Symposium | Schizophrenia：[Symposium 56] Current status of psychiatric research using genetic medicine and genomic medicineImportance of collaborative research among East Asians

Sat. Sep 27, 2025 9:00 AM - 10:30 AM JST | Sat. Sep 27, 2025 12:00 AM - 1:30 AM UTC Session Room 3 (Large Hall A)

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[SY-56-02] Multimodal Genomic and Mobile Sensing Reveals Genetic and Behavioral Signatures in Mood Disorder Phenotypes

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Keywords：antidepressant induce mania、unipolar mania、digital phenotyping

Mood disorders span diverse phenotypes. We integrate genome-wide analyses and digital phenotyping to clarify how inherited risk and real-world mobility inform mood disorder classification and prediction. Among 772 Han Chinese patients with unipolar depression, 145 (19.7%) developed antidepressant-induced mania (AIM) within 28 days of antidepressant exposure or discontinuation. Genome-wide testing identified eight suggestive SNPs, and higher bipolar polygenic risk scores significantly predicted AIM (OR ≈ 1.25, $p < .05$). Clinical risk factors included female sex, postpartum depression, OCD, severe episodes, substance use, and psychoses. Additionally, bipolar patient with unipolar mania (UM) were compared to 1,041 with depressive-manic (D-M) presentations. A genome-wide locus (rs149251101, *THSD7A*) differentiated UM from D-M cases ($p = 5.3 \times 10^{-8}$). PRS for bipolar disorder, major depression, and suicide attempt were positively associated with UM, while insomnia liability was inversely linked. Lastly, in two smartphone cohorts (n=107), passive GPS and mood data over six months revealed over 10,000 person-days. Homestay predicted next-day fatigue, depressed mood, and irritability; higher location variance predicted lower depression. Depressive symptoms, in turn, predicted reduced mobility. Spectral and diurnal analyses identified mood-linked movement cycles and evening mobility declines as digital markers of depression. These multimodal approaches reveal overlapping genetic and behavioral markers in mood disorders, enabling future personalized, movement-informed interventions.