

CHANDAN PAL, PhD

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PERSONAL SUMMARY

I'm a computational biologist working in a broad area of genomics and metagenomics. My best skills are my passion about doing things with quality, pushing for things and the ability to work hard to make things happen. Currently, I'm working as a senior scientist at the Ministry for Primary Industries (MPI) in Auckland, New Zealand. My current work and research activities in biosecurity area are largely dominated by analysing large-scale Next Generation Sequencing (NGS) data of metagenomes and genomes from a variety of sources to identify exotic pests and diseases. I have studied and been trained in both bioinformatics and microbiology areas and I use such multidisciplinary expertise to answer innovative biological questions. I have a deep interest in bacterial genomics, metagenomics, metabarcoding, eDNA, antibiotic, biocide and metal resistances, microbial community ecology and the human, animal and environmental microbiomes. I also have an interest in developing biological databases, bioinformatics software/tools and designing new websites. In January 2017, I finished my PhD from University of Gothenburg in Sweden. As part of my PhD, I studied the effects of antibacterial biocides (e.g. antiseptics, disinfectants) and metals (e.g. copper, silver) on antibiotic resistance using genomic and metagenomic approaches. Previously, I obtained a master degree in Post-genomic science from the University of Liverpool in UK in 2012 and a bachelor degree in microbiology/molecular-biology from Auckland University of Technology (AUT) in New Zealand in 2011.

MAIN RESEARCH INTERESTS

- Large-scale analysis of genomic, metagenomic and transcriptomic data
- Developing bioinformatics software/tools and biological databases
- Human microbiome and its role in health and disease
- Animal and environmental microbiomes
- Food microbiology and food safety risk analysis
- Bacterial genomics, antibiotic resistance, biocide/metal resistance and bacterial virulence
- Plasmid biology, mobile genetic elements and horizontal gene transfer (HGT) in bacteria
- Pest and diseases

EMPLOYMENT HISTORY

Senior Scientist – bioinformatics | March 2017– Current
Ministry for Primary Industries (MPI) | Auckland, New Zealand

Doctoral researcher – bioinformatics | Oct 2012–Jan 2017
University of Gothenburg | Gothenburg, Sweden

EDUCATION & RESEARCH

PhD - Medical Science (Bioinformatics) | Oct 2012–Jan 2017
University of Gothenburg, Sweden | supervisor: Joakim Larsson

MSc - Post-Genomic Science (Genomics & bioinformatics) | Sep 2011–Sep 2012
University of Liverpool, United Kingdom | supervisor: Alistair Darby

BSc - Applied Science (Microbiology) | Feb 2007–Aug 2011
Auckland University of Technology (AUT), New Zealand | supervisor: Darren Saunders (ESR)

OTHER RESEARCH WORK

Research Technician – molecular-biology (voluntary work) | Jul 2008–Jan 2009
Lincoln University, New Zealand | Animal genetics lab of Jon Hickford

Research internship – analytical chemistry | Apr 2011–Jul 2011
Institute of Environmental Science and Research Ltd. (ESR), Christchurch, New Zealand

KEY WORK SKILLS AND ATTRIBUTES

Skills in computational science: UNIX/Linux platform, programming language (Perl); Shell scripting, working on servers, cloud and cluster computing queuing systems such as SLURM; large-scale data storage, management and mining; biological database development and maintenance, relational databases (MySQL) and CGI programming, website development using HTML and CSS.

Skills in bioinformatics: In-depth analysis of NGS data from large-scale 16S rRNA amplicon-sequencing, large-scale genomic and metagenomic projects; specific skills including assembly of metagenomes and genomes, functional and taxonomic characterization of metagenomics data, genome annotation, exome-seq and RNA-seq data analysis; short-read mapping, gene prediction, SNP and indel analysis; developing new bioinformatics tools; pipeline development for large-scale NGS data analysis.

Skills in statistics: R for statistical tests and graphical visualizations and ecological dataset analyses.

Skills in microbiology and molecular-biology: Isolation and culturing of microorganisms; antibiotic sensitivity test, DNA extraction and quantification (Qubit); PCR, gel electrophoresis (agarose, SDS-PAGE, SSCP)

DEVELOPED DATABASES, TOOLS & WEBSITES

1. [FARAO](#) (2016) – a tool for organizing and visualize sequence annotation and coverage information with graphics
2. [Metaxa2](#) (2015) – a tool for taxonomic identification and classification of rRNA in metagenomic Data
3. [BacMet](#) (2014) – a biological database of antibacterial biocide and metal resistance genes
4. [BacMet-Scan](#) (2014) – a tool to scan sequence data against the BacMet database
5. [BacMet website](#) (2013) – designed this database-driven website of a biological database
6. [INTERACT website](#) (2013) – designed this research-oriented website for a 5-yrs research project

AWARDS AND FUNDINGS

- Postdoctoral Fellowship for 2 years at Harvard University by Swedish Society for Medical Research (SSMF), Sweden May 2017
- The Wallenberg Foundation Postdoctoral Research Scholarship for 2 years at Broad Institute of MIT and Harvard by Knut and Alice Wallenberg Foundation, Sweden April 2017
- Travel grant: Conference- ASM microbe 2016, Boston, USA (11011 SEK) March 2016
- Travel grant: Conference- EDAR3, Germany (8640 SEK) March 2015
- Research grant: Wilhelm and Martina Lundgrens Foundation, Sweden (10,000 SEK) May 2015
- Research grant: Wilhelm and Martina Lundgrens Foundation, Sweden (10,000 SEK) May 2014
- Award: ‘Best Analytical Chemistry Student’ by New Zealand Institute of Chemistry March 2009

