

Curriculum Vitae

Bongsoo Park, Ph. D.

Bioinformatics Scientist
Department of Environmental Health and Engineering
Johns Hopkins Bloomberg School of Public Health
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Education and Training

- 2017, Post-doc** Center for Eukaryotic Gene Regulation, The Genome Science Institute, Penn State University
Advisor: B. Franklin Pugh
- 2013, Ph.D** The Pennsylvania State University (Bioinformatics and Genomics)
Advisor: Seogchan Kang, Co-Advisor: Istvan Albert
- 2006, B.S** Seoul National University, South Korea (Applied Biology and Chemistry)
Advisor: Yong-Hwan Lee
- 2006, B.A** Seoul National University, South Korea (Program in Information and Multimedia Culture)

Research and Professional Experience

Research Associate, Bioinformatics and Genomics (2017-current)

Center for Global Health, Biswal Lab
Department of Environmental Health and Engineering
Johns Hopkins University, Bloomberg School of Public Health
Toxico-Epigenomics (TaRGET), Integrative Multi-omics Analysis, Epigenomics Roadmap Project
ChIP-Seq, ATAC-Seq, RNA-seq, DNA-methylation, Deconvolution of mixture cells (blood & liver)

Research Associate, Bioinformatics (2013-2017)

Center for Eukaryotic Gene Regulation
Department of Biochemistry and Molecular Biology
The Pennsylvania State University, USA
Bioinformatics of Gene Regulation, Web-based ChIP-Exo Analysis Platform

USDA-NIFA Microbial Genomics Fellow (2011-2013)

Department of Plant Pathology and Environmental Microbiology
The Pennsylvania State University, USA
Development of plant pathogen database, De-novo assembly of fungal plant pathogens

Graduate Research Assistant and Teaching Assistant (2008-2011)

Bioinformatics and Genomics, Huck Institutes of the Life Sciences
The Pennsylvania State University, USA
Development of plant pathogen database, IBIOS/BMMB 551 (Genomics)

Research Support

1. NIH U01 grant, TaRGET project, Research Scientist, Bioinformatics & Metadata committee, PI: *Shyam Biswal*
2. NIH R01 grant, NCI Lung Adenocarcinoma research, Bioinformatics support, PI: *Shyam Biswal*
3. NIH R21 grant under review, Co-Investigator (Transcriptome analysis support), PI: *Murugappan Ramanathan*
4. NIH P30 grant under review, Baltimore Environmental Health Center, Multi-omics Analysis, PI: *Shyam Biswal*
5. AHA career development grant under review, Cardiovascular disease and Multi-omics Analysis, PI: *Bongsoo Park*

Research Interests: Bioinformatics and Genomics

1. Research infrastructure: Reproducible bioinformatics for Eukaryotic Gene Regulation Studies
 - a. Galaxy-based ChIP-Exo Analysis Platform (2014-2016)
 - b. The automation of the bioinformatics workflow, and quality control pipeline (2015-2016)
 - c. Yeast Regulome project (2016-current)
 - d. Heat shock epigenome analysis (2016-current)
2. Global differential regulation of *Methanosarcina acetivorans* acetoclastic pathway deduced via ChIP-Exo (In collaboration with Ferry lab at Penn State University, 2015-2017)
3. Eukaryotic Comparative Epigenomics Platform, Transcription Factor Database
4. The computational genomics for detecting variations (SNP/SV) in the regulatory regions from cancer cells (In collaboration with Kim lab at Geisinger Health System, 2016-current)
5. SAGA transcription regulation (In collaboration with Kornberg lab, Stanford School of Medicine)
6. Toxic-Epigenomics (Biswal Lab at Johns Hopkins University, 2017-current)
7. HISAT-bisulfite: Population based Whole Genome Bisulfite Sequencing platform (In collaboration with Kim lab at University of Texas South Western Medical School, 2017-current)

Honors and Awards

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| 1. NSF-sponsored Travel Grant to attend the 2010 <i>Oomycete</i> Genetic Network Meeting in Toulouse | 2010 |
| 2. CyberScience Summer Student Research Award from Institute for CyberScience, Penn State. | 2011 |
| 3. USDA-NIFA Microbial Functional Genomics Fellowship (up to four semesters of support) | 2011 |

