

## BIBLIOGRAPHIC REFERENCES:

1. Daane KM, Almeida RPP, Bell VA, Walker JTS, Botton M, Fallahzadeh M, et al. Biology and management of mealybugs in vineyards. In: Arthropod management in vineyards. Dordrecht: Springer; 2012. p. 271–307.
2. Correa MCG, Germain JF, Malausa T, Zaviezo T. Molecular and morphological characterization of mealybugs (Hemiptera: Pseudococcidae) from Chilean vineyards. Bull Entomol Res. 2012;102(5):524–30.
3. Mansour R, Grissa-Lebdi K, Suma P, Mazzeo G, Russo A. Key scale insects (Hemiptera: Coccoidea) of high economic importance in a mediterranean area: Host plants, bio-ecological characteristics, natural enemies and pest management strategies – a review. Plant Prot Sci. 2017;53(1):1–14.
4. Pacheco Da Silva VC, Kaydan MB, Malausa T, Germain JF, Palero F, Botton M. Integrative taxonomy methods reveal high mealybug (Hemiptera: Pseudococcidae) diversity in southern Brazilian fruit crops. Sci Rep. 2017;7:15741.
5. Acevedo FE, Jiménez M, Pimentel JP, Benavides P. Spatial distribution of mealybugs (Hemiptera: Coccoidea) in the root system of pruned and non-pruned coffee arabica trees. J Econ Entomol. 2020;113(1):172–84.
6. Walton VM, Pringle KL. Vine mealybug, *Planococcus ficus* (Signoret) (Hemiptera: Pseudococcidae), a Key Pest in South African vineyards. A Review. South African J Enol Vitic. 2004;25(2):54–62.
7. Charles JG, Cohen D, Walker JTS, Forgie SA, Bell VA, Breen KC. A review of the ecology of grapevine leafroll associated virus type 3 (GLRaV3). New Zeal Plant Prot. 2006;59:330–7.
8. Bordeu E, Troncoso DO, Zaviezo T. Influence of mealybug (*Pseudococcus* spp.) - infested bunches on wine quality in Carmenere and Chardonnay grapes. Int J Food Sci Technol. 2012;47(2):232–9.
9. Le Maguet J, Beuve M, Herrbach E, Lemaire O. Transmission of six ampeloviruses and two vitiviruses to grapevine by *Phenacoccus aceris*. Phytopathology. 2012;102(7):717–23.
10. Herrbach E, Alliaume A, Prator CA, Daane KM, Cooper ML, Almeida RPP. Vector transmission of grapevine leafroll-associated viruses. In: Grapevine viruses: molecular Biology, diagnostics and management. Cham: Springer; 2017. p. 483–503.
11. Moore C. Rechazos por Pseudococcidae y su estatus cuarentenario [Internet]. 2012. Available from: [http://www.fdf.cl/biblioteca/presentaciones/2012/04\\_jt\\_chanco\\_fosfina/Presentacion\\_FDF\\_Copiapo\\_SAG.pdf](http://www.fdf.cl/biblioteca/presentaciones/2012/04_jt_chanco_fosfina/Presentacion_FDF_Copiapo_SAG.pdf)
12. Ripa R, Larral P. Manejo de plagas en paltos y cítricos. In: Colección Instituto de Investigaciones Agropecuarias No 23. Centro Regional de Investigación La Cruz; 2008. p. 399.
13. Charles JG, Bell VA, Lo PL, Cole LM, Chhagan A. Mealybugs (Hemiptera: Pseudococcidae) and their natural enemies in New Zealand vineyards from 1993–2009. New Zeal Entomol. 2010;33(1):84–91.
14. Dreistadt S. Integrated pest management for citrus. Third. Davis: University of California Agriculture and Natural Resources; 2012.
15. García Morales M, Denno BD, Miller DR, Miller GL, Ben-Dov Y, Hardy NB. ScaleNet: a literature-based model of scale insect biology and systematics. Database. 2016;2016:bav118.
16. Many M, Shivaraju C. Mealybugs and their management in agricultural and horticultural crops. Springer India; 2016.
17. Wyatt TD. Pheromones and animal behaviour: communication by smell and taste. Cambridge: Cambridge University Press; 2003.
