An ecological analysis of the global relationship between air pollution and cancer statistics

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Background : Air pollution is a major environmental risk factor for human health. While the link to lung cancer is established, its associations with other cancer types remain less clear on a global scale.

Methods : We conducted an ecological analysis combining cancer incidence and mortality data from GLOBOCAN 2022 with risk factor estimates from the Global Burden of Diseases 2021 database across 179 countries. Lasso regression was used to select key risk factors, followed by multivariable linear regression models adjusted for the socio-demographic index.

Results : Among the 14 risk factors identified by Lasso, particulate matter pollution was linked to the incidence of gallbladder, mesothelioma, bladder, melanoma, testicular, and lung cancers, as well as to mortality from melanoma, mesothelioma, thyroid, and lung cancers. Nitrogen dioxide pollution was associated with the incidence of stomach, thyroid, leukemia, kidney, and pancreatic cancers, and marginally with pancreatic cancer mortality.

Conclusion : This global analysis highlights ecological associations between air pollution and both cancer incidence and mortality across several types of cancer, including lung, mesothelioma, melanoma, and thyroid cancers.

Association of cognitive function with all-cause mortality in a community-dwelling elderly people

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Background : Cognitive function declines with age in elderly people. Cognitive impairment leads to falls, a decrease in quality of life and conditions requiring nursing care. Moreover, some previous studies reported that impaired cognitive function is associated with higher risk of all-cause mortality in elderly people. However, these studies had limitations including a narrow age range of older adults (aged 80 and more), small sample size or short follow-up duration. The present study aimed to investigate the association between cognitive function and all-cause mortality in a community-dwelling elderly people, with a follow-up duration of approximately 15 years.

Methods : This prospective cohort study included 2174 men aged ≥65 years, of whom 2012 completed the baseline survey. Follow-up surveys were conducted five, 10 and 15 years later with mortality as the outcome. Cognitive function was assessed using the Mini-Mental State Examination (MMSE). We divided the MMSE total score into the cognitive impairment (0-23 points), mild cognitive impairment (24-27points), and normal cognitive function (28-30 points). Hazard ratios were calculated for the association between cognitive function and all-cause mortality using Cox proportional hazards models.

Results : Participants with lower MMSE scores had higher age and lower height. Compared to participants with normal cognitive function at baseline, participants with mild cognitive impairment and cognitive impairment had significantly higher mortality risks (hazard ratio (HR): 1.276, 95% confidence interval (CI): 1.057-1.541 and HR: 1.565, 95%CI: 1.091-2.243, respectively), after adjusting for age, education, smoking, drinking and some past medical history.

Conclusions : This study showed that cognitive impairment was associated with a significantly increased risk of mortality in the elderly. Lower cognitive function performance may be independently predicted mortality in the elderly people.

Association between serum leptin concentration and incidence of diabetes mellitus: Toon Health Study

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Background : Leptin, a hormone secreted by adipose tissue, plays a key role in regulating metabolism, insulin resistance, and diabetes mellitus (DM). While interacting with insulin, evidence linking leptin to DM remains inconsistent. This study examined the association between serum leptin and DM incidence among middle-aged Japanese.

Methods : This cohort study, part of the Toon Health Study in Toon City, Ehime, Japan, included 770 adults (239 men, 531 women) after excluding persons with DM at baseline or missing data. Serum leptin was measured by ELISA and categorized into sex-specific quartiles. DM was defined by fasting glucose ≥126 mg/dL or 2-hour post-load glucose after 75g oral glucose tolerance test ≥200 mg/dL or current use of glucose-lowering medication. Odds ratios (ORs) and 95% confidence intervals (CIs) were estimated by logistic regression after adjustment for age, sex, physical activity, smoking, alcohol drinking, and sleep quality. We further adjusted for HOMA-IR and BMI to examine whether these factors affect associations. Same analyses were stratified by median BMI. The study was approved by the Institutional Review Board of Ehime University Hospital (#170511).

