

Alan Péricles Rodrigues Lorenzetti

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1 Formal Education

2016 - 2021

Doctoral degree in Bioinformatics

University of São Paulo (USP), Ribeirão Preto, Brazil

with collaborative period at Institute for Systems Biology (WA, US)

(Advisor: Nitin Baliga)

Field of study: genomics, transcriptomics and proteomics of *Halobacterium salinarum*; Insertion Sequences.

Advisor: Tie Koide

Co-advisor: Ricardo Zorzetto Nicoliello Vencio

Funding: São Paulo Research Foundation (FAPESP)

2014 - 2016

Master's degree in Genetics and Molecular Biology

State University of Londrina (UEL), Londrina, Brazil

Field of study: Plant genomics and small RNAs; Transposable Elements

Advisor: Douglas Silva Domingues

Co-advisor: Alexandre Rossi Paschoal

Funding: Coordination of Superior Level Staff Improvement

2013 - 2014

Specialist degree in Bioinformatics

Federal University of Technology (UTFPR), Cornélio Procópio, Brazil

Field of study: Plant genomics and small RNAs; Transposable Elements

Advisor: Douglas Silva Domingues

Co-advisor: Alexandre Rossi Paschoal

2009 - 2013

Undergraduate degree in Biological Sciences

State University of Londrina (UEL), Londrina, Brazil

Field of study: Plant genomics; Transposable Elements

Advisor: Rogério Fernandes de Souza

2 Complementary Education (most relevant courses)

2020

Proteomics Informatics Course

(Credit Hours: 40h).

Institute for Systems Biology, ISB, Seattle, United States.

2018

Nanopore Community Meeting Workshop

(Credit Hours: 8h).

Oxford Nanopore Technologies, San Francisco, United States.

2016

Algorithms and Computational Techniques for Genome Assembly

(Credit Hours: 25h).

LACTAD/Unicamp, Campinas, Brazil.

2015

Current methodologies in transcriptome analysis

(Credit Hours: 3h).

University of São Paulo, São Paulo, Brasil.

2014

X Summer Course for Bioinformatics (with “Bioconductor fellows”).

(Credit Hours: 70h).

University of São Paulo, Ribeirão Preto, Brasil.

3 Professional experience

3.1 Lieber Institute for Brain Development (current)

Since 11/2022

Role: Postdoctoral Fellow

Duties: Short-read and long-read sequencing data analysis for the molecular characterization of X-linked Dystonia Parkinsonism (XDP) and neurodevelopmental diseases.

3.2 Lieber Institute for Brain Development

06/2022 - 11/2022

Role: Bioinformatics consultant

Duties: Short-read and long-read sequencing data analysis for the molecular characterization of X-linked Dystonia Parkinsonism (XDP)

3.3 Carlos Chagas Institute/Oswaldo Cruz Foundation (Paraná, Brazil)

01/2022 - 05/2022

Role: Bioinformatics technical support

Duties: Proteomics data processing for the discovery of isoforms associated to Alzheimer's disease.

3.4 São Paulo State University (Rio Claro, Brazil)

06/2021 - 12/2021

Role: Bioinformatics technical support

Duties: Establishment of a reference transcriptome for *Quillaja brasiliensis*, a tree species native to Brazil, using the Iso-Seq (PacBio) technology; RNA-Seq analysis of *Coffea arabica*; Chloroplast genome assembly.

4 Articles in Scientific Journals

4.1 Lorenzetti, A. P. R.; Kusebauch, U.; Zaramela, L. S.; Wu, W. J.; de Almeida, J. P.; Turkarslan, S.; de Lomana, L. G.; Gomes-Filho, J. V.; Vêncio, R. Z.; Moritz, R. L.; Koide, T.; Baliga, N. S. A Genome-Scale Atlas Reveals Complex Interplay of Transcription and Translation in an Archaeon. *Msystems*, v. 8, no. 2, 2023. <https://doi.org/10.1128/mSystems.00816-22>

4.2 Lima, L. D. P.; de Santana, E. S.; Lorenzetti, A. P. R.; Lourenço, R. F.; Ceseti, L. D. M.; Riva, L.; Bayer-Santos, E.; Boechat, A. L.; Baldini, R. L.; Farah, C. S.; Koide, T.; Alvarez-Martinez, C. E. The AraC-type transcription factor TagK is a new player in the signaling cascade that induces the anti-eukaryotic T6SS of *Xanthomonas citri*. *Molecular Microbiology*, v. 118, no. 5, 2022. <https://doi.org/10.1111/mmi.14985>