18. Millar JG, Daane KM, Steven Mcelfresh J, Moreira JA, Malakar-Kuenen R, Guillén M, et al. Development and Optimization of Methods for Using Sex Pheromone for Monitoring the Mealybug *Planococcus ficus* (Homoptera: Pseudococcidae) in California Vineyards. J Econ Entomol. 2002;95(4):706–14.
19. Franco José C, Zada A, Mendel Z. Novel approaches for the management of mealybug pests. In: Biorational control of arthropod pests. Dordrecht: Springer; 2009. p. 233–78.
20. Witzgall P, Kirsch P, Cork A. Sex pheromones and their impact on pest management. J Chem Ecol. 2010;36(1):80–100.
21. Uehara T, Honda H. Sex pheromone communication system in hawk moths. In: Insect sex pheromone research and beyond. Singapore: Springer; 2020. p. 19–33.
22. Tabata J. Sex pheromones of mealybugs: implications for evolution and application. In: Insect sex pheromone research and beyond. Singapore: Springer; 2020. p. 35–59.

23. Zou Y, Millar JG. Chemistry of the pheromones of mealybug and scale insects. *Nat Prod Rep*. 2015;32(7):1067–113.
24. El-Sayed AM, Unelius CR, Twidle A, Mitchell V, Manning LA, Cole L, et al. Chrysanthemyl 2-acetoxy-3-methylbutanoate: the sex pheromone of the citrophilous mealybug, *Pseudococcus calceolariae*. *Tetrahedron Lett*. 2010;51(7):1075–8.
25. Unelius CR, El-Sayed AM, Twidle A, Bunn B, Zaviezo T, Flores MF, et al. The Absolute Configuration of the Sex Pheromone of the Citrophilous Mealybug, *Pseudococcus calceolariae*. *J Chem Ecol*. 2011;37(2):166–72.
26. Flores MF, Romero A, Oyarzun MS, Bergmann J, Zaviezo T. Monitoring *Pseudococcus calceolariae* (Hemiptera: Pseudococcidae) in fruit crops using pheromone-baited traps. *J Econ Entomol*. 2015;108(5):2397–406.
27. Beran F, Köllner TG, Gershenzon J, Tholl D. Chemical convergence between plants and insects: biosynthetic origins and functions of common secondary metabolites. *New Phytol*. 2019;223(1):52–67.
28. Demissie ZA, Erland LAE, Rheault MR, Mahmoud SS. The biosynthetic origin of irregular monoterpenes in lavandula: Isolation and biochemical characterization of a novel cis-prenyl diphosphate synthase gene, lavandulyl diphosphate synthase. *J Biol Chem*. 2013;288(9):6333–41.
29. Rivera SB, Swedlund BD, King GJ, Bell RN, Hussey CE, Shattuck-Eidens DM, et al. Chrysanthemyl diphosphate synthase: Isolation of the gene and characterization of the recombinant non-head-to-tail monoterpene synthase from *Chrysanthemum cinerariaefolium*. *Proc Natl Acad Sci U S A*. 2001;98(8):4373–8.
30. Xu H, Moghe GD, Wiegert-Rininger K, Schillmiller AL, Barry CS, Last RL, et al. Coexpression analysis identifies two oxidoreductases involved in the biosynthesis of the monoterpene acid moiety of natural pyrethrin insecticides in *Tanacetum cinerariifolium*. *Plant Physiol*. 2018;176(1):524–37.
31. Yang T, Gao L, Hu H, Stoopen G, Wang C, Jongsma MA. Chrysanthemyl diphosphate synthase operates in planta as a bifunctional enzyme with chrysanthemol synthase activity. *J Biol Chem*. 2014;289(52):36325–35.
32. Thulasiram H V., Erickson HK, Poulter CD. Chimeras of two isoprenoid synthases catalyze all four coupling reactions in isoprenoid biosynthesis. *Science*. 2007;316(5821):73–6.
33. Lee JS, Pan JJ, Ramamoorthy G, Poulter CD. Structure-function studies of *Artemisia tridentata* farnesyl diphosphate synthase and chrysanthemyl diphosphate synthase by site-directed mutagenesis and morphogenesis. *J Am Chem Soc*. 2017;139(41):14556–67.