Professional Activities

1. Organizer for Cancer Genomics Journal Club at Penn State University, University Park
2. Member of Bioinformatics & Genomics and Plant Pathology Association at Penn State University
3. Member of the International Society for Computational Biology
4. Member of American Association for the Advancement of Science
5. Korean-American Scientists and Engineers Association (KSEA)
6. Scientific Program Committee and Paper reviewer, Translational Bioinformatics Conference 2017

Teaching Experience

Teaching Assistant for IBIOS/BMMB 551 (Genomics), Penn State University	Fall, 2010
Teaching Assistant for IBIOS/BMMB 551 (Genomics), Penn State University	Fall, 2011
Invited lecture for Molecular Toxicology 187.632.01 (Topic: Genomics), Johns Hopkins University	Fall, 2017
Invited lecture for Molecular Toxicology 187.682.01 (Topic: Omics tools), Johns Hopkins University	Fall, 2017
Lectures for Genomics, under review, Johns Hopkins Bloomberg School of Public Health	Fall, 2018

Peer-reviewed Publications

1. **Park B**, Rengasamy P, Yin J, Rao X, Reyes-Caballero H, Rajagopalan S, Biswal SS[†]. [Research paper](#): Epigenomic marks of air pollution and insulin resistance. *Manuscript in preparation*
2. **Park B**[†], and Biswal SS[†]. [Review paper](#): Epigenomic signatures and computational tools for deconvolution of blood mixture cells. *Manuscript in preparation* ([†] corresponding author)
3. **Park B**, Tharakan A, Rengasamy P, Yin J, Wang D, Rajagopalan S, Biswal S, Ramanathan M. [Research paper](#): Global transcriptome and epigenetic analysis in mouse nasal tissue exposed to ambient air pollution PM_{2.5} *Manuscript in preparation*
4. Reyes-Caballero H, **Park B**, and Biswal SS. [Research article](#): Integrative analysis of transcriptome, methylome with metabolite data from cigarette smoke exposed mice. *Manuscript in preparation*
5. Lai WKM, Yamada N, Shao D, Von Kuster G, **Park B**, Mahony S, and Pugh BF. [Method paper](#): Galaxy-based ChIP-exo analysis platform. *Manuscript in preparation*

