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OBJECTIVES

A population-based study was conducted to investigate the epidemiology, prevalence and the temporal trend of NMOSD incidence over 12 years (2012 – 2023) at Penang Island, Malaysia, located at the equatorial Southeast Asia.

(2) Population-based prevalence studies and genetic studies of NMOSD worldwide were reviewed.

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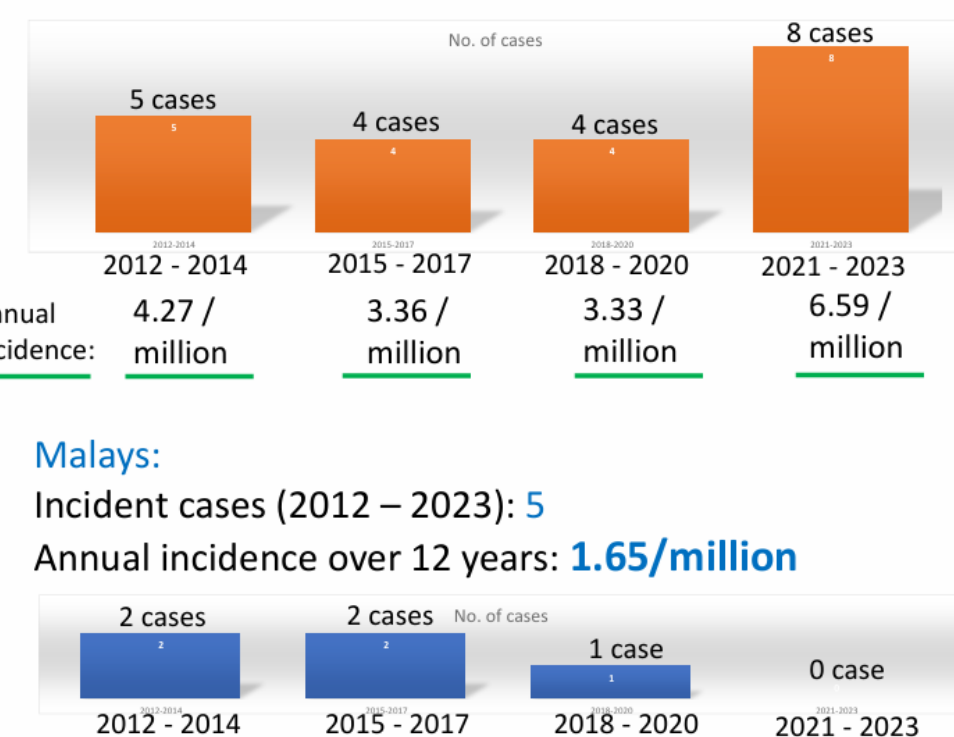
graph TD
    A["AQP4-IgG+ NMOSD patients:  
79 identified"] --> B["Residents of Penang Island: 38"]
    A --> C["Residents of  
neighbouring areas: 37  
Non-citizens: 4  
EXCLUDED"]
    B --> D["Chinese (East Asian  
ancestry): 32"]
    B --> E["Malays (Austronesian  
ancestry): 6"]
    D --> F["Incident cases  
(2012 – 2023)  
Chinese: 21"]
    E --> G["Incident cases  
(2012 – 2023)  
Malays: 5"]
  
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Prevalence Data: Prevalence Day: 31st Dec 2023

	No. of living patients	Prevalence Rate
Chinese (East Asians)	28	6.96 / 100,000
Malays (Austronesians)	4	1.57 / 100,000
Indians (South Asians)	---	