34. Cocco A, Lentini A, Serra G. Mating disruption of *Planococcus ficus* (Hemiptera: Pseudococcidae) in vineyards using reservoir pheromone dispensers. *J Insect Sci*. 2014;14(1):144.
35. Lucchi A, Suma P, Ladurner E, Iodice A, Savino F, Ricciardi R, et al. Managing the vine mealybug, *Planococcus ficus*, through pheromone-mediated mating disruption. *Environ Sci Pollut Res*. 2019;26(11):10708–18.
36. Benelli G, Lucchi A, Thomson D, Ioriatti C. Sex pheromone aerosol devices for mating disruption: Challenges for a brighter future. *Insects*. 2019;10(10):308.
37. Bergmann J, Tapia J, Bravo M, Zaviezo T, Flores MF. Synthesis of citrophilus mealybug sex pheromone using chrysanthemol extracted from Pyrethrum (*Tanacetum cinerariifolium*). *Nat Prod Res*. 2019;33(3):303–8.
38. Gietz RD. Yeast transformation by the LiAc/SS carrier DNA/PEG method. In: *Yeast Genetics*. 3rd ed. New York: Humana Press; 2014. p. 1–12.
39. Dagert M, Ehrlich SD. Prolonged incubation in calcium chloride improves the competence of *Escherichia coli* cells. *Gene*. 1979;6(1):23–8.
40. Mikkelsen MD, Buron LD, Salomonsen B, Olsen CE, Hansen BG, Mortensen UH, et al. Microbial production of indolyglucosinolate through engineering of a multi-gene pathway in a versatile yeast expression platform. *Metab Eng*. 2012;14(2):104–11.
41. Shaw W, Ellis T. Quick and easy CRISPR engineering in *Saccharomyces cerevisiae* [Internet]. 2017. Available from: <https://benchling.com/pub/ellis-crispr-tools>
42. Chen Y, Xiao W, Wang Y, Liu H, Li X, Yuan Y. Lycopene overproduction in *Saccharomyces cerevisiae* through combining pathway engineering with host engineering. *Microb Cell Fact*. 2016;15(1):113.
43. Gilbert LA, Larson MH, Morsut L, Liu Z, Brar GA, Torres SE, et al. CRISPR-mediated modular RNA-guided regulation of transcription in eukaryotes. *Cell*. 2013;154(2):442–51.
44. Smith JD, Suresh S, Schlecht U, Wu M, Wagih O, Peltz G, et al. Quantitative CRISPR interference screens in yeast identify chemical-genetic interactions and new rules for guide RNA design. *Genome Biol*. 2016;17:45.
45. Pollak B, Matute T, Nuñez I, Cerda A, Lopez C, Vargas V, et al. Universal loop assembly: Open, efficient and cross-kingdom DNA fabrication. *Synth Biol*. 2020;5(1):ysaa001.

46. Gibson DG, Young L, Chuang RY, Venter JC, Hutchison III CA, Smith HO. Enzymatic assembly of DNA molecules up to several hundred kilobases. *Nat Methods*. 2009;6(5):343–5.
47. López J, Essus K, Kim I kwon, Pereira R, Herzog J, Siewers V, et al. Production of  $\beta$ -ionone by combined expression of carotenogenic and plant CCD1 genes in *Saccharomyces cerevisiae*. *Microb Cell Fact*. 2015;14(84).
48. Yaws CL. Thermophysical properties of chemicals and hydrocarbons. New York: William Andrew; 2009. p. 499.
49. Aceituno FF, Orellana M, Torres J, Mendoza S, Slater AW, Melo F, et al. Oxygen response of the wine yeast *Saccharomyces cerevisiae* EC1118 grown under carbon-sufficient, nitrogen-limited enological conditions. *Appl Env Microbiol*. 2012;78(23):8340–52.
50. Bicas JL, Molina G, Cavalcante Barros FF, Pastore GM. White biotechnology for sustainable chemistry. RSC Green Chemistry. Cambridge: Royal society of chemistry; 2015.
51. Paramasivan K, Mutturi S. Progress in terpene synthesis strategies through engineering of *Saccharomyces cerevisiae*. *Crit Rev Biotechnol*. 2017;37(8):974–89.
52. Wang C, Liwei M, Park J Bin, Jeong SH, Wei G, Wang Y, et al. Microbial platform for terpenoid production: *Escherichia coli* and Yeast. *Front Microbiol*. 2018;9:2460.
