BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. DO NOT EXCEED FIVE PAGES.

NAME: Whirl-Carrillo, Michelle

eRA COMMONS USER NAME (credential, e.g., agency login): carrillo.michelle

POSITION TITLE: PharmGKB Director

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE (if applicable)	END DATE MM/YYYY	FIELD OF STUDY
Massachusetts Institute of Technology, Cambridge, MA	BS	1993	Biology
Stanford University, Stanford, CA	PHD	2002	Biophysics

A. Personal Statement

I am the Director of the PharmGKB (Pharmacogenomics Knowledge Base) and a Senior Research Scientist in the Department of Biomedical Data Science at Stanford University. My work focuses on pharmacogenomics, the study of the impact of genetics on drug response, and its application to personalized medicine and personal genomics. My projects range from basic research studying gene-variant-drug associations at PharmGKB to translation of pharmacogenomics information into the clinical setting via Clinical Pharmacogenetics Implementation Consortium (CPIC) guidelines. I am the co-director of the CPIC Informatics Working Group which works to reduce barriers to implementing the CPIC guidelines in the clinical electronic environment, in part by addressing Clinical Decision Support (CDS) in Electronic Health Record (EHR). I am particularly interested in translation of human genome sequencing data (whole genome and exome) to pharmacogenomic-based therapeutic recommendations that are actionable in the clinic.

1. Huddart R, Fohner AE, Whirl-Carrillo M, Wojcik GL, Gignoux CR, Popejoy AB, Bustamante CD, Altman RB, Klein TE. Standardized Biogeographic Grouping System for Annotating Populations in Pharmacogenetic Research. Clin Pharmacol Ther. 2019 May;105(5):1256-1262. PubMed PMID: 30506572; PubMed Central PMCID: PMC6465129.
2. Whirl-Carrillo M, McDonagh EM, Hebert JM, Gong L, Sangkuhl K, Thorn CF, Altman RB, Klein TE. Pharmacogenomics knowledge for personalized medicine. Clin Pharmacol Ther. 2012 Oct;92(4):414-7. PubMed PMID: 22992668; PubMed Central PMCID: PMC3660037.
3. McDonagh EM, Whirl-Carrillo M, Garten Y, Altman RB, Klein TE. From pharmacogenomic knowledge acquisition to clinical applications: the PharmGKB as a clinical pharmacogenomic biomarker resource. Biomark Med. 2011 Dec;5(6):795-806. PubMed PMID: 22103613; PubMed Central PMCID: PMC3339046.
4. Whirl-Carrillo M, Woon M, Thorn CF, Klein TE, Altman RB. An XML-based interchange format for genotype-phenotype data. Hum Mutat. 2008 Feb;29(2):212-9. PubMed PMID: 17994540.

B. Positions and Honors

Positions and Employment

2002 - 2007	Research Scientist/Scientific Curator, PharmGKB, Stanford University
2007 - 2008	Research Scientist/Lead Curator, PharmGKB, Stanford University
2008 - 2009	Curation Manager, 23andMe, Inc.
2009 - 2014	Assistant Director, PharmGKB, Stanford University
2014 - 2019	Associate Director, PharmGKB, Stanford University
2015 -	Senior Research Scientist, Stanford University
2019 -	PharmGKB Director, Stanford University

Other Experience and Professional Memberships

Honors

C. Contribution to Science

1. I am the Director of the Pharmacogenomics Knowledge Base (PharmGKB, www.pharmgkb.org). PharmGKB is the premier knowledge resource regarding the impact of genetic variation on drug response and contains thousands of manually curated gene-variant-drug relationships. The PharmGKB team publishes review articles of drug-centered pathways and very important pharmacogenes (many of which I have co-authored) and collaborates with researchers and clinicians around the globe to further pharmacogenomics knowledge and implementation. Having been a part of the PharmGKB team almost since its inception, I have co-developed the curation processes used and evaluated curation methods applied to annotating the scientific literature. Recently, I have helped develop a software tool called PharmCAT that leverages the curated pharmacogenomics knowledge in PharmGKB to translate genomic sequencing results into diplotypes and clinical guidance.

    a. Sangkuhl K, Whirl-Carrillo M, Whaley RM, Woon M, Lavertu A, Altman RB, Carter L, Verma A, Ritchie MD, Klein TE. Pharmacogenomics Clinical Annotation Tool (PharmCAT). Clin Pharmacol Ther. 2019 Jul 15;PubMed PMID: 31306493.
    b. Thorn CF, Whirl-Carrillo M, Hachad H, Johnson JA, McDonagh EM, Ratain MJ, Relling MV, Scott SA, Altman RB, Klein TE. Essential Characteristics of Pharmacogenomics Study Publications. Clin Pharmacol Ther. 2019 Jan;105(1):86-91. PubMed PMID: 30406943; PubMed Central PMCID: PMC6449845.
    c. McDonagh EM, Whirl-Carrillo M, Altman RB, Klein TE. Enabling the curation of your pharmacogenetic study. Clin Pharmacol Ther. 2015 Feb;97(2):116-9. PubMed PMID: 25670512; PubMed Central PMCID: PMC4352230.
    d. Rinaldi F, Clematide S, Garten Y, Whirl-Carrillo M, Gong L, Hebert JM, Sangkuhl K, Thorn CF, Klein TE, Altman RB. Using ODIN for a PharmGKB revalidation experiment. Database (Oxford). 2012;2012:bas021. PubMed PMID: 22529178; PubMed Central PMCID: PMC3332569.

