

DOCTORADO EN CIENCIAS AGROALIMENTARIAS

Claudio Meneses

Publicaciones (2017- 2021)

1. Rojas, B., Suárez, F., Saez, S., Olmedo, P., Zepeda, B., Delgado, J., Defilippi, B., Pedreschi, R., **Meneses, C.**, Pérez, A., Campos, R. 2021. Pre-anthesis cytokinin applications increase table grape berry firmness by modulating cell wall polysaccharides. *Plants*. Q1.
2. Nuñez, G., Ulloa, L., Pavez, C., Riveros, A., Blanco, F., Campos, R., Pedreschi, R., **Meneses, C.** 2021. Unravelling the molecular regulation mechanisms of slow ripening trait in *Prunus persica*. *Plants*, 10: 2380. Q1.
3. Hernández, I., Uarrota, V., Paredes, D., Fuentealba, C., Defilippi, B., Campos, R., **Meneses, C.**, Hertog, M., Pedreschi, R. 2021. Can metabolites at harvest be used as physiological markers for modelling the softening behaviour of Chilean “Hass” avocados destined to local and distant markets? *Postharvest Biology and Technology*. Q1.
4. Antiquero, P., Zuloaga, R., Bastia, M., **Meneses, C.**, Estrada, J., Molina, A., Valdés, J. 2021. Antiquero, P., Zuloaga, R., Bastia, M., Meneses, C., Estrada, J., Molina, A., Valdés, J. *Biology*, 10: 995. Q1.
5. Zuloaga, R., Dettleff, P., Bastias, M., **Meneses, C.**, Altamirano, C., Valdés, J., Molina, A. 2021. RNA-seq-based analysis of cortisol-induced differential gene expression associated with piscirickettsia salmonis infection in rainbow trout (*Oncorhynchus mykiss*) myotubes. *Animals*, 11: 2399. Q1.
6. Rothkegel, K., Espinoza, A., Sanhueza, D., Lillo, V., Riveros, A., Campos, R., **Meneses, C.** 2021. Identification of DNA methylation and transcriptomic profiles associated with fruit mealiness in *Prunus persica* (L.) Batsch. *Frontiers in Plant Science*, 12: 684130. Q1.
7. Salazar, J.A., Vergara, C., Jorquera, C., Zapata, P., Ruiz, D., Martínez, P., Infante, R., **Meneses, C.** 2021. De novo transcriptome sequencing in kiwifruit (*Actinidia chinensis* var. *deliciosa* (a chev) *liang et ferguson*) and development of tissue-specific transcriptomic resources. *Agronomy*, 11: 919. Q1.
8. Olmos, C., Campaña, G., Monreal, V., Pidal, P., Sanchez, N., Airola, C., Sanhueza, D., Tapia, P., Muñoz, A., Corvalan, F., Hurtado, S., **Meneses, C.**, Orellana, A., Montecino, M., Arriagada, G., Bustos, F. 2021. SARS-CoV-2 infection in asymptomatic healthcare workers at a clinic in Chile. *PLoS ONE*. Q2.
9. Salazar, J., Zapata, P., Silva, C., González, M., Pacheco, I., Bastías, M., **Meneses, C.**, Jorquera, C., Moreno, I., Shinya, P., Infante, R. 2021. Transcriptome analysis and postharvest behavior of the kiwifruit '*Actinidia deliciosa*' reveal the role of ethylene-related phytohormones during fruit ripening. *Tree Genetics and Genomes*. Q1.