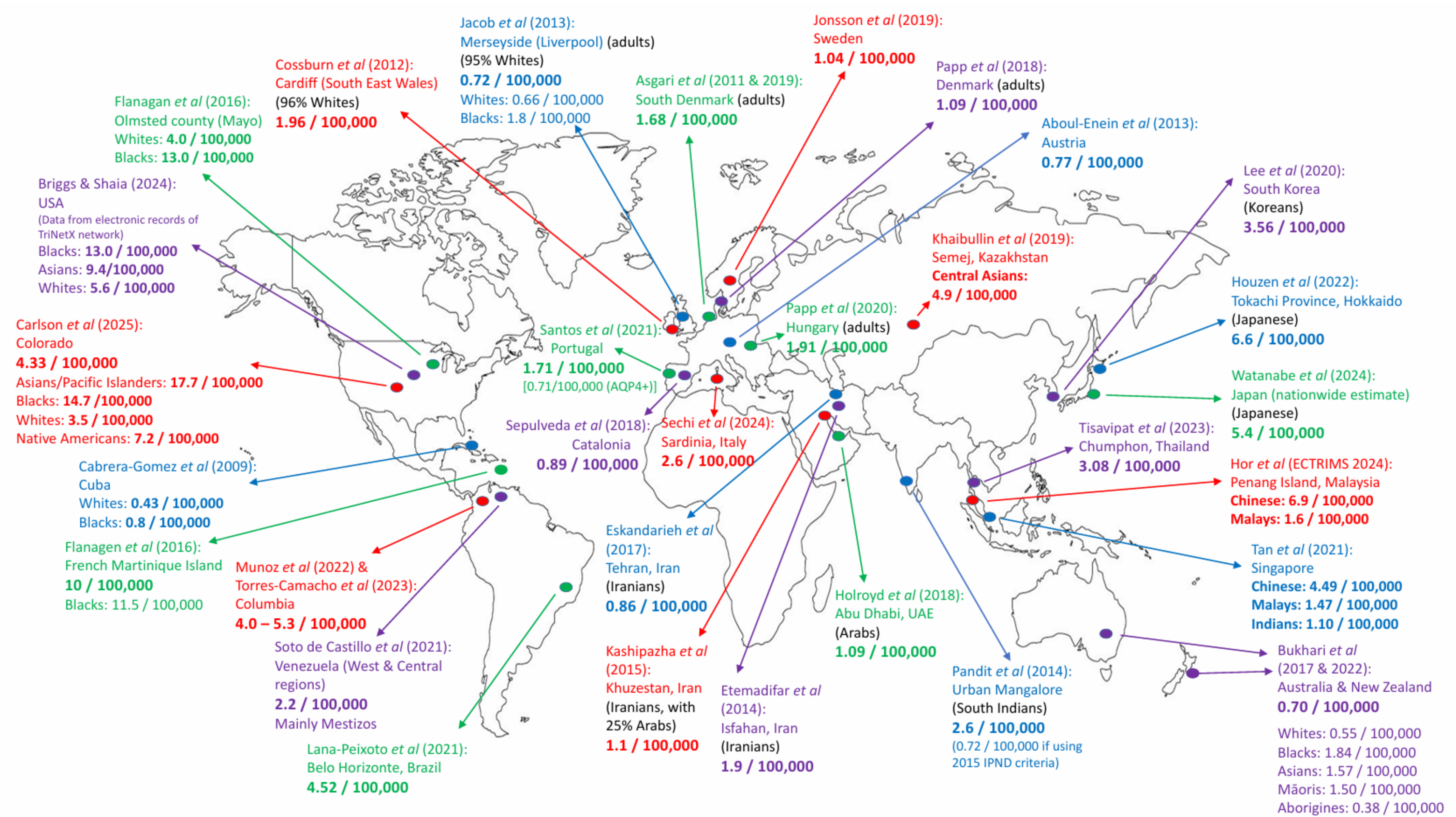
Temporal trend of NMOSD incidence

Chinese:
Incident cases (2012 – 2023): **21**
Annual incidence over 12 years:



The universal Covid19 vaccination in the whole island population in 2021-22 provides a unique opportunity to study the effect of vaccination on the disease onset. Among the Chinese population, in 2021-2023, 2 of the 8 incident cases had onset after Covid19 vaccination.

World Map Showing Prevalence Studies of NMOSD



NO LATITUDE GRADIENT

Modified from Hor *et al.* Front Neurol 2020

Whites / Europeans: ~2 / 100,000
Black Africans: up to 10 / 100,000
East Asians: ~6 / 100,000
Austronesians: ~2 / 100,000
South Asians: ~1 / 100,000
South America: 2.2 - 5 / 100,000
(With genetic contributions from
African ancestry & Native American ancestry)

Whites / Europeans: 0.37 – 1.32 / million
African-Caribbean: up to 7 / million
East Asians: ~ 3 – 4 / million
Austronesians: ~1.5 – 2 / million

Ancestral groups	Risk alleles	Protective alleles	
Asians:			
Chinese	DBP1*05:01 DBR1*16:02	DBR1*09:01	Wang <i>et al.</i>
Japanese	DBP1*05:01 DBR1*16:02 DBR1*08:02 DBR1*12 DQA1*05:03	DBR1*09:01	Isobe <i>et al.</i> Yoshimura <i>et al.</i> Matsushima <i>et al.</i> Ogawa <i>et al.</i>
Koreans	DBR1*03:01		Hyun <i>et al.</i>
Indians	DBR1*03		Pandit <i>et al.</i>
Arabs	DBR1*04:04 DBR1*10:01	DBR1*07 DQB1*02:02	Brill <i>et al.</i>
Other populations:			
Whites / Europeans	DBR1*03 A*01 B*08		Blanco <i>et al.</i> Estrada <i>et al.</i> Brujilstens <i>et al.</i> Tabansky <i>et al.</i>
Afro-Caribbeans	DBR1*03		Deschamps <i>et al.</i>
Brazilians	DBR1*03:01 DBR1*16:02 DQA1*04:05		Brum <i>et al.</i> Alvarenga <i>et al.</i> Kay <i>et al.</i>
Mexicans / Native Americans	DBR1*03 DBR1*10 DQB1*03:01 DBR1*08:02 DBR1*16:02 DBR1*14:06 DQB1*04:02	DBR1*03:02 DQB1*02:02	Alonso <i>et al.</i> Romero-Hidalgo <i>et al.</i>

Modified from Hor *et al.* Neurol Clin Neurosci 2021

Based on our and other population-based studies, there was differential prevalence of NMOSD in populations with different ancestries – Black African (up to 10/100,000), East Asian (~6/100,000), Austronesian (~2/100,000), European (~2/100,000) and South Asian (~1/100,000), despite some of them living in the same environment.

No latitude gradient was observed unlike that seen in multiple sclerosis.

The temporal trend of incidence (new cases) appeared relatively stable over time, apart from a slight increase after universal Covid19 vaccination.

Genetic studies in various populations identified several different HLA risk and protective alleles.

Genetic predisposition may play an important role in the disease prevalence and pathogenesis, and vaccination may be a minor trigger in at-risk population.