
Title

Structural and transcriptional characterization of pyruvate decarboxylase (PDC) gene family during strawberry fruit ripening process

Abstract

Strawberry is one of the most popular fruits in the world, because their high fruit quality, especially with respect to the combination of aroma, flavor, color, and nutritional compounds. Pyruvate decarboxylase (PDC) is the first of two enzymes specifically required for ethanolic fermentation and catalyzes the decarboxylation of pyruvate to yield acetaldehyde and CO₂. The ethanol, an important alcohol which acts as a precursor for the ester and other alcohols formation in strawberry, is produced by the PDC. The objective was found all different PDCs genes present in the strawberry genome and investigate PDC gene expression and ligand-protein interactions in strawberry fruit. Volatile organic compounds were evaluated during the development of the fruit. After this, eight FaPDC were identified with four genes that increase the relative expression during fruit ripening process. Molecular dynamics simulations were performed to analyze the behavior of Pyr and TPP ligands within the catalytic and regulatory sites of the PDC proteins. Results indicated that energy-restrained simulations exhibited minor fluctuations in ligand-protein interactions, while unrestrained simulations revealed crucial insights into ligand affinity. TPP consistently displayed strong interactions with the catalytic site, emphasizing its pivotal role in enzymatic activity. However, FaPDC6 and FaPDC9 exhibited decreased pyruvate affinity initially, suggesting unique binding characteristics requiring further investigation. Finally, the present study contributes significantly to understanding PDC gene expression and the intricate molecular dynamics underlying strawberry fruit ripening, shedding light on potential targets for further research in this critical biological pathway. © 2024 Elsevier Masson SAS

Authors

Hormazábal-Abarza F.; Bustos D.; Rodríguez-Arriaza F.; Sáez D.; Urra G.; Parra-Palma C.; Méndez-Yáñez Á.; Ramos P.; Morales-Quintana L.

Author full names

Hormazábal-Abarza, Francisca (58884555800); Bustos, Daniel (57076160800); Rodríguez-Arriaza, Francisca (58884128000); Sáez, Darwin (23098430700); Urra, Gabriela (58513693600); Parra-Palma, Carolina (56872859400); Méndez-Yáñez, Ángela (57195593304); Ramos, Patricio (54788288200); Morales-Quintana, Luis (36731136500)

Author(s) ID

58884555800; 57076160800; 58884128000; 23098430700; 58513693600; 56872859400; 57195593304; 54788288200; 36731136500

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Affiliations

Multidisciplinary Agroindustry Research Laboratory, Instituto de Ciencias Biomédicas, Facultad de Ciencias de La Salud, Universidad Autónoma de Chile, Cinco Poniente #1670 Talca, Región Del Maule, Chile; Laboratorio de Bioinformática y Química Computacional, Departamento de Medicina Traslacional, Facultad de Medicina, Universidad Católica Del Maule, Talca, 3480094, Chile; Vicerrectoría de Investigación y Postgrado, Universidad Católica Del Maule, Talca, Chile; Programa de Doctorado en Ciencias Biomédicas, Instituto de Ciencias Biomédicas, Facultad de Ciencias de La Salud, Universidad Autónoma de Chile, Chile; Plant Microorganism

Interaction Laboratory, Instituto de Ciencias Biológicas, Universidad de Talca, Talca, Chile

Authors with affiliations

Hormazábal-Abarza F., Multidisciplinary Agroindustry Research Laboratory, Instituto de Ciencias Biomédicas, Facultad de Ciencias de La Salud, Universidad Autónoma de Chile, Cinco Poniente #1670 Talca, Región Del Maule, Chile; Bustos D., Laboratorio de Bioinformática y Química Computacional, Departamento de Medicina Traslacional, Facultad de Medicina, Universidad Católica Del Maule, Talca, 3480094, Chile, Vicerrectoría de Investigación y Postgrado, Universidad Católica Del Maule, Talca, Chile; Rodríguez-Arriaza F., Multidisciplinary Agroindustry Research Laboratory, Instituto de Ciencias Biomédicas, Facultad de Ciencias de La Salud, Universidad Autónoma de Chile, Cinco Poniente #1670 Talca, Región Del Maule, Chile; Sáez D., Multidisciplinary Agroindustry Research Laboratory, Instituto de Ciencias Biomédicas, Facultad de Ciencias de La Salud, Universidad Autónoma de Chile, Cinco Poniente #1670 Talca, Región Del Maule, Chile, Programa de Doctorado en Ciencias Biomédicas, Instituto de Ciencias Biomédicas, Facultad de Ciencias de La Salud, Universidad Autónoma de Chile, Chile; Urra G., Vicerrectoría de Investigación y Postgrado, Universidad Católica Del Maule, Talca, Chile; Parra-Palma C., Multidisciplinary Agroindustry Research Laboratory, Instituto de Ciencias Biomédicas, Facultad de Ciencias de La Salud, Universidad Autónoma de Chile, Cinco Poniente #1670 Talca, Región Del Maule, Chile; Méndez-Yáñez Á., Multidisciplinary Agroindustry Research Laboratory, Instituto de Ciencias Biomédicas, Facultad de Ciencias de La Salud, Universidad Autónoma de Chile, Cinco Poniente #1670 Talca, Región Del Maule, Chile; Ramos P., Vicerrectoría de Investigación y Postgrado, Universidad Católica Del Maule, Talca, Chile, Plant Microorganism Interaction Laboratory, Instituto de Ciencias Biológicas, Universidad

