Pharmacogenomics: Discovery and Implementation.

A Symposium Sponsored by the International Union of Basic and Clinical Pharmacology (IUPHAR)

The 2018 International Congress of Genetics, organized under the auspices of the International Genetics Federation and coordinated by the Brazilian Society of Genetics (SBG) and the Latin American Association of Genetics (ALAG), was held in Foz do Iguaçu, Brazil, on September 10-14. The congress, attended by 1,100 delegates, from 32 countries in all continents, the larger contingent coming from Latin America, offered the opportunity of visiting the magnificent Iguaçu Falls (see photo) at the tri-country border of Brazil, Argentina and Paraguay.



A view of the Iguaçu Falls from the Brazilian side (photo kindly provided by Roger Gaedigk).

The symposium **Pharmacogenomics: Discovery and Implementation**, was coordinated by the Section of Pharmacogenetics/Genomics (PGx), and co-chaired by Guilherme Suarez-Kurtz, past-Chair of the PGx Section and Mara H. Hutz, past-Chair of SBG. The symposium attracted a large audience, at full-capacity lecture hall, and comprised talks by three invited speakers (see photo below) followed by two oral communications selected from the abstracts submitted to the congress.

Andrea Gaedigk, from Children's Mercy Kansas City, provided an in-depth overview of **The Pharmacogene Variation (PharmVar) Consortium,** which in 2017 became the new hub for pharmacogene nomenclature. PharmVar coordinates its efforts with PharmGKB and the Clinical Pharmacogenetics Implementation Consortium (CPIC) to provide standardized pharmacogene variation designation to the PGx community, to facilitate the translation of genotype into phenotype. At the core of PharmVar is a

state-of-the art database which now covers *CYP2C9, CYP2C19* and *CYP2D6*, but will expand beyond *CYP* genes prioritizing those in the CPIC guidelines, such as *NUDT15, DPYD* and *SLCO1B1*.

In his presentation entitled **Translational Pharmacogenomics: Discovery, Education, and Implementation,** Stuart A. Scott summarized the current state of translational pharmacogenomics at the Icahn School of Medicine at Mount Sinai, New York. Focus areas have included drug response association studies and allele discovery, multi-ethnic pharmacogenomics, personalized genotyping and survey-based education programs, and pre-emptive clinical testing implementation. Support for these programs has been provided, in part, by continued development of clinical pharmacogenomic testing assays. Barriers to adoption of these tests, such as provider awareness and education, and recent data on provider adoption of pre-emptive clinical pharmacogenomic testing were discussed.

Pharmacogenomics in Latin America: Impact of Population Admixture was examined by Guilherme Suarez-Kurtz, from Instituto Nacional de Câncer, Rio de Janeiro, and Brazilian Pharmacogenetics Network. The first part of the talk expanded on the notion that pharmacogenomic research and implementation in Latin America must take into account ethnic, cultural, socio-economical, scientific and technological disparities, in addition to genetic heterogeneity. Data on the frequency distribution of polymorphisms in *CYP3A5* and *NUDT15* among Latin American populations were presented to illustrate the pharmacogenomics implications of the population diversity in Latin America.



The invited speakers at the PGx symposium, from left to right: Guilherme Suarez-Kurtz, Andrea Gaedigk and Stuart Scott (photo kindly provided by Roger Gaedigk).

Mariana R Botton (Icahn School of Medicine at Mount Sinai) interrogated the 10q23.33 region across microarray data from 11,096 patients for structural variation at the

CYP2C locus. Seven deletions, all affecting both CYP2C18 and CYP2C19, and one duplication were detected. The observed frequency of these structural variants is consistent with the Database of Genomic Variants, and their identification will likely improve metabolizer phenotype prediction.

Marcelo R.S. Briones (Brazilian Initiative on Precision Medicine, BIPMED) explored the BIPMED Whole Exome Sequencing database for 106 Brazilian individuals, to infer populational structure and ethnicity bias. The data suggested that stratification of the study cohort based on mitochondrial haplogroups is more accurate than self-declared ethnicity and that deviation of Hardy-Weinberg Equilibrium in pharmacogenomic markers is haplogroup specific.

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