

Ryan Pabalate

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GENENTECH, INC., Dixon, California

Genetic Analysis Lab, System Specialist II

2017 – Present

- **Onboarding, managing, training contingent workers**
- **Oversee the process samples for the Genetic Analysis Lab (GAL). Using high-throughput technology, GAL is responsible for overseeing the production genotyping of ~900 rodent colonies for 500-600 scientists in gRED. Annually, we process about 350,000 animal biopsies in order to report out ~750,000 genotypes.**
- **Lead and participate in GAL and cross functional teams to improve quality and efficiency by taking advantage of emerging technologies:**
 - Developed and validated a re-queue system in CMS. This project was able to take sample from the CMS (Colony Management System, a customized of LIMS system) and re-queue those samples so they can be re-assayed in automation or re-assayed manually with a work template.
 - Developed and implemented the Beckman NX 8-Span to automate re-assays at 20uL in 96 plate format. Using Python programming, it is able to take work templates from CMS (Colony Management System, a customized of LIMS system) and format it to be used in the Beckman NX 8-Span instrument. With the design, it can do 7 X 96 plates, 59 DNA source plates, 2 types or more types of master mixes, and 96 diluted primer mixes.
 - Developed and implemented a primer search GUI. This project uses Python programming to search for primer stock, diluted primer mixes, and primers in a 384 plate. The search is searches through ~20 X 384 plates, ~2,700 primer stocks, and 800 diluted primer mixes with in a minute.
 - Developed and implemented DNA Concentration search. With the use of Python programming, a sample in CMS (Colony Management System) DNA concentration can be found within seconds, by searching using a plate number or sample ID number.
 - Developed and implemented automated workflow for the Cryo QC samples. These samples are out of CMS and are need to be genotyped for terminated projects before they are cryogenically frozen. Since these samples are out of CMS they needed to be worked on by hand which requires a lot of cut and paste, but with the use of Python programming, work templates, which include the pairing of assays and samples, are created automatically.
 - Redesign and developed a new process for the DNA giveback system. With the use of Python programming the DNA giveback system is able to show the

- user which samples are to aliquot, which samples are ready to be checked, and which samples are ready to be sent. It also automatically enters the samples in Smartsheets for data archiving.
- o Independently implemented the VIAFLO 384 for DNA transfer and a backup for PCR dilution.
 - o Independently designed and implemented two Combi nL in the ECHO Access system.
 - o Designed a custom reservoir, which was able to purchase through the Research Innovation Fund. The reservoir was used to pool multiple 384 well plates into a reservoir to create a DNA library.
 - o Coordinated and oversee the transition of self-purchased reagents and consumable to using gSupply.
 - o Provide 3D printing services. Created organ models and created 3D prints to improve instrumentation.
 - o Currently developing and testing genotyping using NGS-based workflow. Currently optimizing chemistries and developing genetic analysis software in order to process thousands of animal samples per day. This project requires redesigning at least 30 assays to fit NGS from our current 3730 and Taqman platforms.
 - o Currently developing a system using Benchling automation for samples out of CMS (Colony Management System, a customized of LIMS system).
 - o Currently developing automation using the QiAcuity run digital PCR instead of CNV (Copy Number Variation). Using the ECHO 525 with the QiAcuity will allow us to run an avg of 1000 samples a day without using calibrators and saving money on reagents.
 - o Currently developing automation to detect volumes in the 384 ECHO plates, the diluted primer mixes, primer stock, and PCR plates using the BioMicroLab Volume Check 384.
 - o Scheduled and planned an effective way to keep employees social distanced during the COVID-19 pandemic. Genotyping had never stopped during the pandemic.
 - **Represented the Genetic Analysis Lab in the Leadership Team in the early stages of the COVID Pandemic.**
 - o Presented updates on the Genetic Analysis Lab during Molecular Biology/ department meetings.
 - o Updated the leadership team with GAL's method of social distancing and schedules.
 - o Updated the leadership team of the effects on GAL's as mice cages ramped up.
 - o Update GAL of all changes the leadership team decides.