53. Jiang GZ, Yao MD, Wang Y, Zhou L, Song TQ, Liu H, et al. Manipulation of GES and ERG20 for geraniol overproduction in *Saccharomyces cerevisiae*. *Metab Eng*. 2017;41:57–66.
54. Zhang L, Xiao WH, Wang Y, Yao MD, Jiang GZ, Zeng BX, et al. Chassis and key enzymes engineering for monoterpenes production. *Biotechnol Adv*. 2017;35(8):1022–31.
55. Liu J, Zhang W, Du G, Chen J, Zhou J. Overproduction of geraniol by enhanced precursor supply in *Saccharomyces cerevisiae*. *J Biotechnol*. 2013;168(4):446–51.
56. Lund S, Hall R, Williams GJ. An Artificial pathway for isoprenoid biosynthesis decoupled from native hemiterpene metabolism. *ACS Synth Biol*. 2019;8(2):232–8.
57. Clomburg JM, Qian S, Tan Z, Cheong S, Gonzalez R. The isoprenoid alcohol pathway, a synthetic route for isoprenoid biosynthesis. *Proc Natl Acad Sci U S A*. 2019;116(26):12810–5.
58. Chatzivasilieou AO, Ward V, Edgar SMB, Stephanopoulos G. Two-step pathway for isoprenoid synthesis. *Proc Natl Acad Sci U S A*. 2019;116(2):506–11.
59. Claassens NJ, Burgener S, Vögeli B, Erb TJ, Bar-Even A. A critical comparison of cellular and cell-free bioproduction systems. *Curr Opin Biotechnol*. 2019;60:221–9.
60. Grubbe WS, Rasor BJ, Krüger A, Jewett MC, Karim AS. Cell-free styrene biosynthesis at high titers. *Metab Eng*. 2020;61:89–95.
61. Karim AS, Jewett MC. Cell-Free synthetic biology for pathway prototyping. *Methods Enzymol*. 1st ed. 2018;608:31–57.
62. Karim AS, Dudley QM, Juminaga A, Yuan Y, Crowe SA, Heggestad JT, et al. In vitro prototyping and rapid optimization of biosynthetic enzymes for cell design. *Nat Chem Biol*. 2020; Online ahead of print.
63. Rosano GL, Ceccarelli EA. Recombinant protein expression in *Escherichia coli*: Advances and challenges. *Front Microbiol*. 2014;5:172.
64. Lorsch JR. Practical steady-state enzyme kinetics. 1st ed. Vol. 536, *Methods in Enzymology*. Elsevier; 2014. p. 3–15.
65. Rollin JA, Tam TK, Zhang YHP. New biotechnology paradigm: Cell-free biosystems for biomanufacturing. *Green Chem*. 2013;15(7):1708–19.
66. Alissandratos A, Caron K, Loan TD, Hennessy JE, Easton CJ. ATP recycling with cell lysate for enzyme-catalyzed chemical synthesis, protein expression and PCR. *ACS Chem Biol*. 2016;11(12):3289–93.
67. Wang J, Zheng C, Zhang T, Liu Y, Cheng Z, Liu D, et al. Novel one-pot ATP regeneration system based on three-enzyme cascade for industrial CTP production. *Biotechnol Lett*. 2017;39(12):1875–81.
68. Eisenthal R, Danson MJ, Hough DW. Catalytic efficiency and  $k_{cat}/K_M$ : a useful comparator? *Trends Biotechnol*. 2007;25(6):247–9.
69. Park J, Zielinski M, Magder A, Tsantrizos YS, Berghuis AM. Human farnesyl pyrophosphate synthase is allosterically inhibited by its own product. *Nat Commun*. 2017;8:14132.

70. Apweiler R, Bairoch A, Wu CH, Barker WC, Boeckmann B, Ferro S, et al. UniProt: the Universal Protein knowledgebase. *Nucleic Acids Res.* 2004 Jan;32:D115–D119.
71. Altschul SF, Madden TL, Schäffer AA, Zhang J, Zhang Z, Miller W, et al. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Res.* 1997 Sep;25(17):3389–402.
72. Katoh K, Rozewicki J, Yamada KD. MAFFT online service: Multiple sequence alignment, interactive sequence choice and visualization. *Brief Bioinform.* 2018;20(4):1160–6.