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10. Saona, L., Soria, M., Durán, V., Wörmer, L., Milucka, J., Castro, E., **Meneses, C.**, Contreras, M., Farías, M. 2021. Phosphate-Arsenic Interactions in Halophilic Microorganisms of the Microbial Mat from Laguna Tebenquiche: from the Microenvironment to the Genomes. *Microbial Ecology*. Q1.
11. Vidal, C., Larama, G., Riveros, A., **Meneses, C.**, Cornejo, P. 2021. Main molecular pathways associated with copper tolerance response in *Imperata cylindrica* by de novo transcriptome assembly. *Plants*. Q1.
12. Cárdenas, M., Galleguillos, C., Acevedo, K., Ananias, C., Alarcón, J., Michelson, S., Toledo, J., Montoya, M., **Meneses, C.**, Castro, E., Vásquez-Martínez, Y., Cortez, M. 2020. Rapid sequence modification in the highly polymorphic region (HPR) of the hemagglutinin gene of the infectious salmon anaemia virus (ISAV) suggest intra-segmental template switching recombination. *Journal of Fish Diseases*. Q1.
13. Alarcón, J., Márquez, S., Teunisse, G., Mendoza, C., **Meneses, C.**, Baldini, A., Parra, P., Zamora, P., Boehmwald, F., Castro, E. 2020. Sequences of endophytic fungal and bacterial communities from *Araucaria Araucana* [(Molina) K.Koch, 1869] in the Coastal and Andes mountain ranges, Chile. *Microbiology Resource Announcements*. Q4.
14. Muñoz, C., Di Genova, A., Sanchez, A., Correa, J., Espinoza, A., **Meneses, C.**, Maas, A., Orellana, A., Hinrichsen, P. 2020. Identification of SNPs and InDels associated with berry size in table grapes integrating genetic and transcriptomic approaches. *BMC Plant Biology*. Q1.
15. Rothkegel, K., Sandoval, P., Soto, E., Ulloa, L., Riveros, A., Lillo, V., Cáceres, J., Almeida, A., **Meneses, C.** 2020. Dormant but Active: Chilling accumulation modulates the epigenome and transcriptome of *Prunus avium* during bud dormancy. *Frontiers in Plant Science*. Q1.
16. Guerrero, E., **Meneses, C.**, Castro, E., Guzman, A., Alvarez, A., Quesada, C., Paredes, D., Rodriguez, C. 2020. Origin, genomic diversity and microevolution of the *Clostridium difficile* B1/NAP1/RT027/ST01 strain in Costa Rica, Chile, Honduras and Mexico. *Microbial genomics*. Q1.
17. Lillo, V., Espinoza, A., Rothkegel, K., Rubilar, M., Nilo, R., Pedreschi, R., Campos, R., **Meneses, C.** 2020. Identification of metabolite and lipid profiles in a segregating peach population associated with mealiness in *Prunus persica* (L.) Batsch. *Metabolites*. Q2.
18. Meneses, M., García, M., Muñoz, C., Carrasco, T., Defilippi, B., Gonzalez-Aguero, M., **Meneses, C.**, Infante, R., Hinrichsen, P. 2020. Transcriptomic study of pedicels from GA₃-treated table grape genotypes with different susceptibility to berry drop reveals responses elicited in cell wall yield, primary growth and phenylpropanoids synthesis. *BMC Plant Biology*. Q1.
19. Franck, N., Zamorano, D., Wallberg, B., Hardy, C., Ahumada, M., Rivera, N., Montoya, M., Urra, C., **Meneses, C.**, Balic, I., Mejía, N., Ibacache, A., Zurita, A. 2020. Contrasting grapevines grafted into naturalized rootstock suggest scion-driven transcriptomic changes in response to water deficit. *Scientia Horticulturae*. Q1.

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20. Dettleff, P., Hormazabal, E., Aedo, J., Fuentes, M., **Meneses, C.**, Molina, A., Valdés, J. 2020. Identification and Evaluation of Long Noncoding RNAs in Response to Handling Stress in Red Cusk-Eel (*Genypterus chilensis*) via RNA-seq. Marine Biotechnology. Q1.
21. González, P., Dettleff, P., Valenzuela, C., Estrada, J., Valdés, J., **Meneses, C.**, Molina, A. 2019. Evaluating the genetic structure of wild and commercial red cusk-eel (*Genypterus chilensis*) populations through the development of novel microsatellite markers from a reference transcriptome. Molecular Biology Reports. Q4.
22. Barra, M., **Meneses, C.**, Riquelme, S., Pinto, M., Lague, M., Davidson, C., Tai, H. 2019. Transcriptome profiles of contrasting potato (*Solanum tuberosum* L.) genotypes under water stress. Agronomy. Q1.
23. Aedo, J., Zuloaga, R., Bastías, M., **Meneses, C.**, Boltaña, S., Molina, A., Valdés, J. 2019. Early transcriptomic responses associated with the membrane-initiated action of cortisol in the skeletal muscle of rainbow trout (*Oncorhynchus mykiss*). Physiological Genomics. Q2.
24. Dettleff, P., Hormazabal, E., Aedo, J., Fuentes, M., **Meneses, C.**, Molina, A., Valdés, J. 2019. Identification and Evaluation of Long Noncoding RNAs in Response to Handling Stress in Red Cusk-Eel (*Genypterus chilensis*) via RNA-seq. Marine Biotechnology. Q1.
25. Orellana, M., Pacheco, N., Costa, J.; Mendez, K., Miossec, M., **Meneses, C.**, Castro, E., Marcoleta, A., Poblete, I. 2019. In-depth genomic and phenotypic characterization of the antarctic psychrotolerant strain *Pseudomonas* sp. MPC6 reveals unique metabolic features, plasticity, and biotechnological potential. Frontiers in Microbiology. Q1.
26. Pardo, C., Castro, J., Krüger, G., Cabezas, C., Briones, A., Aguirre, C., Morales, N., Baquedano, M., Sulbaran, Y., Hidalgo, A., **Meneses, C.**, Poblete, I., Castro, E., Valvano, M., Saavedra, C. 2019. The transcription factor ARCA modulates *Salmonella*'s metabolism in response to neutrophil hypochlorous acid-mediated stress. Frontiers in Microbiology. Q1.
27. Mendez, K., Hoare, A., Soto, C., Bugueño, I., Olivera, M., **Meneses, C.**, Pérez, J., Castro, E., Bravo, D. 2019. Variability in Genomic and Virulent properties of *Porphyromonas gingivalis* Strains isolated from healthy and severe chronic periodontitis individuals. Frontiers in cellular and infection microbiology. Q1.
28. Herrera, H., García, I., **Meneses, C.**, Pereira, G., Arriagada, C. 2019. Orchid mycorrhizal interactions on the Pacific side of the andes from Chile. A review. Journal of Soil Science and Plant Nutrition. Q2.
29. Pedreschi, R., Uarrota, V., Fuentealba, C., Alvaro, J., Olmedo, P., Defilippi, B., **Meneses, C.**, Campos, R. 2019. Primary metabolism in avocado fruit. Frontiers in Plant Science. Q1.

