Yearly Trends in Social Support for HPV Vaccine Completion Among Young Japanese Women: A Repeated Cross-Sectional Study (2022–2025)

Mari Mizumachi (1)
Yuichiro Nishida (1), Takuma Furukawa (1,3), Ai Sakakibara (1,4), Toshiko Nakamura (1,5), Takaomi Kobayashi (1)
Wakaba Fukushima (2), Megumi Hara(1),

1 : Department of Preventive Medicine, Faculty of Medicine, Saga University
2 : Department of Public Health, Graduate School of Medicine, Osaka Metropolitan University
3 : Saga University Hospital
4 : Department of Nursing, Faculty of Medicine, Saga University
5 : Department of Nursing, Faculty of Fukuoka Medical Technology, Teikyo University

Background : Human papillomavirus (HPV) vaccination is an effective strategy for preventing cervical cancer. In Japan, uptake dropped sharply after the government suspended active recommendation in 2013, creating a generation of under-vaccinated women. Although catch-up vaccination resumed in 2022, completion of the three-dose series remains low. Social support from healthcare providers, family, and peers influences vaccine behavior, but little is known about how its impact has changed during this recovery phase.

Objective : This study examined the association between social support and HPV vaccine completion among young Japanese women in the catch-up generation and explored annual trends from 2022 to 2025.

Methods : We used data from annual nationwide cross-sectional surveys conducted from 2022 to 2025, targeting women around age 20 (total n=2,400). Completion of three vaccine doses was the outcome. Perceived support from healthcare providers, family, and peers was treated as dichotomous variables. Modified Poisson regression was performed for each year to estimate adjusted prevalence ratios (aPRs), adjusting for age.

Results : Completion increased from 5.0% in 2022 to 19.3% in 2025. Support from healthcare providers was significantly associated with vaccine completion each year (aPRs: 3.95 in 2022, 2.69 in 2023, 1.94–2.65 in 2024–2025). Family support was also consistently significant (aPRs: 3.09 in 2022, 3.94 in 2023, 1.78–2.03 in 2024–2025). Peer support was significant only in 2022 (aPR=2.25, 95%CI: 1.17–4.33). Age was not a significant confounder.

Conclusion : Support from healthcare providers and family members has remained a stable determinant of vaccine completion. Enhancing communication and ongoing recommendation may improve uptake among the catch-up generation.

Global modelling analysis of trends in suicide mortality rates, 1990–2021, with projections to 2050

Selin Woo (1)
Dong Keon Yon (1)

1 : Center for Digital Health, Medical Science Research Institute, Kyung Hee University Medical Center, Kyung Hee University College of Medicine, Seoul, South Korea

Suicide is a major global health issue influenced by complex socioeconomic and demographic factors. Understanding trends and projections is critical for developing effective prevention strategies. However, few studies have comprehensively evaluated both historical trends and future patterns across a large number of countries using standardized global data. We analyzed age-standardized suicide mortality rates from 1990 to 2021 across 102 countries using the WHO Mortality Database. Trends were estimated with LOESS regression. Associations with Human Development Index(HDI), Sociodemographic Index(SDI), reverse Gender Gap Index(rGGI), Gender Inequality Index(GII), and latitude were assessed via linear regression. Future rates to 2050 were projected using a Bayesian age–period–cohort(BAPC) model. Decomposition analysis quantified effects of population growth, aging, and epidemiological change. Global suicide mortality declined from 10.33(95% CI: 9.67–10.99) per 100,000 in 1990 to 7.24(6.58–7.90) in 2021. Males showed a drop from 16.41 to 11.51, and females from 4.65 to 3.22. High-income countries decreased from 12.68(11.96–13.40) to 8.61(7.89–9.33), while low- and middle-income countries decreased from 7.88(6.93–8.84) to 5.73(4.77–6.69). Rates were positively associated with HDI (β=24.250, P=0.001), SDI (β=0.091, P<0.001), and latitude (β=23.732, P<0.001), and inversely with rGGI (β=−39.913, P=0.002); GII was also significant (β=13.229, P=0.016). BAPC projections indicate a decline from 8.60 (95% CrI: 8.40–8.83) in 2021 to 6.49 (2.19–17.57) in 2050. Decomposition showed demographic shifts increased deaths, while epidemiologic changes reduced them. Suicide mortality has declined globally over the past three decades and is projected to continue decreasing. However, disparities by sex, age, income, and region remain, underscoring the need for targeted interventions and stronger mental health systems in vulnerable populations and low-resource settings.

Long-Term Risk of Diabetes-Related Complications in Youth- or Young-Onset Diabetes

Dae Jung Kim (1)
Kyoung Hwa Ha (1,2,3), Ja Young Jeon (1)

1 : Department of Endocrinology and Metabolism, Ajou University School of Medicine
2 : Department of Preventive Medicine, Yonsei University College of Medicine
3 : Institute for Innovation in Digital Healthcare, Yonsei University

Aims : To compare the long-term risks of diabetes-related complications and all-cause mortality in individuals diagnosed with type 1 diabetes mellitus (T1DM) or type 2 diabetes mellitus (T2DM) before the age of 40.

Methods : This study included 72,917 individuals newly diagnosed with T1DM or T2DM between 2003 and 2006 and followed them through 2023 (median follow-up, 18.9 years), using data from the Korean National Health Insurance database. Participants were stratified by age at diagnosis: 0–19 years (T1DM, n=693; T2DM, n=1,988) and 20–39 years (T1DM, n=3,008; T2DM, n=67,228). Outcomes included acute, severe microvascular, and cardiovascular complications, and all-cause mortality. Cumulative incidence and hazard ratios (HRs) with 95% confidence intervals (CIs) were compared between T1DM and T2DM by age group.