Genetic Analysis Lab, Scientific Researcher

2011 – 2017

- **Design, process, and analyze data for the Genetic Analysis lab using the AB 9700 Thermalcyclers, BioRad CT1000 and the AB3730xl DNA Analyzer.**
- **Lead and participate in GAL and cross functional teams to improve quality and efficiency by taking advantage of emerging technologies:**
 - Assign weekly responsibilities for four full time employees and 1-4 contractors.
 - Responsible for overseeing all members of Genetic Analysis Lab production training.
 - Troubleshoot and maintain all instruments in the lab (Beckman FX (x2), Beckman NX (x2), ECHO 525 (x2), OASIS LM 600, AB3730xl DNA Analyzer (x2), BioRad CFX (x4), AB 9700 Thermalcyclers, BioRad CT1000, BioRad QX20 ddPCR, and Thermo Scientific Ion Torrent (x2)).
 - Ensure that results are consistently being reported within the 2-3 day turnaround time.
 - Created and validated the protocol for the ECHO 525 acoustic droplet ejection (ADE) and Labcyte Access system for PCR assembly. This required designing the GAL GUI to include ECHO functionality. With the use of the ECHO, the time for the 384 gDNA samples with their respective assays was reduced from 67 minutes to 10 minutes.
 - Created and validated the protocol for the Liquid Re-array System which fully automates sample consolidation. After determining the failures on the vendor's side and teaching them how to optimize their instrument timings, the processing speed had increased nearly 100% (4 plates from 90 minutes to 45 minutes). Along with changing the process/ protocol of when to start tail processing this instrument frees 1 FTE and shortens the turnaround time from 3-4 days to 2-3 days.
 - Created and validated the protocol to implement the GAL DNA extraction. The GAL DNA extraction method uses the Beckman FX with the Agencourt DNAdvance kit. This system is currently the highest throughput mammalian tissue gDNA prep system available. This system allows us to extract pure gDNA using green chemistry to yield a full 96 prepped box every 20 minutes.
 - Modified the lab instruments to accommodate the switch from a 96 well plate to a 384 plate. This process includes validating the BioRad 384 thermocyclers, creating and validating the protocol for the qPCR genetic analyzer, creating a protocol on the LM 600 OASIS to dilute 384 plates, creating and validating the protocol for the Beckman NX 384 well head, and modifying the AB3730xl DNA Analyzer to read 384 plates. The use of 384 plates decreased cost by using less volume, less consumables, and less reagents. It also decreased the use of instruments, instead of using 4 thermalcyclers for 384 samples, only 1 instrument is needed.
 - Created a workflow for Copy Number Variation (CNV) on the Tecan EVO. This includes creating Excel macros for both normalization of samples and PCR assembly for CNV. This workflow transitioned from a workflow which required a lot of hand pipetting. With the use of the Tecan EVO, we were able to make fewer mistakes and make the CNV pipeline more efficient.

- o Created a workflow for CNV on the ECHO 525 system. This includes creating an Excel macro for PCR assembly for CNV. Using the ECHO 525 decreased reagent use and decreased the turnaround time for CNV.
- o Decreased GAL's reagent spending by nearly half from 2.0 Mil (2012) to 1.1 Mil (2016) by negotiating with vendors and distributors.
- o Independent managing the relationship Integrative DNA outsource vendor, Integrative DNA Technologies (IDT). We've outsourced our complex ~5,400 oligos to IDT replacing the efforts of 1 GAL FTE. Managing includes having to be in constant communication with IDT on the performance of the assays and making sure new assays are plated biweekly and shipped to Dixon for just-in-time supply to our ECHO reaction assembly workstation.
- o Tested and implemented the VIAFLO 96 pipette used for DNA extraction and DNA transfer
- o Independently validated and implemented the BioTek plate reader and stacker. This was used for to QC DNA quality and quantification. A 96 well plate take less than 5 minutes to read and calculate the DNA concentration, and take 10 minutes to get the spectral.

