

CLINICAL PHARMACY GUEST SEMINAR

Beyond Conventional GWAS: Leveraging Local Ancestry and Multi-Omics to Advance Precision Pharmacogenomics in Admixed Populations.

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The promise of precision medicine depends on capturing the full spectrum of human genomic diversity. Yet, conventional genome-wide association studies (GWAS) and pharmacogenomic prediction models often rely on global ancestry or broad population labels that may not adequately represent the complex genetic architecture of admixed populations. Caribbean Hispanics provide a compelling example, with extensive three-way admixture and substantial heterogeneity in linkage disequilibrium, allele frequencies, and ancestry-specific genetic effects. Using clopidogrel response in Caribbean Hispanics as a translational model, this seminar will explore how moving from global to local ancestry can uncover pharmacogenomic associations that may be missed by conventional GWAS. We will examine how local ancestry-informed approaches can reveal ancestry-specific effects and how integrating genomic, transcriptomic, and proteomic data can provide a more comprehensive understanding of variability in drug response. Finally, we will discuss how these discoveries can be translated into risk prediction and clinical decision-support strategies, while addressing challenges related to transferability, generalizability, and population representativeness. Together, this work illustrates how ancestry-aware, multi-omic approaches can help bridge genomic discovery and clinical implementation and advance more precise and equitable pharmacotherapy.