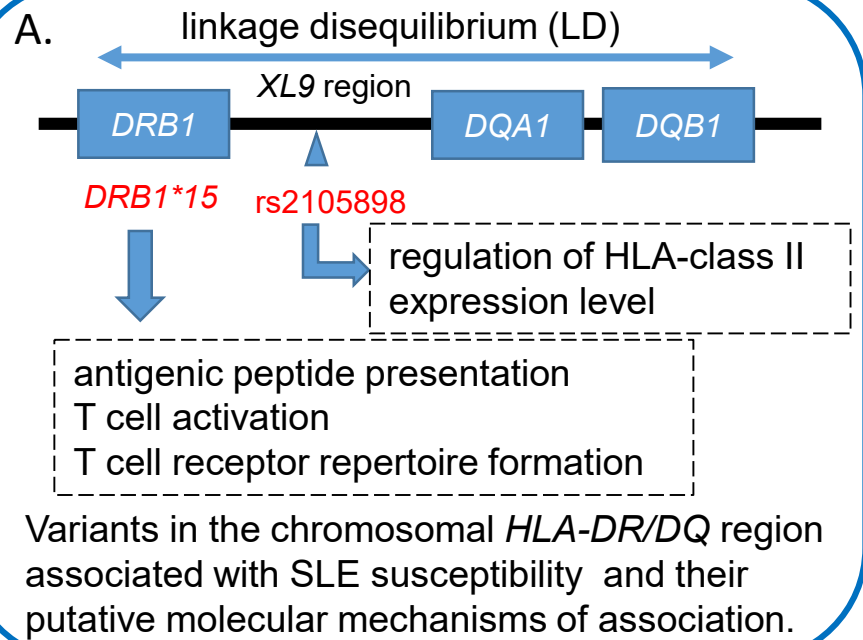


From Molecular and Genetic Epidemiology Laboratory

Genetic dissection of *HLA-DRB1*15:01* and XL9 region variants in Japanese patients with systemic lupus erythematosus (SLE): primary role for *HLA-DRB1*15:01*.



B.

haplotype		SLE susceptibility	population	LD
<i>HLA-DRB1</i>	rs2105898 (XL9)			
*15:01	T	risk	European	strong
*15:03	T	risk	African	strong
*15:01	T	risk	Japanese	moderate
*15:02	T	non-risk		

Due to strong LD between *HLA-DRB1*15* and XL9 region variants, it was impossible to dissect genetic contributions from both variants in the European or African populations, which was not the case in the Japanese population.

C.

	P unconditional	P conditional on <i>DRB1*15:01</i>	P conditional on rs2105898
<i>DRB1*15:01</i>	5.1×10^{-8}	-	7.6×10^{-6}
rs2105898	0.0017	0.83	-

Conditional logistic regression analysis supported a primary role of *DRB1*15:01* in the Japanese population.

Reference: Aya Kawasaki et al., *RMD Open* 2023;9:e003214.

Contact: Aya Kawasaki, Naoyuki Tsuchiya

SUMMARY

Leveraging the differences in the genetic background among populations, we demonstrated that *DRB1*15:01*, rather than XL9 region variants, is primarily associated with SLE in the Japanese population.