Genotyping/ Genetic Analysis Lab, Research Assistant

2009

– 2011

- **Process samples for the Genetic Analysis Lab (GAL). Using high-throughput technology, GAL is responsible for overseeing the production genotyping of ~900 rodent colonies for 500-600 scientists in gRED. Annually, we process about 350,000 animal biopsies in order to report out ~750,000 genotypes.**
- **Participate in GAL and cross functional teams to improve quality and efficiency by taking advantage of emerging technologies:**
 - o Partnered with the Sanger Sequencing Core in South San Francisco to sequence over 100 loci to help design Taqman assays and to troubleshoot assays. With the sequences, assays from the 3730 platform were converted to the Taqman platform. The Taqman platform, when compared to the 3730 platform, has more specificity, less subjectivity, and a faster turnaround time of 1-2 days rather than the 3730 platform of 2-3 days.
 - o Independently redesigned the DNA giveback system. This is a delivery system to provide investigators in South San Francisco extracted gDNA. This system includes an Excel macro which would provide GAL and investigators a list of colonies and samples which will be aliquoted and sent for delivery.
 - o Independently validated and implemented gelRed as a substitute for Ethidium Bromide. With gelRed, GAL no longer has to work with Ethidium Bromide which is a mutagen which is a health and environmental hazard.
 - o Validated and implemented Taqman genotyping using the ABI7900
 - o Designed assays 5 Taqman Assays (RON, RAG2, APOBEC1, NIK, OVACD8_APO)
 - o Help facilitate the move from South San Francisco to Dixon and validate all instrumentations.

- o Independently designed and validated an ELISA for mice fecal testing for corticosterone. The experiment was used to see if the detection of corticosterone in the mice could correlate to mice's stress level.

Bio Analytical Assays, Research Assistant

2006 – 2009

- Performed pharmacokinetic and antibody ELISA in the BioAnalytical Assays (BA) department. The BA implements biological matrix assays and automated systems in a compliant environment to deliver the highest quality data for Genentech's clinical and preclinical studies. Research assistants must be trained in GLP and 21 CFR Part 11.
 - o Validated system for GLP, the TECAN ELISA station, AT Hamilton Dilutor and Tecan Aquarius, were used to run up to 20 ELISA plates within 4 hours.
 - o Ran electrochemiluminescence assays (ECLA) for some clinical samples.
 - o Train new employees the processes within the workgroup.
- Study Coordinator for 7 studies in Rituxan. Reviewed protocols and dilution memos, handle assay documentation and maintain awareness of project timelines/priorities to schedule sample analysis.
- Assay Maintainer for all Rituxan assays. Assay Maintainer ensures sufficient reagent supply and performance, extend reagent expiration before reagent expires and/or incorporate new reagents, monitors assay performance and quality through quantitative measures, performs partial validations as required, updates Assay Validation Reports, reviews and updates SOPs current practices and any new information, maintain a history of the assays, and ensure worksheets and master and study assays are up to date.
- Member of the Notebook Committee which transition compliant lab notebooks into compliant lab binders. The lab binder reduced the cutting and pasting paper into notebooks. Lab binders also kept things in order and did not require signatures for every page.
- Managed pipet outsourcing to Rainin for calibration. The responsibilities included making sure calibration certificates were filled out correctly; making sure pipettes are calibrated on time and make sure there are spares for each pipet.

Cell Genesys, Inc., South San Francisco, California

2004-2006

Assay Services, R&D Associate

- Perform routine and non-routine immunoassays (e.g. ELISAs), PCR-based assays (e.g. TaqMan), and cell-based assays (e.g. plaque assays and cell secretion assays), according to defined procedures in the Assays Services department.

- o Maintain detailed documentation of assay performance.
- o Write and modify procedures as needed.
- o Perform peer review of work from other Assay Services associates.
- o Perform moderately complex quantitative data analysis and trending.
- o Coordinate scheduling and execution of activities with multiple internal client groups (e.g. Process Development, Assay Development, Research, and Clinical) for timely completion of service requests.
- o Track samples and maintain sample inventory
- o Track/tabulate activities and communicate in monthly reports.
- o Share responsibilities for routine lab operation and maintenance.

Awards:

- o gRed 2012 Key Researcher Award
- o gRed 2015 Key Researcher Award

Education:

- o University of California at Berkeley, Bachelor of Arts in Integrative Biology, December 2002
- o City College of San Francisco, Biotechnician Certificate, December 2003

Publication:

Carol Cain-Hom, **Ryan Pabalate**, Anna Pham, Hetal N. Patel, Rhonda Wiler, and J. Colin Cox (2016). Mammalian genotyping using acoustic droplet ejection for enhanced data reproducibility, superior throughput, and minimized cross-contamination. *J Lab Autom*, **21**, 37-48.