Results : Over the follow-up, 36 new DM cases occurred. In multivariable models, the highest leptin quartile (Q4) had a higher risk of DM; the OR (95%CIs) for Q4 was 2.77 (1.05–7.35, p for trend = 0.01) compared with Q1. However, the association was non-significant after adjustment for HOMA-IR (OR: 1.90; 95% CIs: 0.67–5.42; p for trend = 0.11) and BMI (OR: 1.31; 95% CIs: 0.37–4.70; p for trend = 0.07). In stratified analyses, leptin concentration was associated with DM only in subjects with BMI ^{3} median (OR per 1 unit increment: 1.07; 95% CI: 1.01–1.14) and was insignificant after adjusting for HOMA-IR.

Conclusion : Higher leptin levels were linked to greater DM risk, particularly in those with higher BMI, but this was largely explained by insulin resistance in higher body weight individuals.

Cross cohort proteomics reveals muscle mass biomarkers i n UKB and YMoC study

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Background : Skeletal muscle mass is a key determinant of mobility and metabolic health. Circulating proteomes capture muscle-related pathways.

Objective: To identify plasma proteins associated with whole-body muscle mass and assess their significance.

Methods : We used a two-stage discovery–replication design with a discovery cohort from UK Biobank (UKB; n=43,434; age 56.8 ± 8.2; 54.2% female) and a replication cohort from the Yamanashi Multi-omics Cohort study (YMoC; n=162; age 54.4 ± 7.4; 40.1% female). We estimated whole-body muscle mass by bioelectrical impedance (BIA), quantified plasma proteins by Olink NPX, and energy-adjusted nutrient intakes from the food frequency questionnaire (FFQ). We first tested the protein-muscle mass associations by multivariable linear regression adjusted for age, sex, smoking, physical activity, and income, applying Benjamini–Hochberg FDR ($q<0.05$). The primary overlap comprised proteins significant in both cohorts. Second, we assessed the associations between replicated proteins and FFQ-derived nutrients using partial Spearman correlations.

Results : In UKB, we identified plasma proteins significantly associated with muscle mass (FDR $q<0.05$); seven replicated in YMoC with concordant directions (IGSF3, CKB, IGFBP2, THBS4, CRYBB2, COMP, CTHRC1). Through functional annotation, we implicated extracellular matrix integrity (THBS4, COMP) and growth-factor signaling (IGFBP2) and included novel candidates with limited prior evidence in skeletal muscle (IGSF3, CRYBB2). In secondary analyses in YMoC, we observed IGSF3–α-carotene (positive) and THBS4–ethanol (inverse) associations (FDR $q<0.1$).

Conclusion : Through cross-cohort replication, we identified a proteomic signature of muscle mass implicated in key biological pathways. However reliance on BIA-derived estimates of muscle mass, and the relative NPX scale, causal inference and clinical application warrant further investigation.

Evaluation of Methylation Risk Scores for type 2 diabetes in the Japanese general population

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Background : Genetic risk factors for type 2 diabetes (T2D) have been well documented and increasing attention has been directed toward epigenetic factors such as DNA methylation. Recent studies have identified T2D-associated methylation sites, and methylation risk scores (MRS) have emerged as a promising tool for assessing diabetes risk. However, evidence from Japanese populations remains limited.

Methods : In this study, we analyzed data from 512 participants randomly selected from the Japan Multi-Institutional Collaborative Cohort (J-MICC) Study, Saga region, with DNA methylation array measurements performed on blood samples. MRSs were calculated based on DNA methylation sites and effect sizes reported in epigenome-wide association study (EWAS) of Indian Asians and in meta-analysis of European populations. The MRS values for each participant were calculated as the weighted sum of the methylation rates at each methylation site. Logistic regression analysis was used to analyze odds ratios (OR) for diabetes prevalence by MRS levels. Classification accuracy was evaluated using the area under the receiver operating characteristic curve (AUC). The analysis was adjusted for age, sex, white blood cell differential, and the top five principal components.

Results : Higher MRS quantiles were associated with higher OR of diabetes in both MRSs. Per one standard deviation increase in MRS, the ORs for diabetes were 2.30 (Indian Asian-based MRS) and 2.69 (European-based MRS). The AUC was 0.861 for the Indian Asian MRS, and 0.825 for European MRS, indicating that both scores provide high discriminatory ability for diabetes risk.

Conclusion : Our findings indicate that the MRSs calculated from EWAS data exhibit strong classification performance for T2D and may be useful for identifying individuals at elevated risk. Further research is warranted to refine epigenomic profiling and develop population-specific MRSs, which could enhance prediction and support preventive strategies for diabetes.