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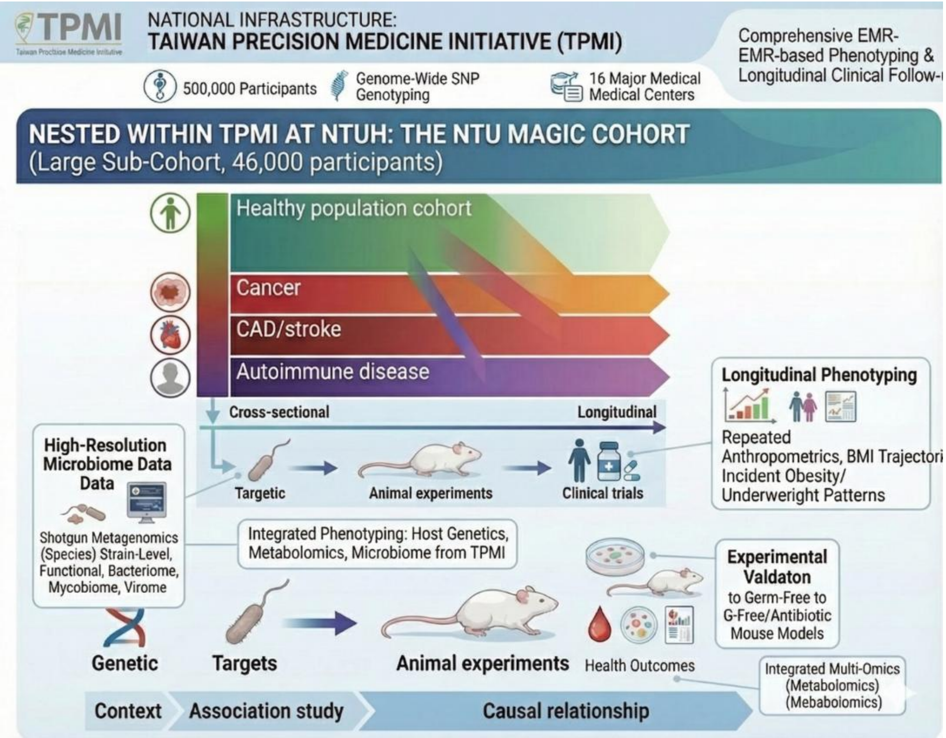
<tr><th colspan="2">SPEECH INFORMATION (For Conference Program Book)</th></tr>
<tr><td>Topic</td><td>The e NTU MAGIC (Microbiota and Genetic Integrated Cohort)</td></tr>
<tr><td>Abstract</td><td>

TPMI is a national precision medicine infrastructure led by Academia Sinica in collaboration with 16 major medical centers across Taiwan, integrating genome-wide SNP genotyping with comprehensive electronic medical record (EMR)–based phenotyping and longitudinal clinical follow-up. Within TPMI, the NTU MAGIC (Microbiota and Genetic Integrated Cohort) represents a large hospital-based sub-cohort at National Taiwan University Hospital (NTUH), comprising approximately 46,000 participants. The cohort includes a healthy population as well as individuals with major disease categories, including cancer, coronary artery disease (CAD)/stroke, and autoimmune diseases, enabling cross-sectional and longitudinal analyses across a broad clinical spectrum. Participants are followed longitudinally with repeated anthropometric measurements, detailed clinical data, and EMR linkage, allowing reconstruction of BMI trajectories and identification of incident obesity or underweight patterns.High-resolution microbiome profiling is performed using shotgun metagenomic sequencing of stool samples, providing species-level, strain-level, functional, and multi-kingdom information, including bacteriome, mycobiome, and virome. These microbiome data are integrated with host genetic data from TPMI and with additional omics layers, such as metabolomics, to achieve comprehensive phenotyping. The platform is designed to move from observational association studies to causal inference. Candidate microbial taxa, genes, or pathways identified in human analyses are prioritized as targets for experimental validation. Microbiota transfer experiments using germ-free or antibiotic-treated mouse models, together with downstream metabolic and health outcome assessments, enable mechanistic testing of host–microbiome interactions. This integrated framework supports translation from population-based genomic and microbiome associations to biological mechanisms and potential clinical interventions.



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