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30. Nilo, R., Vizoso, P., Sanhueza, D., Balic, I., Meneses C., Orellana, A., Campos, R. 2019. A *Prunus persica* genome-wide RNA-seq approach uncovers major differences in the transcriptome among chilling injury sensitive and non-sensitive varieties. *Physiologia Plantarum*. Q1.
31. Molina, M.A., Ballesteros, G., Castro, E., **Meneses, C.**, Gallardo, J., Torres, C. 2019. A first insight into the structure and function of rhizosphere microbiota in Antarctic plants using shotgun metagenomics. *Polar Biology*. Q2.
32. Núñez, G., Balladares, C., Pavez, C., Urra, C., Sanhueza, D., Vendramin, E., Dettori, M., Arús, P., Verde, I., Blanco, F., Campos, R., **Meneses, C.** 2019. High-density genetic map and QTL analysis of soluble solid content, maturity date, and mealiness in peach using genotyping by sequencing. *Scientia Horticulturae*. Q1.
33. Carrasco, T., Muñoz, C., Riveros, A., Pedreschi, R., Arus, P., Campos, R., **Meneses, C.** 2019. Expression QTL (eQTLs) analyses reveal candidate genes associated with fruit flesh softening rate in peach [*Prunus persica* (L.) Batsch]. *Frontiers in Plant Science*. Q1.
34. Parra, J., Largo, A., Carrasco, T., Celiz, J., Sepulveda, P., Temple, H., Sanhueza, D., Reyes, F., **Meneses, C.**, Saez, S., Orellana. 2019. New steps in mucilage biosynthesis revealed by analysis of the transcriptome of the UDP-rhamnose/UDP-galactose transporter 2 mutant. *Journal of Experimental Botany*. Q1.
35. Ortiz, J., Soto, J., Fuentes, J., Herrera, H., **Meneses, C.**, Arriagada, C. 2019. The endophytic Fungus *Chaetomium cupreum* regulates expression of genes involved in the tolerance to metals and plant growth promotion in *Eucalyptus globulus* roots. *Microorganisms*. Q2.
36. Gavicho, V., Fuentealba, C., Hernández, I., Defilippi, B., **Meneses, C.**, Campos, R., Lurie, S., Hertog, M., Carpentier, S., Poblete, C., Pedreschi, R. 2019. Integration of proteomics and metabolomics data of early and middle season Hass avocados under heat treatment. *Food Chemistry*. Q1.
37. Vergara, C., Rothkegel, K., González, M., Pedreschi, R., Campos, R., Defilippi, B., **Meneses, C.** 2019. De novo assembly of *Persea americana* cv. 'Hass' transcriptome during fruit development. *BMC Genomics*. Q2.
38. Zepeda, B., Olmedo, P., Ejsmentewicz, T., Sepúlveda, P., Balic, I., Balladares, C., Delgado, J., Fuentealba, C., Moreno, A., Defilippi, B., **Meneses, C.**, Pedreschi, R., Campos, R. 2018. Cell wall and metabolite composition of berries of *Vitis vinifera* (L.) cv. Thompson Seedless with different firmness. *Food Chemistry*. Q1.
39. Arraño, P., Domínguez, J., Herrera, A., Zavala, D., Medina, J., Vicente, J., **Meneses, C.**, Canessa, P., Moreno, A., Blanco, F. 2018. WRKY7, -11 and -17 transcription factors are modulators of the bZIP28 branch of the unfolded protein response during PAMP-triggered immunity in *Arabidopsis thaliana*. *Plant Science*. Q1.