Results : Among individuals diagnosed at 0–19 years, the cumulative incidence of acute complications in T1DM reached approximately 30% at 10 years and 40% at 20 years, while remaining below 10% in T2DM. Severe microvascular complications increased after 10 years in both groups, reaching ~20% at 20 years. In this age group, T1DM was associated with higher risks of acute complications (HR 5.94; 95% CI 4.78–7.39) and severe microvascular complications (1.32; 1.06–1.66) compared with T2DM. Among individuals diagnosed at 20–39 years, the cumulative incidence of severe microvascular complications in T1DM approached 30% by 20 years, compared with ~10% in T2DM. T1DM was associated with increased risks of acute complications (7.84; 7.16–8.58), severe microvascular complications (2.37; 2.19–2.57), cardiovascular complications (2.16; 1.79–2.60), and all-cause mortality (2.41; 2.21–2.62).

Conclusion : In early-onset diabetes, the cumulative burden of diabetes-related complications and all-cause mortality was substantial, particularly in those with T1DM. Complication patterns and timing differed by diabetes type and age at diagnosis.

Machine learning-based dietary patttern development for personalized prevention

Hyobin Lee (1,2)
Dongseok Heo (3), Sukhong Min (1), Sinyoung Cho (1,4), So-Yoon Lee (1), Bongwon Suh (5), Daehee Kang (1,2)

1 : Seoul National University College of Medicine / Department of Preventive Medicine
2 : Seoul National University Graduate School / Integrated Major in Innovative Medical Science
3 : Seoul National University / Interdisciplinary Program in Artificial Intelligence
4 : Seoul National University Hospital / Department of Family Medicine
5 : Seoul National University / Department of Intelligence and Information

Background & Aims : Dietary pattern analysis plays a pivotal role in nutritional epidemiology by capturing the complex interactions among various foods. While clustering methods are widely applied in dietary pattern analysis, the role of dimensionality reduction in improving clustering performance remains underexplored. This study aimed to systematically compare Principal Component Analysis (PCA), Uniform Manifold Approximation and Projection (UMAP), and Autoencoders (AE) for dietary pattern development.

Methods : Data were obtained from participants of the large-scale prospective cohort study, Health Examinees-Gem (HEXA-G) study (2004-2013). After exclusions, 130,472 participants were included in the analysis. Dietary intake was assessed using a 106-item food frequency questionnaire. PCA, UMAP, and AE were applied for dimensionality reduction, followed by k-means clustering. Cluster quality was assessed with silhouette coefficients, and variable contributions were evaluated using SHAP values.

Results : Notable differences in clustering performance were observed. Without dimensionality reduction, the silhouette coefficient was 0.05. PCA rarely exceeded 0.2 except at two dimensions. UMAP maintained stable performance around 0.4 across different dimensions and cluster numbers (k). AE consistently achieved coefficients above 0.35, with modest variation by k. SHAP analysis revealed that PCA and UMAP relied heavily on a few dominant variables, whereas AE captured more balanced contributions.

Conclusion : Among the tested methods, AE achieved the most favorable balance of cluster quality and interpretability. This framework demonstrates the utility of machine learning–based approaches for dietary pattern development and their potential application in personalized prevention.

Genetic determinants of hepatitis B vaccine response in the Taiwanese population

Chih-Ching Yeh (1)
Moreen Maliko (1), Fu-Hsiung Su (2), Abram Bunya Kamiza (3)
1 : School of Public Health, College of Public Health, Taipei Medical University
2 : Department of Family Medicine, Cardinal Tien Hospital, Fu Jen Catholic University
3 : Sydney Brenner Institute for Molecular Bioscience, Faculty of Health Sciences, University of the Witwatersrand

Background : Hepatitis B virus (HBV) vaccination has successfully reduced infection rates in Taiwan, yet variability in immune response remains a challenge. While many individuals develop durable immunity, others show weak or waning protection, suggesting the influence of host genetic factors. However, genetic determinants of HBV vaccine response in the Taiwanese population remain underexplored.

Methods : We conducted a genome-wide association study (GWAS) using data from 108,490 unrelated participants aged 20–70 years in the Taiwan Biobank. Based on serological markers, individuals were classified into three groups: (1) susceptible (waning vaccine effect, anti-HBs <5 IU/L, negative HBsAg and anti-HBc), (2) vaccinated with weak immunity (anti-HBs >50 to ≤100 IU/L), and (3) vaccinated with strong immunity (anti-HBs ≥100 IU/L). Two case-control analyses were performed: weak immunity vs. susceptible, and strong immunity vs. susceptible. After quality control, 3.56 million SNPs were analyzed using logistic regression, adjusting for age, sex, and population stratification.

Results : No genome-wide significant loci were identified in the weak vs. susceptible comparison. In contrast, the strong vs. susceptible analysis (n=9075) identified a novel variant, rs78980954, located between *HLA-DPB1* and *HLA-DPB2*, reaching genome-wide significance (OR=0.75, $P=7.35\times10^{-9}$). Strong responders were slightly younger and more often female compared with susceptibles ($P=0.001$). Validation in Biobank Japan did not replicate this association for vaccine response, though the variant has been linked to chronic HBV infection, suggesting a phenotype-specific role.

Conclusion : This study identifies rs78980954 near *HLA-DPB1/DPB2* as a novel locus for strong HBV vaccine response in the Taiwanese population. The findings highlight genetic contributions to vaccine effectiveness and support further research toward personalized vaccination approaches.