4.3 Lima, L. D. P.; Pereira, J. B.; Flores, A. J. F.; Lorenzetti, A. P. R.; Boechat, A. L.; Pereda, M. C.; Gualtieri, S.; do Prado, D. F.; Rocha, D.; Ceseti, L. D. M.; Baldini, R. L.; Farah, C. S.; Koide, T.; Benedetti, C. E.; Alvarez-Martinez, C. E. An Extracytoplasmic Function Sigma Factor Required for Full Virulence in *Xanthomonas citri* pv. *citri*. *Journal of Bacteriology*, v. 204, no. 5, 2022. <https://doi.org/10.1128/jb.00624-21>

4.4 Araújo, H. L.; Martins, B. P.; Vicente, A. M.; Lorenzetti, A. P. R.; Koide, T.; Marques, M. V. Cold Regulation of Genes Encoding Ion Transport Systems in the Oligotrophic Bacterium *Caulobacter crescentus*. *Microbiology Spectrum*, v. 9, no. 1, 2021. <https://doi.org/10.1128/Spectrum.00710-21>

4.5 Ibrahim, A. G. A. E.-R.; Vêncio, R. Z. N.; Lorenzetti, A. P. R.; Koide, T. *Halobacterium salinarum* and *Haloferax volcanii* Comparative Transcriptomics Reveals Conserved Transcriptional Processing Sites. *Genes*, v. 12, no. 7, 2021. <https://doi.org/10.3390/genes12071018>

4.6 de Lomana, A. L. G.; Kusebauch, U.; Raman, A. V.; Pan, M.; Turkarslan, S.; Lorenzetti, A. P. R.; Moritz, R. L.; Baliga, N. S. Selective Translation of Low Abundance and Upregulated Transcripts in *Halobacterium salinarum*. *mSystems*, v. 5, 2020. <http://doi.org/10.1128/mSystems.00329-20>

4.7 Silva, L. G.; Lorenzetti, A. P. R.; Ribeiro, R. A.; Alves, I. R.; Leaden, L.; Galhardo, R. S.; Koide, T.; Marques, M. V. OxyR and the hydrogen peroxide stress response in *Caulobacter crescentus*. *Gene*, v. 700, 2019. <http://doi.org/10.1016/j.gene.2019.03.003>

4.8 De Almeida, J. P. P.; Vêncio, R. Z. N.; Lorenzetti, A. P. R.; Ten-Caten, F.; Gomes-Filho, J. V.; Koide, T. The Primary Antisense Transcriptome of *Halobacterium salinarum* NRC-1. *Genes*, v. 10, 2019. <https://doi.org/10.3390/genes10040280>

4.9 Dos Santos, T. B.; Soares, J. D. M.; Lima, J. E.; Silva, J. C.; Ivamoto, S. T.; Baba, V. Y.; Souza, S. G. H.; Lorenzetti, A. P. R.; Paschoal, A. R.; Meda, A. R.; Nishiyama Júnior, M. Y.; De Oliveira, Ú. C.; Mokochinski, J. B.; Guyot, R.; Junqueira-De-Azevedo, I. L. M.; Figueira, A. V. O.; Mazzafera, P.; Júnior, O. R.; Vieira, L. G. E.; Pereira, L. F. P.; Domingues, D. S. An integrated analysis of mRNA and sRNA transcriptional profiles in *Coffea arabica* L. roots: insights on nitrogen starvation responses. *Functional & Integrative Genomics*, v. 1, 2018. <http://doi.org/10.1007/s10142-018-0634-8>

4.10 Ten-Caten, F.; Vêncio, R. Z. N.; Lorenzetti, A. P. R.; Zaramela, L. S.; Santana, A. C.; Koide, T. Internal RNAs overlapping coding sequences can drive the production of alternative proteins in archaea. *RNA Biology*, 2018. <http://doi.org/10.1080/15476286.2018.1509661>

4.11 Leaden, L.; Silva, L. G.; Ribeiro, R. A.; Dos Santos, N. M.; Lorenzetti, A. P. R.; Alegria, T. G. P.; Schulz, M. L.; Medeiros, M. H. G.; Koide, T.; Marques, M. V. Iron Deficiency Generates Oxidative Stress and Activation of the SOS Response in *Caulobacter crescentus*. *Frontiers in Microbiology*, v. 9, 2018. <http://doi.org/10.3389/fmicb.2018.02014>