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40. Rodríguez, F., Laporte, D., González, A., Mendez, K., Castro, E., **Meneses, C.**, Huidobro-, J., Moenne. 2018. Copper-induced increased expression of genes involved in photosynthesis, carotenoid synthesis and C assimilation in the marine alga *Ulva compressa*. BMC Genomics. Q2.
41. Cabezas, C, Briones, A., Aguirre, C., Pardo, C., Castro, J., Salinas, C., Baquedano, M., Hidalgo, A., Fuentes, J., Morales, E., **Meneses, C.**, Castro, E., Saavedra, C. 2018. The transcription factor SlyA from *Salmonella Typhimurium* regulates genes in response to hydrogen peroxide and sodium hypochlorite. Research in Microbiology. Q2.
42. Gutierrez, I., Miossec, M., Valenzuela, S., **Meneses, C.**, Dos Santos, V, Castro, E., Poblete, I. 2018. Genome sequence of two members of the chloroaromatic-degrading MT community: Pseudomonas reinekei MT1 and Achromobacter xylosoxidans MT3 (2018). Journal of Biotechnology. Q2.
43. Cifuentes, N., Celiz, J., Henriquez, C., Mitina, I., Arraño, P., Moreno, A., **Meneses, C.**, Blanco, F., Orellana, A. 2018. bZIP17 regulates the expression of genes related to seed storage and germination, reducing seed susceptibility to osmotic stress. Journal of Cellular Biochemistry. Q2.
44. Biondi, E., Zamorano, A., Vega, E., Ardizzi, S., Sitta, D., De Salvador, F., Campos, R., **Meneses, C.**, Perez, S., Bertaccini, A., Fiore, N. 2018. Draft whole genome sequence analyses on Pseudomonas syringae pv. actinidiae hypersensitive response negative strains detected from kiwifruit bleeding sap samples. Phytopathology. Q1.
45. Nardocci, G., Carrasco, M., Acevedo, E., Hodar, C., **Meneses, C.**, Montecino, M. 2018. Identification of a novel long noncoding RNA that promotes osteoblast differentiation. Journal of Cellular Biochemistry. Q2.
46. Mendez, K., Zuloaga, R., Valenzuela, C, Bastias, M., **Meneses, C.**, Vizoso, P., Valdés, J., Molina. 2018. A. RNA-seq analysis of compensatory growth in the skeletal muscle of fine flounder (*Paralichthys adspersus*). Aquaculture. Q1.
47. Balic, I., Vizoso, P., Nilo, R., Sanhueza, D., Olmedo, P., Sepúlveda, P., Arriagada, C., Defilippi, B., **Meneses, C.**, Campos, R. 2018. Transcriptome analysis during ripening of table grape berry cv. Thompson Seedless. PLoS ONE. Q2.
48. Olmedo, P., Moreno, A., Sanhueza, D., Balic, I., Silva, C., Zepeda, B., Verdonk, J., Arriagada, C., **Meneses, C.**, Campos, R. 2017. A catechol oxidase AcPPO from cherimoya (*Annona cherimola* Mill.) is localized to the Golgi apparatus. Plant Science. Q1.
49. Aballai, V., Aedo, J., Maldonado, J., Bastias, M., Silva, H., **Meneses, C.**, Boltaña, S., Reyes, A., Molina, A., Valdés, J. 2017. RNA-seq analysis of the head-kidney transcriptome response to handling-stress in the red cusk-eel (*Genypterus chilensis*). Comparative Biochemistry and Physiology - Part D: Genomics and Proteomics. Q3.

