

Background

Ménière's disease (MD) is an inner ear characterized disorder by dysfunctional endolymph resorption endolymph that in results accumulation and a classical triad of unilateral vertigo, peripheral hearing loss and sensorineural unilateral tinnitus. Multiple etiologies have been proposed including an resorption endolymph predisposition, vascular viral infections, and an allergies, autoimmune component.

Human Leukocyte Antigen (HLA) are variable genes that encode numerous Major Histocompatibility Complex (MHC). MHC's function as antigen presenting proteins which have roles in nearly all human cell lines in regard to immunity and detection of Autoimmune malignancies. pathologies have been associated with quantifiable levels of specific HLA alleles

Purpose

- The goal of this systematic review is to further elucidate the association between MD and HLA alleles in characterizing the autoimmune component by analyzing literature on the linkage of the HLA-A, HLA-B, HLA-C, and HLA-DR serotypes to MD.
- Calculate odds ratio and forest plot of these allele's association with MD.

Data Analysis

- Systematic literature review with exclusion of articles that included small sample sizes, and subjects considered deceased, animal, or cell subjects/samples.
- **PRISMA guidelines for a was** utilized

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HLA and Ménière's disease Susceptibility: A Meta-analysis of Worldwide Studies

Methods

Study Design

In this systematic review, multiple HLA-A, HLA-B, HLA-C, and HLA-DR serotypes and the odds of developing MD were explored.

- PubMed, Google Scholar, ScienceDirect, and Cochrane Library were consulted, and articles were included if living subjects were used, odds ratio was available or could be ascertained from the study, and if it was not a metaanalysis of other researcher's works.
- MetaXL software was used to generate data for analysis and a forest plot was generated for each.
- Eleven studies conducted between 1998 and 2018 met study selection criteria for the combined MD metaanalysis (790 patient alleles and 3,229 control alleles). ¹⁻¹¹

