INCREASING SAMPLE DIVERSITY IN PSYCHIATRIC GENETICS:
INTRODUCING A NEW COHORT OF SCHIZOPHRENIA PATIENTS AND CONTROLS FROM VIETNAM

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Introduction:
Numerous genome-wide association studies (GWAS) have successfully revealed genetic risk variants for schizophrenia (SCZ) and other psychiatric traits. However, a major challenge in current GWAS endeavors is that most samples are from European populations, which limits their power and clinical utility. For example, polygenic risk scores (PRS) show decreased predictive power when applied to non-European populations.

Objectives:
Our main objective is to establish long-term scientific cooperation between the Charité Universitätsmedizin Berlin and the Hanoi Medical University and address this limitation by recruiting a large genetic cohort of schizophrenia patients and controls in Vietnam.

Methods:
A pilot study was conducted at the Department of Psychiatry of the Hanoi Medical University. Data collection encompassed i) genome-wide SNP genotyping of 200 schizophrenia patients and 200 control subjects ii) structured interviews to assess symptom severity (PANSS), iii) clinical parameters (e.g. duration of illness, medication) and demography.

Results:
Schizophrenia PRS of the pilot sample (N=200/200) were generated using three different training data sets: i) European, ii) East-Asian and iii) mixed GWAS summary statistics from the Psychiatric Genomics Consortium's latest SCZ discovery publication (Trubetskoy et al., 2022). As expected, most variance explained was observed when using a mixed discovery sample (R2 liability=0.053, p=3.11*10-8, Pd <0.5), followed by PRS based on the East-Asian summary statistics (R2 liability=0.0503, p=6.78*10-8, Pd <1) and the European sample (R2 liability=0.0363, p = 4.26*10-6, Pd <0.01).

Conclusions:
We established efficient recruitment procedures, as well as genotyping and data analysis pipelines for this pilot project. Our results corroborate previous findings indicating that the transferability of PRS across populations depends on the ancestral composition of the initial discovery dataset. In the future, a more comprehensive phenotyping battery will be added to the study protocol. This includes the validation of previously not translated diagnostic tools into Vietnamese. We are currently expanding our data collection efforts across multiple sites in order to improve risk prediction across diverse populations.