OTHER RESPONSIBILITIES

- Webmaster for research group (www.biomedicine.gu.se/joakimlarsson) and a research program- ‘INTERACT’ (www.interact.gu.se): Dec 2012-Jan 2017
- Curator for a biological database on resistance genes – BacMet (<http://bacmet.biomedicine.gu.se>): Jan 2014-Current

- Assisting internal and external research groups in bioinformatics analyses in multiple projects at University of Gothenburg Oct 2012-Jan 2017
- Ad hoc referee: Antibiotics (MDPI), Microbiome

PRESENTATIONS AT INTERNATIONAL CONFERENCES

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| 1. ASM Microbe 2016 - Annual American Society for Microbiology meeting, June 16-20; 2016 (<u>Poster</u>) | Boston, USA |
| 2. International Conference on Evolution and Transfer of Antibiotic Resistance (ICETAR), June 24-26; 2015 (<u>Poster</u>) | Amsterdam, the Netherlands |
| 3. 3rd International Symposium of Environmental Dimension of Antibiotic Resistance (EDAR-3), May 17-21; 2015 (<u>Oral</u>) | Wernigerode, Germany |

LIST OF PUBLICATIONS

1. Marathe N, Pal C, Gaikwad SS, Kristiansson E, Larsson DGJ. (2017) **Untreated urban waste contaminates Indian river sediments with resistance genes to last resort antibiotics.** *Water Research. Accepted for Publication.*
2. Hao X*, Li X*, Pal C*, Hobman JL, Rosen BP, Larsson DGJ, Zhu YG, Rensing C. (2017) **Bacterial resistance to arsenic protects against protest killing.** *Biometals.* DOI: [10.1007/s10534-017-0003](https://doi.org/10.1007/s10534-017-0003). (*-co-first authors)
3. Pal C, Asiani K, Arya S, Rensing C, Stekel DJ, Larsson DGJ, Hobman JL. (2017) **Metal resistance and its association with antibiotic resistance.** *Advances in Microbial Physiology.* DOI: [10.1016/bs.ampbs.2017.02.001](https://doi.org/10.1016/bs.ampbs.2017.02.001).
4. Flach CF, Pal C, Svensson CJ, Kristiansson E, Östman M, Bengtsson-Palme J, Tysklind M, Larsson DGJ. (2017) **Does antifouling paint select for antibiotic resistance?** *Science of the Total Environment.* DOI: [10.1016/j.scitotenv.2017.01.213](https://doi.org/10.1016/j.scitotenv.2017.01.213).
5. Pal C, Bengtsson-Palme J, Kristiansson E, Larsson DGJ. (2016) **The structure and diversity of human, animal and environmental resistomes.** *Microbiome*; 4:54. DOI: [10.1186/s40168-016-0199-5](https://doi.org/10.1186/s40168-016-0199-5)
6. Bengtsson-Palme J, Boulund F, Edström R, Feizi A, Johnning A, Jonsson VA, Karlsson FH, Pal C, Pereira MB, Rehammar A, Sanchez J, Sanli K, Thorell K. (2016) **Strategies to improve usability and preserve accuracy in biological sequence databases.** *Proteomics.* DOI: [10.1002/pmic.20160003](https://doi.org/10.1002/pmic.20160003). (co-authors listed alphabetically)
7. Hammarén R, Pal C, Bengtsson-Palme J. (2016) **FARAO – The Flexible All-Round Annotation Organizer.** *Bioinformatics.* DOI: [10.1093/bioinformatics/btw499](https://doi.org/10.1093/bioinformatics/btw499).
8. Bengtsson-Palme J, Hammarén R, Pal C, Östman M, Björleinius B, Flach CF, Fick J, Kristiansson E, Tysklind M, Larsson DGJ. (2016) **Elucidating selection processes for antibiotic resistance in sewage treatment plants using metagenomics.** *Science of the Total Environment.* DOI: [10.1016/j.scitotenv.2016.06.228](https://doi.org/10.1016/j.scitotenv.2016.06.228).

9. Pal C, Bengtsson-Palme J, Kristiansson E, Larsson DGJ. (2015) **Co-occurrence of resistance genes to antibiotics, biocides and metals reveals novel insights into their co-selection potential.** *BMC Genomics*; 16:964. [DOI: 10.1186/s12864-015-2153-5](https://doi.org/10.1186/s12864-015-2153-5).
10. Bengtsson-Palme J, Hartmaan M, Eriksson KM, Pal C, Thorell K, Larsson DGJ, Nilsson NH. (2015) **Metaxa2: Improved Identification and Taxonomic Classification of Small and Large Subunit rRNA in Metagenomic Data.** *Molecular Ecology Resources*. 15:1403-1414. [DOI: 10.1111/1755-0998.12399](https://doi.org/10.1111/1755-0998.12399).
11. Pal C, Bengtsson-Palme J, Rensing C, Kristiansson E, Larsson DGJ. (2014) **BacMet: antibacterial biocide and metal resistance genes database.** *Nucleic Acids Research*. 42(1):D737-D743. [DOI: 10.1093/nar/gkt1252](https://doi.org/10.1093/nar/gkt1252).

Under review:

12. Higgins D, Pal C, Sulaiman IM, Jia C, Zerwekh T, Banerjee P. (2017) **Assessment of microbiota in retail foods available in low and high socioeconomic neighborhoods using Next Generation Sequencing.** *Submitted*