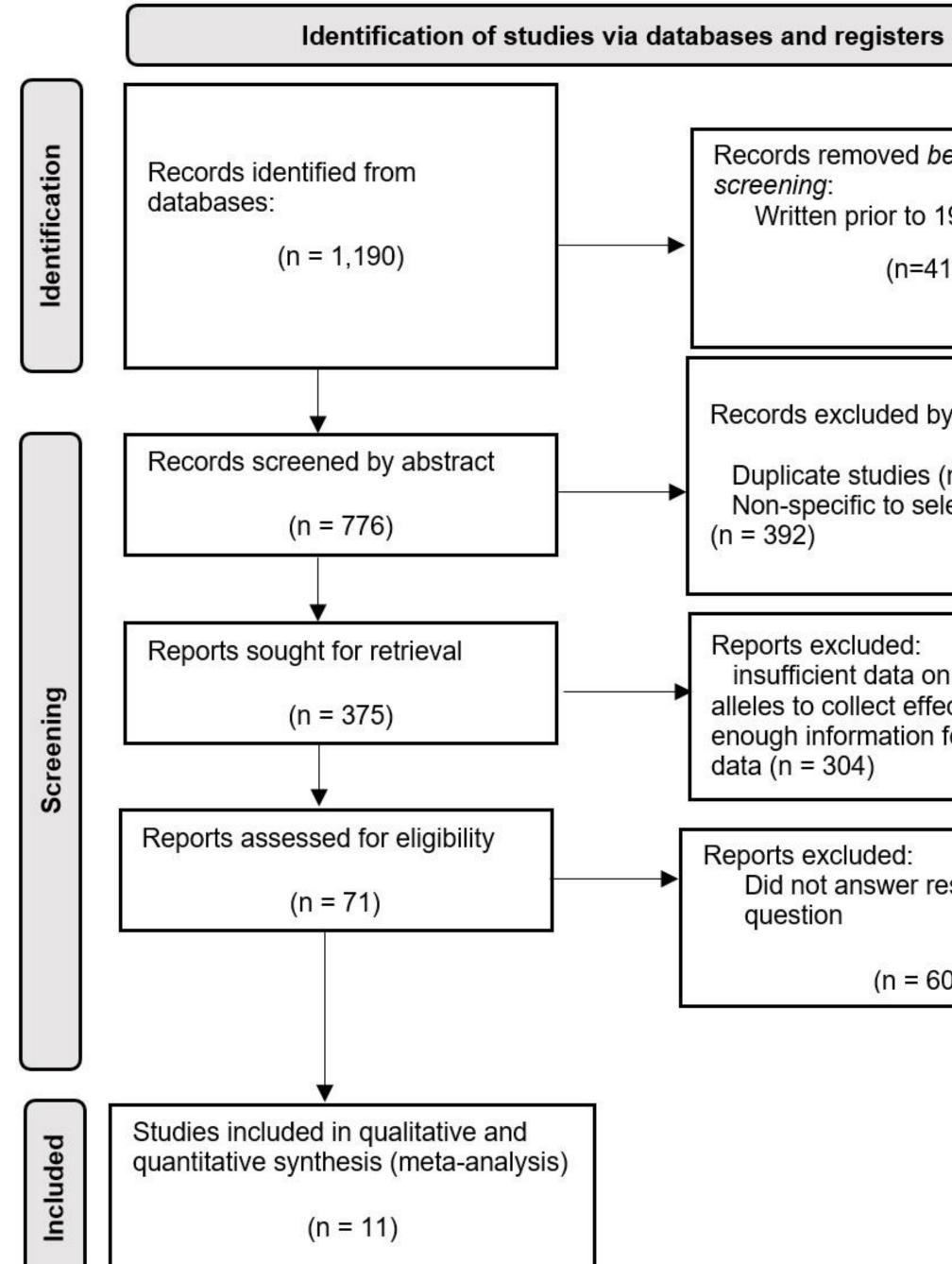


Figure 1. PRISMA flow guideline/checklist for meta-analysis. Figure represents included articles from 1989 – 2018 that met study criteria.

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Records removed before screening: Written prior to 1989 (n=414) Records excluded by abstract: Duplicate studies (n = 9)Non-specific to selected genes (n = 392) Reports excluded: insufficient data on the HLA alleles to collect effect size or not enough information for needed data (n = 304) Reports excluded: Did not answer research question (n = 60)

- MD as compared to healthy controls. This result is shown in figure 2.
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HLA	Serotype
HLA-A	A1, A2, A11
HLA-B	B7, B8, B13, B27, B35,
HLA-C	C1, C2, C3, C4, C5, C6,
HLA-DR	DR1, DR3, DR4, DR7, 1

DR8, DR9, DR10, DR11, DR12, DR13, DR15, DR16 **Table 1.** HLA serotypes that were analyzed for significance in Ménière's disease

	Protection		Susceptibility		
Study or Subgroup	Events	Total	Events	Total	W
1.8.10 HLA-DR11					
Futaki et al, 1989	1	44	4	120	
Yeo et. al, 1998	3	39	24	199	
Lopez et. al, 2002	18	52	112	534	
Koo 2003	3	41	11	226	
Lopez et. al, 2007	30	80	49	250	1
Subtotal (95% CI)		256		1329	3
Total events	55		200		
Heterogeneity: Chi ² = 5	.03, df = 4	4 (P = 0).28); l² = 2	20%	
Test for overall effect: Z	' = 3.26 (F	> = 0.00	01)		
1.8.11 HLA-DR13					
	0		00	400	
Futaki et al, 1989	8	44	20	120	
Yeo et. al, 1998	5	78	53	398	1
Lopez et. al, 2002	10	52	109	534	1
Koo 2003	3	82	55	452	1
Lopez et. al, 2007	16	160 416	77	500 2004	2
Subtotal (95% CI)	40	410	044	2004	0
Total events	42	4 /D - 0	314 20): 12 - 2	10/	
Heterogeneity: Chi ² = 5		`		1%	
Test for overall effect: Z	. = 2.00 (1	² = 0.00	18)		
Total (95% CI)		672		3333	10
Total events	97		514		
Heterogeneity: Chi ² = 2	6.81, df =	9 (P =	0.002); l ² :	= 66%	
Test for overall effect: Z	<u>′</u> = 0.08 (F	⊃ = 0.94	4)		

Test for subgroup differences: $Chi^2 = 17.58$, df = 1 (P < 0.0001), $l^2 = 94.3\%$