73. Kumar S, Stecher G, Li M, Knyaz C, Tamura K. MEGA X: Molecular evolutionary genetics analysis across computing platforms. *Mol Biol Evol.* 2018;35(6):1547–9.
74. Rivera-Perez C, Nyati P, Noriega FG. A corpora allata farnesyl diphosphate synthase in mosquitoes displaying a metal ion dependent substrate specificity. *Insect Biochem Mol Biol.* 2015;64:44–50.
75. Lua RC, Wilson SJ, Konecki DM, Wilkins AD, Venner E, Morgan DH, et al. UET: a database of evolutionarily-predicted functional determinants of protein sequences that cluster as functional sites in protein structures. *Nucleic Acids Res.* 2016 Jan;44(D1):D308–12.
76. Lemmon G, Meiler J. Rosetta ligand docking with flexible XML protocols. In: *Computational drug discovery and design*. New York: Springer; 2012. p. 143–55.
77. Fecker T, Galaz-Davison P, Engelberger F, Narui Y, Sotomayor M, Parra LP, et al. Active site flexibility as a hallmark for efficient PET degradation by *I. sakaiensis* PETase. *Biophys J.* 2018;114(6):1302–12.
78. Reetz MT, Carballeira JD. Iterative saturation mutagenesis (ISM) for rapid directed evolution of functional enzymes. *Nat Protoc.* 2007;2(4):891–903.
79. Barja MV, Rodríguez-Concepción M. A simple In vitro assay to measure the activity of geranylgeranyl diphosphate synthase and other short-chain prenyltransferases. In: *Plant and food carotenoids*. New York: Humana; 2020. p. 27–38.
80. Bordbar A, McCloskey D, Zielinski DC, Sonnenschein N, Jamshidi N, Palsson BO. Personalized whole-cell kinetic models of metabolism for discovery in genomics and pharmacodynamics. *Cell Syst.* 2015;1(4):283–92.
81. Chakrabarti A, Miskovic L, Soh KC, Hatzimanikatis V. Towards kinetic modeling of genome-scale metabolic networks without sacrificing stoichiometric, thermodynamic and physiological constraints. *Biotechnol J.* 2013;8(9):1043–57.
82. Saa PA, Nielsen LK. Construction of feasible and accurate kinetic models of metabolism: A Bayesian approach. *Sci Rep.* 2016;6:29635.
83. Steuer R, Gross T, Selbig J, Blasius B. Structural kinetic modeling of metabolic networks. *Proc Natl Acad Sci U S A.* 2006;103(32):11868–73.
84. Tran LM, Rizk ML, Liao JC. Ensemble modeling of metabolic networks. *Biophys J.* 2008;95(12):5606–17.
85. Gutenkunst RN, Waterfall JJ, Casey FP, Brown KS, Myers CR, Sethna JP. Universally sloppy parameter sensitivities in systems biology models. *PLoS Comput Biol.* 2007;3(10):1871–8.
86. Saa P, Nielsen LK. A general framework for thermodynamically consistent parameterization and efficient sampling of enzymatic reactions. *PLoS Comput Biol.* 2015;11(4):e1004195.
87. Saa PA, Nielsen LK. A probabilistic framework for the exploration of enzymatic capabilities based on feasible kinetics and control analysis. *Biochim Biophys Acta - Gen Subj.* 2016;1860(3):576–87.
88. Theisen MK, Lafontaine Rivera JG, Liao JC. Stability of ensemble models predicts productivity of enzymatic systems. *PLoS Comput Biol.* 2016;12(3):e1004800.
89. Stergiou PY, Foukis A, Filippou M, Koukouritaki M, Parapouli M, Theodorou LG, et al. Advances in lipase-catalyzed esterification reactions. *Biotechnol Adv.* 2013;31(8):1846–59.
90. Divakar S, Manohar B. Use of lipases in the industrial production of esters. In: *Industrial Enzymes*. Dordrecht: Springer; 2007. p. 283–300.
91. Garlapati VK, Banerjee R. Solvent-free synthesis of flavour esters through immobilized lipase mediated transesterification. *Enzyme Res.* 2013;2013:367410.