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50. Muñoz, C., Espinosa, E., Bascuñán, R., Tapia, S., **Meneses, C.**, Almeida, A. 2017. Development of a molecular marker for self-compatible S4' haplotype in sweet cherry (*Prunus avium* L.) using high-resolution melting. *Plant Breeding*. Q2.
51. Fuentealba, C., Hernández, I., Olaeta, J, Defilippi, B., **Meneses C.**, Lurie S., Carpentier, S., Pedreschi R. 2017. New insights into the heterogeneous ripening in Hass avocado via LC-MS/MS proteomics. *Postharvest Biology and Technology*. Q1.
52. Naour, S., Espinoza, B., Aedo, J., Zuloaga, R., Maldonado, J., Bastia, M., Silva, H., **Meneses, C.**, Gallardo, C., Molina, A., Valdés, J. 2017. Transcriptomic analysis of the hepatic response to stress in the red cusk-eel (*Genypterus chilensis*): Insights into lipid metabolism, oxidative stress and liver steatosis. *PLoS ONE*. Q2.

Proyectos con financiamiento externo últimos 5 años (adjudicado y/o ejecutado)

1. Study of epigenetic control of maturity date in *Prunus persica* by integrating transcriptomic and epigenomic approaches.
Financiamiento: FONDECYT
Rol: Director
Duración: 2020-2023
Año adjudicación: 2019
2. Study of cytokinin applications in early stages of berry development on changes in cell wall metabolism and its effect on the grape firmness in *Vitis vinifera*.
Financiamiento: FONDECYT
Rol: Co-investigador
Duración: 2020-2023
Año adjudicación: 2019
3. AgroIA: Innovación basada en visión computacional y Deep Learning para el sector productivo de uva de mesa y vino.
Financiamiento: FONDEF, IDeA
Rol: Asociado
Duración: 2019-2021
Año adjudicación: 2019
4. Unveiling the bases of temperature modulation in ethylene response on avocado: another chilling dilemma for fruit ripening?
Financiamiento: FONDECYT
Rol: Asociado
Duración: 2017-2021
Año adjudicación: 2017

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5. Influence of drought on the efficiency of arbuscular mycorrhizal symbiosis in phosphorus acquisition by plants growing in Andisols from Southern Chile: wheat as a crop model.
Financiamiento: FONDECYT
Rol: Asociado
Duración: 2017-2021
Año adjudicación: 2017
6. Identification of biomarkers associated with mealiness in peach using mQTL and meQTL
Financiamiento: FONDECYT
Rol: Director
Duración: 2016-2020
Año adjudicación: 2016
7. Centro de Regulación del genoma (CRG)
Financiamiento: FONDAP
Rol: Asociado
Duración: 2016-2020
Año adjudicación: 2016
8. Centro de Excelencia UC Davis-Chile (Línea II): Whole Genome Analytics-Genetics identification of clones/rootstocks for grapevine
Financiamiento: CORFO
Rol: Director
Duración: 2016-2018
Año adjudicación: 2016
9. Centro de Excelencia UC Davis-Chile (Línea II): Whole Genome Analytics-Genetics identification of clones/rootstocks for grapevine. ETAPA II
Financiamiento: CORFO
Rol: Director
Duración: 2018-2020
Año adjudicación: 2018
10. Discovery of Biomarker candidates linked to table grape berry firmness based on transcriptomic and metabolomic analyses
Financiamiento: FONDECYT
Rol: Asociado
Duración: 2015-2020
Año adjudicación: 2015
11. Análisis fisiológico y molecular de la textura del mesocarpo de bayas de uva de mesa
Financiamiento: FONDECYT
Rol: Patrocinante
Duración: 2014-2017
Año adjudicación: 2014

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- 12.** Implementación de una plataforma de marcadores genéticos de apoyo al mejoramiento genético
Financiamiento: CORFO
Rol: Director
Duración: 2014-2019
Año adjudicación: 2014
- 13.** Generación de marcadores moleculares asociados a requerimiento de frío y fecha de floración en cerezos
Financiamiento: CORFO
Rol: Director
Duración: 2014-2019
Año adjudicación: 2014
- 14.** Generación de marcadores para atributos de calidad de impacto económico en postcosecha de duraznos y nectarines
Financiamiento: CORFO
Rol: Director
Duración: 2014-2019
Año adjudicación: 2014
- 15.** Identificación y validación de marcadores moleculares asociados a calidad de fruto en duraznero a través de genómica y metabolómica
Financiamiento: FONDEF
Rol: Asociado
Duración: 2014-2019
Año adjudicación: 2014
- 16.** Programa de mejora genética de kiwi Chile-Italia. Plataforma de selección asistida
Financiamiento: FONDEF
Rol: Asociado
Duración: 2012-2019
Año adjudicación: 2012