6. Nagai S*, **Park B**, Pugh BF, and Kornberg R. *Research article*: Structural inference of SAGA transcription regulation using ChIP-Exo. *Manuscript in preparation*
7. Almishwat M*, **Park B***, Murakami K, Mahony S, Pugh BF, and Ferry JG. *Research article*: Global differential regulation of *Methanosarcina acetivorans* acetoclastic pathway deduced via ChIP-Exo. *Manuscript in preparation* (*co-first author)
8. Vinayachandran V, Reja R, **Park B**, Rossi MJ, and Pugh BF. *Research article*: Genome-wide reprogramming of transcription machinery under physiological perturbation in budding yeast. *Manuscript in preparation*
9. Krietenstein N, Wal M, Watanabe S, **Park B**, Peterson CL, Pugh BF, and Korber P. Genomic nucleosome organization reconstituted with pure proteins. *Cell*. 2016 Accepted.
10. de Dieuleveult M, Yen K, Hmitou I, Depaux A, Boussouar F, Dargham DB, Jounier S, Humbertclaude H, Ribierre F, Baulard C, Farrell NP, **Park B**, Keime C, Carrière L, Berlivet S, Gut M, Gut I, Werner M, Deleuze JF, Olaso R, Aude JC, Chantalat S, Pugh BF, Gérard M. Genome-wide nucleosome specificity and function of chromatin remodellers in ES cells. *Nature*. 2016 Feb 04;530:113-116
11. Han GC, Vinayachandran V, Bataille AR, **Park B**, Chan-Salis KY, Keller CA, Long M, Mahony S, Hardison RC, Pugh BF. Genome-wide organization of GATA1 and TAL1 determined at high resolution. *Molecular and Cellular Biology*. *Mol Cell Biol*. 2015 Oct 26;36(1):157-72
12. Chang GS, Chen XA, **Park B**, Rhee HS, Li P, Han KH, Mishra T, Chan-Salis KY, Li Y, Hardison R, Wang Y, Pugh BF. A comprehensive and High Resolution Genome-wide Response of p53 to Stress. *Cell Reports*. 2014 Jul 24;8(2):514-27
13. **Park B***, Martin FN*, Geiser DM, Kim HS, Mansfield M, Nikolaeva E, Park SY, Coffey M, Russo J, Kim S, Balci Y, Abad G, Burgess T, Grunwald NJ, Cheong K, Choi J, Lee YH, Kang S. *Phytophthora* Database 2.0: Update and future direction. *Phytopathology*. 2013 Dec; 103(12):1204-8 (*co-first author)
14. O'Donnell K, Humber RA, Geiser DM, Kang S, **Park B**, Robert V, Crous PW, Johnston P, Aoki T, Rooney AP, Rehner SA. Phylogenetic diversity of insecticolous fusaria inferred from multilocus DNA sequence data and their molecular identification via FUSARIUM-ID and Fusarium MLST. *Mycologia*. 2012 104:427-445.
15. Moktali V, Park J, Fedorova-Abrams ND, **Park B**, Choi J, Lee YH, Kang S. Systematic and searchable classification of cytochrome P450 proteins encoded in fungal and oomycete genomes. *BMC Genomics*. 2012 **13**: 525 doi:10.1186/1471-2164-13-525.
16. **Park B***, Park J*, Cheong KC, Choi J, Jung K, Kim D, Lee YH, Ward TJ, O'Donnell K, Geiser DM, Kang S. Cyber infrastructure for *Fusarium*: three integrated platforms supporting strain identification, phylogenetics, comparative genomics and knowledge sharing. *Nucleic Acids Research*. 2011 39 (Database issue):D640-646. (*co-first author)
17. O'Donnell K, Sutton DA, Rinaldi MG, Sarver BA, Balajee SA, Schroers HJ, Summerbell RC, Robert VA, Crous PW, Zhang N, Aoki T, Jung K, Park J, Lee YH, Kang S, **Park B**, Geiser DM. An Internet-Accessible DNA Sequence Database for Identifying Fusaria from Human and Animal Infections. *Journal of Clinical Microbiology*. 2010 48(10):3708-3718.
18. Kang S*, Mansfield MA*, **Park B***, Geiser DM, Ivors KL, Coffey MD, Grünwald NJ, Martin FN, Lévesque CA, Blair JE. The promise and pitfalls of sequence-based identification of plant-pathogenic fungi and oomycetes. *Phytopathology*. 2010 100(8):732-737. (*co-first author)
19. Lee W, Park J, Choi J, Jung K, **Park B**, Kim D, Lee J, Ahn K, Song W, Kang S, Lee YH, Lee S. IMGd: an integrated platform supporting comparative genomics and phylogenetics of insect mitochondrial genomes. *BMC Genomics*. 2009 10(1):148
20. Park J, Park J, Jang S, Kim S, Kong S, Choi J, Ahn K, Kim J, Lee S, Kim S, **Park B**, Jung K, Kim S, Kang S, Lee YH. FTFD: an informatics pipeline supporting phylogenomic analysis of fungal transcription factors. *Bioinformatics (Oxford, England)*. 2008 24(7):1024-1025.