de Talca, Talca, Chile; Morales-Quintana L., Multidisciplinary Agroindustry Research Laboratory, Instituto de Ciencias Biomédicas, Facultad de Ciencias de La Salud, Universidad Autónoma de Chile, Cinco Poniente #1670 Talca, Región Del Maule, Chile

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References

Aharoni A., Keizer L.C., Bouwmeester H.J., Sun Z., Alvarez-Huerta M., Verhoeven H.A., Blaas J., van Houwelingen A.M., De Vos R.C., van der Voet H., Jansen R.C., Guis M., Mol J., Davis R.W., Schena M., van Tunen A.J., O'Connell A.P., Identification of the SAAT gene involved in strawberry flavor biogenesis by use of DNA microarrays, *Plant Cell*, 12, pp. 647-662, (2000); Baek M., DiMaio F., Anishchenko I., Dauparas J., Ovchinnikov S., Lee G.R., Wang J., Cong Q., Kinch L.N., Schaeffer R.D., Millan C., Park H., Adams C., Glassman C.R., DeGiovanni A., Pereira J.H., Rodrigues A.V., van Dijk A.A., Ebrecht A.C., Opperman D.J., Sagmeister T., Buhlheller C., Pavkov-Keller T., Rathinaswamy M.K., Dalwadi U., Yip C.K., Burke J.E., Garcia K.C., Grishin N.V., Adams P.D., Read R.J., Baker D., Accurate prediction of protein structures and interactions using a three-track neural network, *Science*, 373, pp. 871-876, (2021); Caleb O.J., Fawole O.A., Mphahlele R.R., Opara U.L., Impact of preharvest and postharvest factors on changes in volatile compounds of pomegranate fruit and minimally processed arils-review, *Sci. Hortic.*, 188, pp. 106-114, (2015); Chou K.-C., Shen H.-B., Plant-mPLOC: a top-down strategy to augment the power for predicting plant protein subcellular localization, *PLoS One*, 5, (2010); Defilippi B.G., Manriquez D., Luengwilai K., Gonzalez-Aguero M., Chapter 1 aroma volatiles: biosynthesis and mechanisms of modulation during fruit ripening, *Advances in Botanical Research*, pp. 1-37, (2009); Edger P.P., Poorten T.J., VanBuren R., Hardigan M.A., Colle M., McKain M.R., Smith R.D., Teresi S.J., Nelson A.D.L., Wai C.M., Alger E.I., Bird K.A., Yocca A.E., Pumpllin N., Ou S., Ben-Zvi G., Brodt A., Baruch K., Swale T., Shiue L., Acharya C.B., Cole G.S., Mower J.P., Childs K.L., Jiang N., Lyons E., Freeling M., Puzey J.R., Knapp S.J., Origin and evolution of the octoploid strawberry genome, *Nat.*