Oral Presentations:

J. Colin Cox, Mykle Gaynor, **Ryan Pabalate**, and Gregg Sy “3D printing special interest group 1st annual meeting: background, applications, and answers.” February 2-6, 2019, 8th Annual Society for Laboratory Automation and Screening (SLAS) Conference and Exhibition, Washington DC.

Ryan Pabalate and J. Colin Cox, “3D printing to cut out the middle man: rapid prototyping to innovate robots and save money.” February 2-6, 2019, 8th Annual Society for Laboratory Automation and Screening (SLAS) Conference and Exhibition, Washington DC.

Ryan Pabalate, Hetal Patel, and J. Colin Cox, “Breaking through the next HTP barrier: the continuing evolution of genetic analysis in Dixon.” November 20, 2017, Laboratory Automation & Robotics Forum Series, Genentech, Inc., South San Francisco, CA

J. Colin Cox, Carol Cain-Hom, **Ryan Pabalate**, Anna Pham, and Rhonda Wiler, “Ultra-high throughput genotyping: a novel platform that curtails cross-contamination and increases data-quality”. January 23-27, 2016, 5th Annual Society for Laboratory Automation and Screening (SLAS) Conference, San Diego, CA.

J. Colin Cox, Carol Cain-Hom, **Ryan Pabalate**, Anna Pham, and Rhonda Wiler, “Quashing qPCR contamination: ADE is more than just faster and smaller”. January 25, 2016, Labcyte Tutorial at SLAS 2016, San Diego, CA.

J. Colin Cox, Carol Cain-Hom, **Ryan Pabalate**, Anna Pham, and Rhonda Wiler, “Sound and the furry: A tail of using ADE for complex, HTP genotyping”. October 28-29, 2015, Labcyte Symposium, Boston, MA.

J. Colin Cox, **Ryan Pabalate**, Carol Cain-Hom and Rhonda Wiler, “Using sound to pipette: massive reduction of cross-contamination and other tasty treats”. April 21, 2015, Integrated DNA Technologies (IDT) Inc., Coralville, IA.

- J. Colin Cox, Carol Cain-Hom, **Ryan Pabalate**, Anna Pham and Rhonda Wiler, "Achieving massive throughput and quality gains via acoustic-dispensing technology: Genentech's new workflow for mammalian genotyping". February 7-11, 2015, 4th Annual Society for Laboratory Automation and Screening (SLAS) Conference and Exhibition, Washington DC.
- J. Colin Cox, Anna Pham, Carol-Cain Hom, **Ryan Pabalate** and Rhonda Wiler, "Genotyping genetically engineered animal models: preparing for increased needs and new paradigms". June 4th, 2014, Labcyte Inc., Sunnyvale, CA
- J. Colin Cox, Robert Schwingendorf, Carol Cain-Hom, Anna Pham, Gregg Sy, **Ryan Pabalate**, Jessenia Perez, Emily Hunley, and Rhonda Wiler, "A High-Throughput & Robust Genotyping Pipeline at Genentech's Research Support Facility (gRsf)". October 2-6, 2011, 62nd American Association for Laboratory Animal Science (AALAS) National Meeting, San Diego, CA.

Posters:

- Gregg Sy, Hetal N. Patel, **Ryan Pabalate**, Lina Planutyte, and J. Colin Cox, "Incorporating Python programming with 3D printing: the ultimate open-source marriage for customized, vendor-free laboratory solutions". February 2-6, 2019, 8th Annual Society for Laboratory Automation and Screening (SLAS) Conference and Exhibition, Washington DC.
- Hetal N. Patel, **Ryan Pabalate**, Deborah Siler, Carol Cain-Hom, Emily Hunley, Anna Pham, Maria Martinez, Gregg Sy, Sanjeet Aujla, and J. Colin Cox. Implementation of acoustic droplet ejection (ADE) for high throughput mammalian genotyping in rapidly changing R&D landscapes. January 23-27, 2016, 5th Annual Society for Laboratory Automation and Screening (SLAS) Conference, San Diego, CA.
- Emily Hunley, Deborah Siler, Carol Cain-Hom, **Ryan Pabalate**, Anna Pham, Maria Martinez, Gregg Sy, Rhonda Wiler, and J. Colin Cox. New challenges in mammalian genotyping: complex loci, droplet digital PCR and pipetting with sound. August 9-12, 2015, UC Davis Transgenic Animal Research Conference (TARC) X Conference, Tahoe City, CA.
- J. Colin Cox, Carol Cain-Hom, Maria Martinez, **Ryan Pabalate**, Anna Pham, and Rhonda Wiler, "Migrating to acoustic-based liquid dispensing for ultra-high throughput genetic screening of cancer and neurology models used in drug discovery efforts". February 7-11, 2015, 4th Annual Society for Laboratory Automation and Screening (SLAS) Conference, Washington DC.
- Ryan Pabalate**, Robert Schwingendorf, Deborah Siler, Gregg Sy, and J. Colin Cox, "A Method for the Conversion of PCR-based Fragment Analysis Genotyping Assays to 5' Nuclease Assay (TaqMan)". October 2-6, 2012, Mouse Molecular Genetics 2012, Pacific Grove, CA.
- Robert Schwingendorf, Vida Asghari, Tamara Franzmann, Doug Garrett, Carol Cain-Hom, Emily Hunley, **Ryan Pabalate**, Gregg Sy, Anna Pham, Jessenia Perez, Rhonda Wiler, and J. Colin Cox, "Advantageous Outcomes by

Transitioning From PCR Fragment Analysis-Based Genotyping to 5' Nuclease Assay (TaqMan™) in an Ultrahigh-Capacity Genetic Model Facility". February 4-8, 2012, 1st Annual Society for Laboratory Automation and Screening (SLAS) Conference and Exhibition, San Diego, CA.

Anna Pham, **Ryan Pabalate**, Daniel Tran, Carol Cain-Hom, Robert Schwingendorf, Rhonda Wiler, and J. Colin Cox, "Development of a Copy Number Variation (CNV) Analysis Methodology for Rapid Gene Copy Determination of Genetic Models in the Context of a High-Throughput Genetic Analysis Pipeline". February 4-8, 2012, 1st Annual Society for Laboratory Automation and Screening (SLAS) Conference and Exhibition, San Diego, CA.

Robert Schwingendorf, Carol Cain-Hom, Anna Pham, Gregg Sy, **Ryan Pabalate**, Jessenia Perez, Emily Hunley, Rhonda Wiler, and J. Colin Cox, "A High-Throughput & Robust Genotyping Pipeline at Genentech's Research Support Facility (gRsf)". October 24-26, 2011, 10th Transgenic Technology Meeting (ISTT), St. Pete Beach, FL.

Internal Posters

Hetal N. Patel, Deborah Siler, Carol Cain-Hom, **Ryan Pabalate**, Anna Pham, Emily Hunley, Maria Martinez, Gregg Sy, Sanjeet Aujla, Rhonda Wiler, and J. Colin Cox, "Genetic Analysis Lab: Typing your complex animals with clever assays and cool new tools". Poster presented October 11-13, 2015 for Asilomar 2015 Research Conference.

Emily Hunley, Deborah Siler, Carol Cain-Hom, Robert Schwingendorf, Anna Pham, **Ryan Pabalate**, Maria Martinez, Gregg Sy, Kimberly Pretchtl, William Christie, Rachel Miller, Merritt Clark, Doug Garrett, Tamara Franzmann, Erik Bierwagen, Rhonda Wiler & J. Colin Cox, "Genetic Analysis: Meeting the needs of gRED now and in the future". Poster presented May 18-20, 2014 for Asilomar 2014 Research Conference.

Orla Cagney, Carol Cain-Hom, Aiman Diaz, Emily Hunley, **Ryan Pabalate**, Jessenia Perez, Anna Pham, Rob Schwingendorf, Deborah Siler, Gregg Sy, Rhonda Wiler & J. Colin Cox, "Mouse Genetics Analysis Lab (mGAL) – More than genotyping". Poster presented October 21-24, 2012 for Asilomar 2012 Research Conference.

Carol Cain-Hom, Rob Schwingendorf, Anna Pham, Jessenia Perez, Emily Hunley, **Ryan Pabalate**, Gregg Sy, Rhonda Wiler & J. Colin Cox, "gRSF – High-throughput solutions and innovations in the Genotyping Lab". Poster presented May 15-18, 2011 for Asilomar 2011 Research Conference.