2. I have done extensive work in knowledge modeling and terminology/ontology development for pharmacogenomics. I have constructed knowledge models for multiple types of data annotations in PharmGKB, including annotated drug labels from multiple international agencies, and variant and clinical annotations that identify and summarize specific variant-drug associations and their meta-data. I co-developed a terminology for classifying subjects of pharmacogenomics studies by biogeographical group used by PharmGKB. My early work in pharmacogenomics focused on the development of knowledge models and informatics tools to capture gene-drug relationships, raw genotype and phenotype data, and pathway knowledge. I co-developed the PharmGKB XML schema description of genotype, sequencing and SNP-discovery data; constructed data models for pharmacogenomic phenotype information; developed a preliminary ontology for data annotation; and co-designed the format and development process for the iconic PharmGKB drug-centered pathways.

    a. Huddart R, Fohner AE, Whirl-Carrillo M, Wojcik GL, Gignoux CR, Popejoy AB, Bustamante CD, Altman RB, Klein TE. Standardized Biogeographic Grouping System for Annotating Populations in Pharmacogenetic Research. Clin Pharmacol Ther. 2019 May;105(5):1256-1262. PubMed PMID: 30506572; PubMed Central PMCID: PMC6465129.
    b. Whirl-Carrillo M, McDonagh EM, Hebert JM, Gong L, Sangkuhl K, Thorn CF, Altman RB, Klein TE. Pharmacogenomics knowledge for personalized medicine. Clin Pharmacol Ther. 2012 Oct;92(4):414-7. PubMed PMID: 22992668; PubMed Central PMCID: PMC3660037.
    c. McDonagh EM, Whirl-Carrillo M, Garten Y, Altman RB, Klein TE. From pharmacogenomic knowledge acquisition to clinical applications: the PharmGKB as a clinical pharmacogenomic biomarker resource. Biomark Med. 2011 Dec;5(6):795-806. PubMed PMID: 22103613; PubMed Central PMCID: PMC3339046.

d. Whirl-Carrillo M, Woon M, Thorn CF, Klein TE, Altman RB. An XML-based interchange format for genotype-phenotype data. Hum Mutat. 2008 Feb;29(2):212-9. PubMed PMID: 17994540.

3. I have worked collaboratively on many pharmacogenomics research projects. As part of the PharmVar steering committee and multiple PharmVar gene expert panels, I focus on gene allele nomenclature. I have worked on nomenclature projects with the CDC concerning pharmacogenomic test result reports. I work to define variants that should be included on pharmacogenomic testing panels ss part of the AMP PGx working group. As part of multiple inter-disciplinary collaborations, I have annotated primary human genome sequence data with relevant pharmacogenomic associations that are potentially actionable for multiple subjects, including a family quartet where inheritance of pharmacogenomic variation can be observed.

   a. Pratt VM, Cavallari LH, Del Tredici AL, Hachad H, Ji Y, Moyer AM, Scott SA, Whirl-Carrillo M, Weck KE. Recommendations for Clinical CYP2C9 Genotyping Allele Selection: A Joint Recommendation of the Association for Molecular Pathology and College of American Pathologists. J Mol Diagn. 2019 Sep;21(5):746-755. PubMed PMID: 31075510.
   b. Gaedigk A, Sangkuhl K, Whirl-Carrillo M, Twist GP, Klein TE, Miller NA. The Evolution of PharmVar. Clin Pharmacol Ther. 2019 Jan;105(1):29-32. PubMed PMID: 30536702; PubMed Central PMCID: PMC6312487.
   c. Kalman LV, Agúndez J, Appell ML, Black JL, Bell GC, Boukouvala S, Bruckner C, Bruford E, Caudle K, Coulthard SA, Daly AK, Del Tredici A, den Dunnen JT, Drozda K, Everts RE, Flockhart D, Freimuth RR, Gaedigk A, Hachad H, Hartshorne T, Ingelman-Sundberg M, Klein TE, Lauschke VM, Maglott DR, McLeod HL, McMillin GA, Meyer UA, Müller DJ, Nickerson DA, Oetting WS, Pacanowski M, Pratt VM, Relling MV, Roberts A, Rubinstein WS, Sangkuhl K, Schwab M, Scott SA, Sim SC, Thirumaran RK, Toji LH, Tyndale RF, van Schaik R, Whirl-Carrillo M, Yeo K, Zanger UM. Pharmacogenetic allele nomenclature: International workgroup recommendations for test result reporting. Clin Pharmacol Ther. 2016 Feb;99(2):172-85. PubMed PMID: 26479518; PubMed Central PMCID: PMC4724253.
   d. Dewey FE, Chen R, Cordero SP, Ormond KE, Caleshu C, Karczewski KJ, Whirl-Carrillo M, Wheeler MT, Dudley JT, Byrnes JK, Cornejo OE, Knowles JW, Woon M, Sangkuhl K, Gong L, Thorn CF, Hebert JM, Capriotti E, David SP, Pavlovic A, West A, Thakuria JV, Ball MP, Zaranek AW, Rehm HL, Church GM, West JS, Bustamante CD, Snyder M, Altman RB, Klein TE, Butte AJ, Ashley EA. Phased whole-genome genetic risk in a family quartet using a major allele reference sequence. PLoS Genet. 2011 Sep;7(9):e1002280. PubMed PMID: 21935354; PubMed Central PMCID: PMC3174201.