92. Geng B, Wang M, Qi W, Su R, He Z. Cinnamyl acetate synthesis by lipase-catalyzed transesterification in a solvent-free system. *Biotechnol Appl Biochem.* 2012;59(4):270–5.
93. Bhavsar K V., Yadav GD. Synthesis of geranyl acetate by transesterification of geraniol with ethyl acetate over *Candida antarctica* lipase as catalyst in solvent-free system. *Flavour Fragr J.* 2019;34(4):288–93.

94. Ferraz LIR, Possebom G, Alvez EV, Cansian RL, Paroul N, de Oliveira D, et al. Application of home-made lipase in the production of geranyl propionate by esterification of geraniol and propionic acid in solvent-free system. *Biocatal Agric Biotechnol*. 2015;4(1):44–8.
95. Lotti M, Alberghina L. Lipases: molecular structure and function. In: *Industrial Enzymes*. Dordrecht: Springer; 2007. p. 263–81.
96. Martins AB, Da Silva AM, Schein MF, Garcia-Galan C, Záchia Ayub MA, Fernandez-Lafuente R, et al. Comparison of the performance of commercial immobilized lipases in the synthesis of different flavor esters. *J Mol Catal B Enzym*. 2014;105:18–25.
97. Ortiz C, Ferreira ML, Barbosa O, Dos Santos JCS, Rodrigues RC, Berenguer-Murcia Á, et al. Novozym 435: The “perfect” lipase immobilized biocatalyst? *Catal Sci Technol*. 2019;9(10):2380–420.
98. Martins AB, Graebin NG, Lorenzoni ASG, Fernandez-Lafuente R, Ayub MAZ, Rodrigues RC. Rapid and high yields of synthesis of butyl acetate catalyzed by Novozym 435: Reaction optimization by response surface methodology. *Process Biochem*. 2011;46(12):2311–6.
99. Blackmer JL, Rodriguez-Saona C, Byers JA, Shope KL, Smith JP. Behavioral response of *Lygus hesperus* to conspecifics and headspace volatiles of alfalfa in a Y-tube olfactometer. *J Chem Ecol*. 2004;30(8):1547–64.
100. Cataldo VF, Arenas N, Salgado V, Camilo C, Ibáñez F, Agosin E. Heterologous production of the epoxycarotenoid violaxanthin in *Saccharomyces cerevisiae*. *Metab Eng*. 2020;59:53–63.
101. López J, Cataldo VF, Peña M, Saa PA, Saitua F, Ibaceta M, et al. Build Your Bioprocess on a Solid Strain— $\beta$ -Carotene Production in Recombinant *Saccharomyces cerevisiae*. *Front Bioeng Biotechnol*. 2019;7:171.
102. Werner N, Ramirez-Sarmiento CA, Agosin E. Protein engineering of carotenoid cleavage dioxygenases to optimize  $\beta$ -ionone biosynthesis in yeast cell factories. *Food Chem*. 2019;299:125089.
103. Ramírez-Sarmiento CA, Engelberger F, Guixé V. An evolutionary marker of the ribokinase superfamily is responsible for zinc-mediated regulation of human pyridoxal kinase. *Catalysts*. 2020;10(5):555.
104. Medina E, Villalobos P, Coñuecar R, Ramírez-Sarmiento CA, Babul J. The protonation state of an evolutionarily conserved histidine modulates domainswapping stability of FoxP1. *Sci Rep*. 2019;9(1):5441.
105. Saa PA, Nielsen LK. Formulation, construction and analysis of kinetic models of metabolism: A review of modelling frameworks. *Biotechnol Adv*. 2017;35(8):981–1003.
106. Saa PA, Cortés MP, López J, Bustos D, Maass A, Agosin E. Expanding metabolic capabilities using novel pathway designs: computational tools and case studies. *Biotechnol J*. 2019;14(9):e1800734.
107. Torres P, Saa PA, Albiol J, Ferrer P, Agosin E. Contextualized genome-scale model unveils high-order metabolic effects of the specific growth rate and oxygenation level in recombinant *Pichia pastoris*. *Metab Eng Commun*. 2019;9:e00103.
108. Daane KM, Middleton MC, Sforza R, Cooper ML, Walton VM, Walsh DB, et al. Development of a multiplex PCR for identification of vineyard Mealybugs. *Environ Entomol*. 2011;40(6):1595–603.