)	2 (2.20)	9 (9.89)	19 (20.88)	45 (49.45)	16 (17.58)
Female	3 (2.75)	2 (1.83)	9 (8.26)	24 (22.02)	51 (46.79)	20 (18.35)

Table 2. Summary of ten SNPs analyzed in this study

SNP	Nearest gene	Location		P value
				OR (95%CI)
rs10490924	LOC387715	10q26	Allele	9.70×10^{-15}
				4.00 (2.79-5.74)
			Genotype	2.41×10^{-13}
			Heterozygote	6.11×10^{-6}
				3.61 (2.02-6.46)
			Homozygote	1.19×10^{-13}
				8.29 (4.62-14.89)
rs3750848	LOC387715	10q26	Allele	1.65×10^{-14}
				3.97 (2.77-5.69)
			Genotype	3.39×10^{-13}

			Heterozygote	1.38 x 10 ⁻¹³
				3.57 (1.99-6.39)
			Homozygote	6.48 x 10 ⁻⁶
				8.24 (4.59-14.80)
rs2672587	HTRA1	10q26	Allele	1.67 x 10 ⁻¹⁰
				3.14 (2.20-4.48)
			Genotype	8.02 x 10 ⁻⁹
			Heterozygote	1.08 x 10 ⁻⁵
				3.73 (2.01-6.92)
			Homozygote	2.91 x 10 ⁻⁸
				4.63 (2.68-7.98)
rs2874794	SH3BGRL2	6q14	Allele	5.56 x 10 ⁻⁶
				2.23 (1.58-3.17)
			Genotype	6.46 x 10 ⁻⁶

			Heterozygote	3.05 x 10 ⁻⁶
				2.21 (1.22-3.99)
			Homozygote	0.0087
				3.93 (2.22-6.96)
rs12462443	ZNF507	19q13	Allele	0.00016
				1.96 (1.39-2.76)
			Genotype	1.53 x 10 ⁻⁵
			Heterozygote	3.70 x 10 ⁻⁶
				3.94 (2.12-7.30)
			Homozygote	0.15
				1.60 (0.87-2.95)
rs2714212	LRP1B	2q22	Allele	0.0084
				1.87 (1.17-2.99)
			Genotype	4.04 x 10 ⁻⁶

			Heterozygote	1.68 x 10 ⁻⁴
				0.32 (0.088-1.16)
			Homozygote	0.089
				2.88 (1.65-5.05)
rs9599819	DACH1	13q21	Allele	0.61
				1.11 (0.75-1.65)
			Genotype	5.08 x 10 ⁻⁶
			Heterozygote	5.77 x 10 ⁻⁴
				1.73 (1.06-2.81)
			Homozygote	0.034
rs3763022	SH2TC2	5q33	Allele	2.18 x 10 ⁻⁶
				6.44 (2.53-16.36)
			Genotype	1.78 x 10 ⁻⁵
			Heterozygote	0.17

			Homozygote	5.59 x 10 ⁻⁶
				6.62 (2.54-17.22)
rs12595534	TRPM1	15q13	Allele	4.26 x 10 ⁻⁵
				2.13 (1.48-3.08)
			Genotype	1.10 x 10 ⁻⁵
			Heterozygote	0.011
				8.91 (2.69-29.52)
			Homozygote	5.98 x 10 ⁻⁶
				1.94 (1.19-3.16)
rs10510110	PLEKHA1	10q26	Allele	4.93 x 10 ⁻⁶
				2.35 (1.62-3.43)
			Genotype	2.07 x 10 ⁻⁵
			Heterozygote	9.50 x 10 ⁻⁶
				2.92 (1.25-6.81)

Homozygote	0.014
	3.09 (1.88-5.09)

Genome positions refer to the human March 2008 (build 36.3) assembly. *P* values were calculated for three models (allele, genotype, heterozygote and homozygote) using Fisher's exact test. OR, odds ratio; CI, confidence interval. ORs and CIs were calculated using Woolf's method.

難治性疾患克服研究事業

黄斑変性カニクイザルを用いた補体活性抑制剤による加齢黄斑変性の
予防・治療法の確立と情報収集システムの開発
(H18 - 難治 - 一般 - 001)

平成 18-20 年度 総合研究報告書

主任研究員 岩田 岳

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