21. Park J, **Park B**, Jung K, Jang S, Yu K, Choi J, Kong S, Park J, Kim S, Kim H, Kim S, Kim JF, Blair JE, Lee K, Kang S, Lee YH. CFGP: a web-based, comparative fungal genomics platform. *Nucleic Acids Research*. 2008 36(Database issue):D562-571.
22. Park J*, **Park B***, Veeraraghavan N*, Jung K, Lee Y, Blair E J, Geiser M D, Isard S, Mansfield A M, Nikolaeva E, Park S, Russo J, Kim H S, Greene M, Ivors L K, Balci Y, Peiman M, Erwin C D, Coffey D M, Rossman A, Farr D, Cline E, Grünwald J N, Luster G D, Schrandt J, Martin F, Ribeiro K O, Makalowska I, Kang S. *Phytophthora* Database: A Forensic Database Supporting the Identification and Monitoring of *Phytophthora*. *Plant Disease*. 2008 92(6):966-972. (*co-first author)
23. Park J, Lee S, Choi J, Ahn K, **Park B**, Park J, Kang S, Lee YH. Fungal cytochrome P450 database. *BMC Genomics*. 2008 9:402
24. Jung K, Park J, Choi J, **Park B**, Kim S, Ahn K, Choi J, Choi D, Kang S, Lee YH. SNUGB: a versatile genome browser supporting comparative and functional fungal genomics. *BMC genomics*. 2008 9(1):586
25. Jeon J, Park SY, Chi MH, Choi J, Park J, Rho HS, Kim S, Goh J, Yoo S, Choi J, Park JY, Yi M, Yang S, Kwon MJ, Han SS, Kim BR, Khang CH, **Park B**, Lim SE, Jung K, Kong S, Karunakaran M, Oh HS, Kim H, Kim S, Park J, Kang S, Choi WB, Kang S, Lee YH. Genome-wide functional analysis of pathogenicity genes in the rice blast fungus. *Nature Genetics*. 2007 39(4):561-565.
26. Park J, Kim H, Kim S, Kong S, Park J, Kim S, Han HY, **Park B**, Jung K, Lee YH. Comparative Genome-Wide Analysis of GATA Transcription Factors in Fungi. *Genomics & Informatics*. 2006 4:147-160.

News Letters

1. Inderbitzin P, **Park B**, *et al.* VertShield – an online resource for *Verticillium* species identification and research. *Phytopathology news*
2. Discovered: How to unlock in accessible genes. *Penn State Science News*. 29 January, 2016
3. Research network helps Penn State researchers study gene regulation. *Penn State the Institutes for CyberScience News*. 2 November, 2016

Book Chapters

1. Kang S, Mansfield M, **Park B**, Martin F. (2016) Molecular identification of *Phytophthora* isolates using a DNA sequence based approach and the *Phytophthora* Database. In: K. Ivors (ed.) *Laboratory Protocols for Phytophthora Species*. APS Press, St. Paul, MN

Presentations and Talks

The 2017 American Diabetes Association. Bongsoo Park, et al. Epigenomic Marks of Air Pollution and Insulin Resistance

The 2017 TaRGET-II Project update at NIEHS, National Institute of Environmental Health Science. Shyam Biswal, and Bongsoo Park. Air Pollution PM_{2.5} and insulin resistance

Invited Talk 2016, Johns Hopkins Department of Environmental Health Sciences. Bongsoo Park. Epigenome analysis using High-resolution biochemical assays and Reproducible web-framework

The Spring 2015, Penn State Genomics Seminar, Center for Systems Genomics. Bongsoo Park. Research Cyber-infrastructure for Eukaryotic Gene Regulation Studies

The 2014 Galaxy Community Conference, Lightning Talk. Bongsoo Park. Plan for Galaxy based ChIP-Exo Analysis Platform

Invited lecture for Introduction to Genomics Course (IBIOS/BMMB 551 Genomics). Bongsoo Park. Analyzing Next Generation Sequencing (NGS) data through Web-based Tools: GALAXY, BLAST, and ClustalW

The 2012 American Phytopathological Society. David M Geiser, Bongsoo Park, et al. Challenges and opportunities for species recognition in *Fusarium* provided by genomics

The 2011 Asia Pacific Bioinformatics Conference. Bongsoo Park, et al. Cyber-infrastructure for *Phytophthora* (CiP): A comprehensive cyber-infrastructure supporting research and education on *Phytophthora*

The 2009 American Phytopathological Society. Bongsoo Park, et al. *Phytophthora* and *Pythium* Databases: A growing cyber-infrastructure supporting the identification and monitoring of major pathogen groups

The 2007 Korea Genome Organization Conference. Bongsoo Park, et al. Phyloviewer, web-based integrated environment for phylogenomic analysis based on the Bioinformatics Portal System

The 2006 Korea Society of Bioinformatics Conference. Bongsoo Park, et al. Object System : A new standard for integrating heterogeneous biological data object-oriented bioinformatics system

References

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