The 8th AAMLS & 2025 8th Congress of Asia Association of Medical Laboratory Scientists in conjunction with 16th Asia-Pacific Forum of Medical Laboratory Sciences



Taiwan WGS Consortium: Disease Cohort, **Clinical Application, Health Policy**

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The Taiwan WGS Consortium (TWC) was created to establish a database for disease diagnosis and precision medicine purposes that are suitable for Taiwan's population and that will remain viable financially in the long term. Target diseases initially included genetic diseases with risk alleles affecting 0.1% to 5% of the Taiwan population, metabolic-associated fatty liver disease and liver cancer, lung cancer, colorectal cancer, breast cancer, prostate cancer, diabetes, and chronic kidney disease. These all are areas in which we have significant clinical datasets already. Up to the present, TWC has already have operated five significant projects in phase one (2023-2024). Our intention is to have collected a minimum of 50,000 patient samples by the end of 2026. Importantly, as a control, we have completed WGS on 2,468 individuals from the general population who are part of the Healthy Aging Longitudinal Study in Taiwan (HALST) Cohort. Starting in 2009, 5663 healthy individuals who were aged over 55 have been recruited from seven community hospitals in urban and rural areas of Taiwan. These individuals have been followed up with home interview every other year and hospital-based examination every five years. Thus, we have established a resources hub for aging studies that target chronic diseases, such as diabetes, hypertension, osteoporosis, kidney disease, and dementia, as well as providing a control population for other projects.





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In order to incorporate population genomics and preventive medicine into our aging research program, we have added genomic data that enhances the HALST objectives (geHALST); this genomic data on the HALST subjects was obtained using DNA array technology and whole genome sequencing. Initially we analyzed dichotomous 3 (monogenic) and continuous (polygenic) traits with respect to chronic kidney disease in order to showcase the value of geHALST as a publicly available resources for population health research in Asia. Finally, using the geHALST dataset, we have been able to identify in the Taiwanese population known and new genetic loci associated with the insulin resistance phenotype of metabolic syndrome; similarly, we have identified loci linked to the presence of reduced glomerular filtration rate and proteinuria in chronic kidney disease



