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Microbial community assembly in an evolving ecosystem

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Curriculum Vitae

About the author

Francisco Dini Andreote was born on the 26th of February 1985 in Piracicaba, Sao Paulo, Brazil. He graduated as agronomist in 2008 at the “Luiz de Queiroz” College of Agriculture, University of Sao Paulo (ESALQ/USP). During five years as an undergraduate student, Francisco interned at the Department of Genetics, being trained as a molecular microbiologist. From 2009 to 2011, Francisco followed a Master program in the same department (ESALQ/USP). His master’s thesis focused on the genetic mechanisms involved in the interaction between a methylotrophic bacterium and the root surface of soybean plants. Afterwards, in January 2012, Francisco obtained the Ubbo Emmius grant to pursue his PhD in Microbial Ecology at the University of Groningen, The Netherlands. His research focuses mostly on the understanding of the eco-evolutionary mechanisms that govern the spatiotemporal changes in microbial communities. Currently, Francisco continues to work at the University of Groningen as a postdoctoral researcher, examining the structure, variation, and assembly of the root-associated microbiomes of grapevines (EU Project: VitiSmart)



List of publications.

**this thesis

*articles published during the PhD period (2012 to 2016)

- (1**) **Dini-Andreote F**, Pylro VS, van Elsas JD, Salles JF. (2016). Ecological succession reveals potential signatures of marine-terrestrial transition in salt marsh fungal communities. *The ISME Journal*. *In press*.
- (2**) **Dini-Andreote F**, Brossi MJL, van Elsas JD, Salles JF. (2016). Reconstructing the genetic potential of the microbially-mediated nitrogen cycle in a salt marsh ecosystem. *Frontiers in Microbiology*, 7: 902.
- (3*) Lima-Perim JE, Ramagnoli EM, **Dini-Andreote F**, Durrer A, Dias ACF et al. (2016). Linking the composition of bacterial and archaeal communities to characteristics of soil and flora composition in the Atlantic rainforest. *PLoS One*, 11: e0146566.
- (4**) **Dini-Andreote F**, Stegen JC, van Elsas JD, Salles JF. (2015). Disentangling mechanisms that mediate the balance between stochastic and deterministic processes in microbial succession. *Proceedings of the National Academy of Sciences USA*, 112: E1326–E1332. (**F1000PRIME RECOMMENDED**).
- (5*) Jiménez DJ, **Dini-Andreote F**, Ottoni JR, Oliveira VM, van Elsas JD et al. (2015). Compositional profile of α/β -hydrolase fold proteins in mangrove soil metagenomes: prevalence of epoxide hydrolases and haloalkane dehalogenases in oil-contaminated sites. *Microbial Biotechnology*, 8: 604–613.

- (6*) Araújo WL, Santos DS, **Dini-Andreote F**, Salgueiro-Londoño JK, Neves AAC et al. (2015). Genes related to antioxidant metabolism are involved in *Methylobacterium mesophilicum*-soybean interaction. *Antonie van Leeuwenhoek*, 108: 951–963.
- (7*) Lima AB, Cannavan FS, Germano MG, **Dini-Andreote F**, Paula AM et al. (2015). Effects of vegetation and seasonality on bacterial communities in Amazonian dark earth and adjacent soils. *African Journal of Microbiology Research*, 9: 2119–2134.
- (8**) **Dini-Andreote F**, Pereira e Silva MC, Triadó-Margarit X, Casamayor EO, van Elsas JD et al. (2014). Dynamics of bacterial community succession in a salt marsh chronosequence: evidences for temporal niche partitioning. *The ISME Journal*, 8: 1989–2001.
- (9*) Santos HF, Carmo FL, Duarte G, **Dini-Andreote F**, Castro CB et al. (2014). Climate change affects key nitrogen-fixing bacterial populations on coral reefs. *The ISME Journal*, 8: 2272–2279.
- (10*) Lourenço MVM, **Dini-Andreote F**, Aguilar-Vildoso CI, Basso LC. (2014). Biotechnological potential of *Candida* spp. for the bioconversion of D-xylose to xylitol. *African Journal of Microbiology Research*, 8: 2030–2036.
- (11*) Jiménez DJ, **Dini-Andreote F**, van Elsas JD. (2014). Metataxonomic profiling and prediction of functional behaviour of wheat straw degrading microbial consortia. *Biotechnology for Biofuels*, 7: 92.
- (12*) Grizard S, **Dini-Andreote F**, Tieleman IB, Salles JF. (2014). Dynamics of bacterial and fungal communities associated with eggshells during incubation. *Ecology and Evolution*, 4: 1140–1157.
- (13*) Marcon J, Taketani RG, **Dini-Andreote F**, Mazzero GI, Soares FL et al. (2014). Draft genome sequence of *Bacillus thuringiensis* strain BrMgv02-JM63, a chitinolytic bacterium isolated from oil-contaminated mangrove soil in Brazil. *Genome Announcements*, 2: e01264-13.
- (14*) **Dini-Andreote F**, van Elsas JD. (2013). Back to the basics: the need for ecophysiological insights to enhance our understanding of microbial behaviour in the rhizosphere. *Plant and Soil*, 373: 1–15. (MARSCHNER REVIEW).
- (15*) Lima AOS, Cabral A, Andreote FD, Cavalett A, Pessatti ML, **Dini-Andreote F** et al. (2013). Draft genome sequence of *Bacillus stratosphericus* LAMA 585, isolated from the Atlantic deep sea. *Genome Announcements*, 1: e00204-13.
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- (20*) Andreote FD, Jiménez DJ, Chaves D, Dias ACF, Luvizotto DM, **Dini-Andreote F** et al. (2012). The microbiome of Brazilian mangrove sediments as revealed by metagenomics. *PLoS One*, 7: e38600.
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- (22) Dias ACF, **Dini-Andreote F**, Taketani RG, Tsai SM, Azevedo JL et al. (2011). Archaeal communities in the sediments of three contrasting mangroves. *Journal of Soils and Sediments*, 11: 1466–1476.

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- (25) **Dini-Andreote F**, Andreote FD, Costa R, Taketani RG, van Elsas JD et al. (2010). Bacterial soil community in a Brazilian sugarcane field. *Plant and Soil*, 336: 337–349.
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