Figure 2. Forest Plots for HLA-DR11 and HLA-DR13 in Ménière's disease

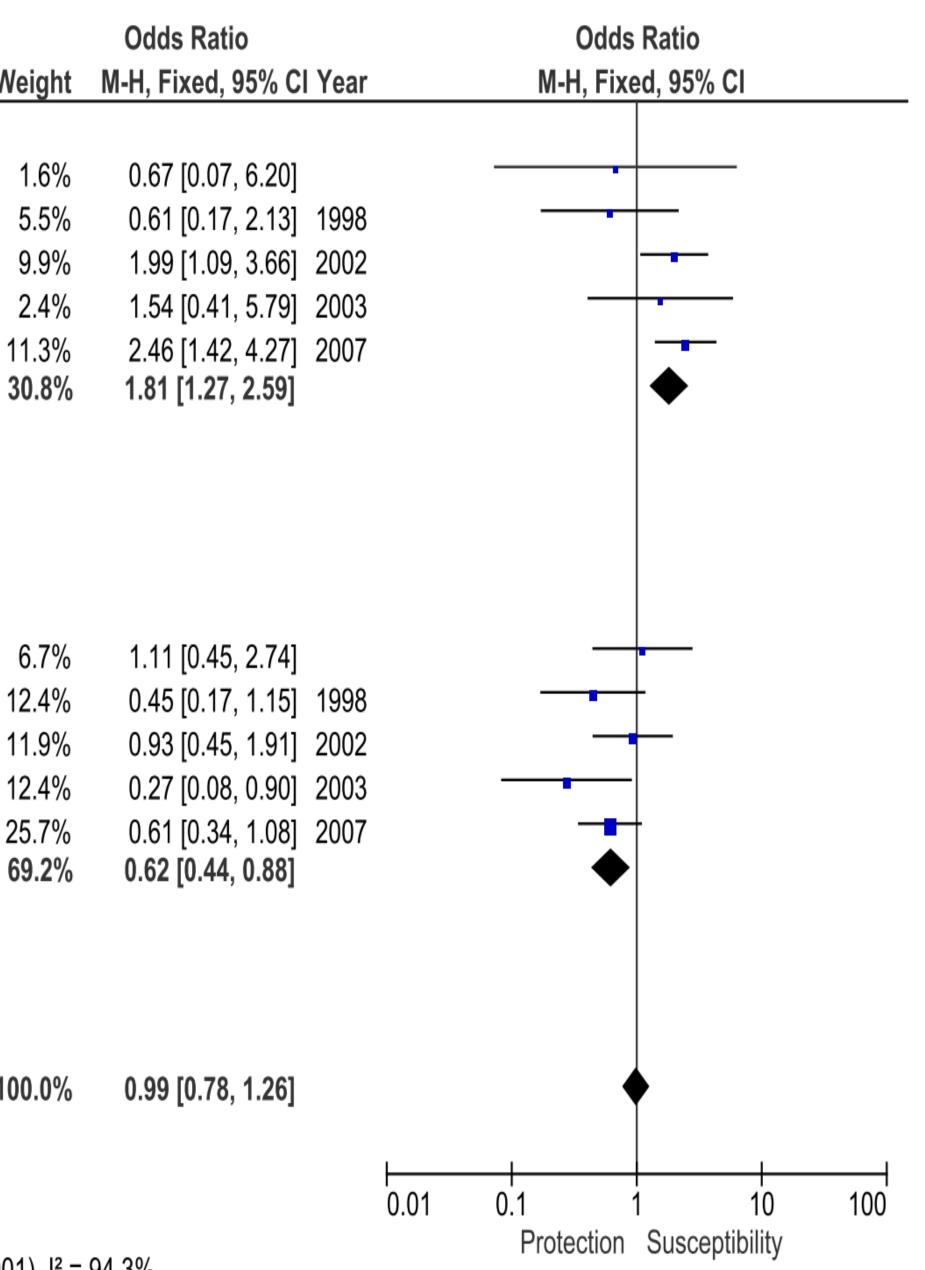
Results

• Thirty-six investigated serotypes with a minimum of three studies were eligible for analysis. 3 HLA-A serotypes, 14 HLA-B serotypes, 7 HLA-C serotypes, and 12 HLA-DR serotypes met the meta-analysis requirements. These alleles are showed in table 1. • Combined odds ratio was calculated using an Inverse Variance Heterogeneity Model and plotted using a Forest Plot. Analysis with I² value for heterogeneity > 25% did not meet significance criteria and were not eligible to be considered significant.

• The presence of the HLA-DR11 conferred 1.81 times increased odds of developing

• The presence of the HLA-DR11 conferred 0.62 times decreased odds of developing

B37, B38, B39, B44, B51, B52, B55, B57, B58 6, C7, C8



- MD.^{12,13}
- MD.¹⁴

- Immunology (2011): 119-122.
- laryngologica 122.8 (2002): 851-856.
- disease." Acta oto-laryngologica 122.5 (2002): 26-29.
- Immunology (2011): 119-122.
- 396-402
- Laryngology & Otology, 100(1), 21-24.

Discussion

• The query returned a total of 1,190 studies, and 11 of those trials met the inclusion criteria. 790 MD patient alleles 3,229 control alleles in 11 trials were assessed.

• Demographic groups included in these studies consisted of ethnically Japanese, South Korean, Iranian, Spanish, and British populations.

• Despite the extensive investigation of autoimmunity within MD, the findings of this comprehensive meta-analysis identified only two HLA serotypes that had significance among the combined patient population.

• Odds of MD was increased in patients with HLA-DR11 (OR=1.81, 95% CI [1.27, 2.59], I2=20%, p<0.05) as compared to normal controls.

• Odds of MD was decreased in patients with HLA-DR13 (OR=0.62, 95% CI [0.44, 0.88], I2=21%, p<0.05) as compared to normal controls.

A majority of the studies focused on the effect of a single haplotype on prevalence MD, with few also comparing effects of linkage disequilibrium, or combined HLA allele frequencies on disease prevalence.

• Future research should focus on combined haplotypes such as the HLA A1-B8-DR3 which has shown significance in individual studies in sensorineural hearing loss and

Another potential for investigation is the HLA class III genes "HSPA1" that represent the heat shock protein genes that are often tested in clinical practice when diagnosing

Conclusion

• The evidence on HLA-DR11 as a risk factor for MD and HLA-DR13 as a protective factor across several ethnic backgrounds is significant. These results warrant further investigation into a more global subset of patients with MD, with an emphasis in frequencies of combined haplotypes such as HLA A1-B8-DR3 common ancestry gene and the HSPA1 heat shock protein gene.

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