4.12 Pedro, D. L. F.; Lorenzetti, A. P. R.; Domingues, D. S.; Paschoal, A. R. PlaNC-TE: a comprehensive knowledgebase of non-coding RNAs and transposable elements in plants. *Database - The Journal of Biological Databases and Curation*, 2018. <http://doi.org/10.1093/database/bay078>

4.13 Marcon, H. S.; Costa-Silva, J.; Lorenzetti, A. P. R.; Marino, C. L.; Domingues, D. S. Genome-wide analysis of EgEVE_1, a transcriptionally active endogenous viral element associated to small RNAs in *Eucalyptus* genomes. *Genetics and Molecular Biology*, v. 40, 2017. <http://doi.org/10.1590/1678-4685-gmb-2016-0086>

4.14 Lorenzetti, A. P. R.; De Antonio, G. Y. A.; Paschoal, A. R.; Domingues, D. S. PlanTE-MIR DB: a database for transposable element-related microRNAs in plant genomes. *Functional & Integrative Genomics*, v. 16, 2016. <http://doi.org/10.1007/s10142-016-0480-5>

5 Poster presentations and lectures (most relevant)

5.1 Lorenzetti, A. P. R. Investigação da regulação de mRNAs codificadores de transposase e da morfologia de transcritos utilizando a plataforma MinION. Workshop de Sequenciamento de Terceira Geração (S3G). University of São Paulo, 2019.

5.2 Lorenzetti, A. P. R.; Almeida, J. P. P.; Gomes, C. S.; Vencio, R. Z. N.; Koide, T. Detecting Insertion Sequence activity in Archaea using multiplex long-read DNA sequencing. Nanopore Community Meeting. San Francisco, 2018.

5.3 Lorenzetti, A. P. R.; Zaramela, L. S.; Almeida, J. P. P.; Gomes-Filho, J. V.; Vencio, R. Z. N.; Koide, T. Association of Hfq/LSm protein with insertion sequence-derived RNAs is a prevalent phenomenon in prokaryotes. X-Meeting. Águas de São Pedro, 2017.

5.4 Lorenzetti, A. P. R.; Zaramela, L. S.; ten-Caten, F.; De Almeida, J. P. P.; Gomes-Filho, J. V.; Vencio, R. Z. N.; Koide, T. Large-scale survey of LSm-bound transcripts in *Halobacterium salinarum* NRC-1. I Workshop in Microbial Molecular Biology. São Paulo, 2017.

5.5 Lorenzetti, A. P. R.; Gomes-Filho, J. V.; Zaramela, L. S.; ten-Caten, F.; Vencio, R. Z. N.; Koide, T. Lsm-bound antisense RNAs play role in *Halobacterium salinarum* NRC-1 transposition regulation. X-Meeting. Belo Horizonte, 2016.

6 Awarded grants and honors

Awarded grants

6.1 Grant number: 21/03947-5

Support type: Technical Training Program

Principal researcher: Douglas Silva Domingues

Grantee: Alan Lorenzetti

June 01, 2021 - December 31, 2021

Title: Integrative bioinformatics of *Quillaja brasiliensis*: Transcriptome analysis and identification of genes related to triterpenic saponins

Source: <https://bv.fapesp.br/en/bolsas/196751/>

6.2 Grant number: 19/13440-5

Support type: Research Internship Abroad

Principal researcher: Tie Koide

Grantee: Alan Lorenzetti

Supervisor abroad: Nitin Baliga

October 18, 2019 - October 17, 2020

Title: Detection of Insertion Sequence-encoded transposases using proteome data

Source: <https://bv.fapesp.br/en/bolsas/186921/>

6.3 Grant number: 17/03052-2

Support type: Doctorate Scholarship

Principal researcher: Tie Koide

Grantee: Alan Lorenzetti

June 01, 2017 - March 07, 2021

Title: Non-coding RNAs derived from insertion sequences in the halophilic archaeon *Halobacterium salinarum* NRC-1

Source: <https://bv.fapesp.br/en/bolsas/171520/>

Honors

6.4 Best poster in the “RNA and Transcriptomics” category, with the study entitled “Association of Hfq/LSm protein with insertion sequence-derived RNAs is a prevalent phenomenon in prokaryotes”. Awarded during X-Meeting (Águas de São Pedro - SP - 2017), an event promoted by AB3C.

6.5 Honorable mention during the international X-Meeting (Belo Horizonte - MG - 2014), promoted by AB3C and ISCB. The poster entitled “Identification of miRNA-related Transposable Elements in Plant Genomes” was awarded the second place according to “People Awards”.

7 Role as reviewer

7.1 Genomics (Elsevier; ISSN: 1089-8646; IF 4.4)