4. I am co-Director of the Clinical Pharmacogenetics Implementation Consortium (CPIC) Informatics Working Group and the Stanford CPIC coordinator. With CPIC, I have worked to create standardized terminology for pharmacogene allele functionality and phenotype terms that can be used across platforms for the return of pharmacogenetic test results. We have also developed resources to support clinical decision support (CDS) for CPIC guideline implementation. We are creating a database and API to store all CPIC materials including prescribing recommendations and supplemental resources to enable querying of data, making it more accessible to electronic health record (EHR) systems. We continue to work to develop resources that will support clinical implementation of guidelines in the EHR. In addition, I have co-authored multiple CPIC guidelines and guideline updates.

   a. Caudle KE, Keeling NJ, Klein TE, Whirl-Carrillo M, Pratt VM, Hoffman JM. Standardization can accelerate the adoption of pharmacogenomics: current status and the path forward. Pharmacogenomics. 2018 Jul 1;19(10):847-860. PubMed PMID: 29914287; PubMed Central PMCID: PMC6123879.
   b. Caudle KE, Dunnenberger HM, Freimuth RR, Peterson JF, Burlison JD, Whirl-Carrillo M, Scott SA, Rehm HL, Williams MS, Klein TE, Relling MV, Hoffman JM. Standardizing terms for clinical pharmacogenetic test results: consensus terms from the Clinical Pharmacogenetics Implementation Consortium (CPIC). Genet Med. 2017 Feb;19(2):215-223. PubMed PMID: 27441996; PubMed Central PMCID: PMC5253119.

c. Caudle KE, Gammal RS, Whirl-Carrillo M, Hoffman JM, Relling MV, Klein TE. Evidence and resources to implement pharmacogenetic knowledge for precision medicine. Am J Health Syst Pharm. 2016 Dec 1;73(23):1977-1985. PubMed PMID: 27864205; PubMed Central PMCID: PMC5117674.

d. Hoffman JM, Dunnenberger HM, Kevin Hicks J, Caudle KE, Whirl Carrillo M, Freimuth RR, Williams MS, Klein TE, Peterson JF. Developing knowledge resources to support precision medicine: principles from the Clinical Pharmacogenetics Implementation Consortium (CPIC). J Am Med Inform Assoc. 2016 Jul;23(4):796-801. PubMed PMID: 27026620; PubMed Central PMCID: PMC6080683.

5. My graduate work focused on constructing and assessing molecular models of RNA, including the E.coli 30S ribosomal subunit, based on published biochemical and molecular experimental data. At the time, the x-ray crystal structure of the ribosome had proved difficult to elucidate so distance data gathered from experimental methods was the available knowledge and models were the best estimation. Subsequently, several ribosomal structures were resolved through x-ray crystallography, which allowed us to retrospectively assess the quality of the experimental distance data that had been previously reported in the literature. Distance measurements continued to be instrumental in understanding the dynamics of the ribosome not revealed by static structures.

   a. Gabashvili IS, Whirl-Carrillo M, Bada M, Banatao DR, Altman RB. Ribosomal dynamics inferred from variations in experimental measurements. RNA. 2003 Nov;9(11):1301-7. PubMed PMID: 14561879; PubMed Central PMCID: PMC1287051.

   b. Whirl-Carrillo M, Gabashvili IS, Bada M, Banatao DR, Altman RB. Mining biochemical information: lessons taught by the ribosome. RNA. 2002 Mar;8(3):279-89. PubMed PMID: 12003488; PubMed Central PMCID: PMC1370250.

   c. Joseph S, Whirl ML, Kondo D, Noller HF, Altman RB. Calculation of the relative geometry of tRNAs in the ribosome from directed hydroxyl-radical probing data. RNA. 2000 Feb;6(2):220-32. PubMed PMID: 10688361; PubMed Central PMCID: PMC1369908.

D. Additional Information: Research Support and/or Scholastic Performance