Genet., 51, pp. 541-547, (2019); Gasteiger E., Gattiker A., Hoogland C., Ivanyi I., Appel R.D., Bairoch A., ExPASy: the proteomics server for in-depth protein knowledge and analysis, *Nucleic Acids Res.*, 31, pp. 3784-3788, (2003); Halgren T.A., Murphy R.B., Friesner R.A., Beard H.S., Frye L.L., Pollard W.T., Banks J.L., Glide: a new approach for rapid, accurate docking and scoring. 2. Enrichment factors in database screening, *J. Med. Chem.*, 47, pp. 1750-1759, (2004); Higo K., Ugawa Y., Iwamoto M., Korenaga T., Plant cis-acting regulatory DNA elements (PLACE) database: 1999, *Nucleic Acids Res.*, 27, pp. 297-300, (1999); Hummer K.E., Nathewet P., Yanagi T., Decaploidy in *Fragaria iturupensis* (rosaceae), *Am. J. Bot.*, 96, pp. 713-716, (2009); Jia H.-F., Chai Y.-M., Li C.-L., Lu D., Luo J.-J., Qin L., Shen Y.-Y., Abscisic acid plays an important role in the regulation of strawberry fruit Ripening1[W][OA], *Plant Physiol.*, 157, pp. 188-199, (2011); Ke D., Yahia E., Mateos M., Kader A.A., Ethanol fermentation of Bartlett pears as influenced by ripening stage and atmospheric composition, *J. Am. Soc. Hortic. Sci. U. S.*, 119, (1994); Ke D., Zhou L., Kader A.A., Mode of oxygen and carbon dioxide action on strawberry ester biosynthesis, *J. Am. Soc. Hortic. Sci.*, 119, pp. 971-975, (1994); Kyriacou M.C., Leskovar D.I., Colla G., Roupheal Y., Watermelon and melon fruit quality: the genotypic and agro-environmental factors implicated, *Sci. Hortic.*, 234, pp. 393-408, (2018); Kutter S., Weiss M.S., Wille G., Golbik R., Spinka M., König S., Covalently bound substrate at the regulatory site of yeast pyruvate decarboxylases triggers allosteric enzyme activation, *J. Biol. Chem.*, 284, pp. 12136-12144, (2009); Kutter S., Wille G., Relle S., Weiss M.S., Hubner G., König S., The crystal structure of pyruvate decarboxylase from *Kluyveromyces lactis*. Implications for the substrate activation mechanism of this enzyme, *FEBS J.*, 273, pp. 4199-4209, (2006); Mithran M., Paparelli E., Novi G., Perata P., Loreti E., Analysis of the role of the pyruvate decarboxylase gene family in *Arabidopsis thaliana* under low-oxygen conditions, *Plant Biol. Stuttg. Ger.*, 16, pp. 28-34, (2014); Morales-Quintana L., Ramos P., Chilean strawberry (*Fragaria chiloensis*): an integrative and comprehensive review,

Food Res. Int., 119, pp. 769-776, (2019); Moyano E., Encinas-Villarejo S., Lopez-Raez J.A., Redondo-Nevado J., Blanco-Portales R., Bellido M.L., Sanz C., Caballero J.L., Munoz-Blanco J., Comparative study between two strawberry pyruvate decarboxylase genes along fruit development and ripening, post-harvest and stress conditions, Plant Sci., 166, pp. 835-845, (2004); Ms E., K M., Decarboxylation of pyruvate to acetaldehyde for ethanol production by hyperthermophiles, Biomolecules, 3, (2013); Muller Y.A., Lindqvist Y., Furey W., Schulz G.E., Jordan F., Schneider G., A thiamin diphosphate binding fold revealed by comparison of the crystal structures of transketolase, pyruvate oxidase and pyruvate decarboxylase, Struct. Lond. Engl., 1, pp. 95-103, (1993); Munoz M.T., Escribano M.I., Merodio C., Ethanol metabolism in cherimoya fruit during storage at ambient and under high CO₂ atmospheres, J. Hortic. Sci., 72, pp. 363-370, (1997); Olsson M.H.M., Sondergaard C.R., Rostkowski M., Jensen J.H., PROPKA3: consistent treatment of internal and surface residues in empirical pK_a predictions, J. Chem. Theor. Comput., 7, pp. 525-537, (2011); Parra-Palma C., Ubeda C., Gil M., Ramos P., Castro R.I., Morales-Quintana L., Comparative study of the volatile organic compounds of four strawberry cultivars and its relation to alcohol acyltransferase enzymatic activity, Sci. Hortic., 251, pp. 65-72, (2019); Ramos P., Parra-Palma C., Figueroa C.R., Zuniga P.E., Valenzuela-Riffo F., Gonzalez J., Gaete-Eastman C., Morales-Quintana L., Cell wall-related enzymatic activities and transcriptional profiles in four strawberry (*Fragaria x ananassa*) cultivars during fruit development and ripening, Sci. Hortic., 238, pp. 325-332, (2018); Rombauts S., Dehais P., Van Montagu M., Rouze P., PlantCARE, a plant cis-acting regulatory element database, Nucleic Acids Res., 27, pp. 295-296, (1999); Roos K., Wu C., Damm W., Reboul M., Stevenson J.M., Lu C., Dahlgren M.K., Mondal S., Chen W., Wang L., Abel R., Friesner R.A., Harder E.D., OPLS3e: extending Force Field Coverage for Drug-Like Small Molecules, J. Chem. Theor. Comput., 15, pp. 1863-1874, (2019); Shahan R., Li D., Liu Z., Identification of genes preferentially expressed in wild strawberry receptacle fruit and

demonstration of their promoter activities, *Hortic. Res.*, 6, (2019); Sievers F., Wilm A., Dineen D., Gibson T.J., Karplus K., Li W., Lopez R., McWilliam H., Remmert M., Soding J., Thompson J.D., Higgins D.G., Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega, *Mol. Syst. Biol.*, 7, (2011); Stanke M., Diekhans M., Baertsch R., Haussler D., Using native and syntenically mapped cDNA alignments to improve de novo gene finding, *Bioinforma. Oxf. Engl.*, 24, pp. 637-644, (2008); Staudt G., Strawberry biogeography, genetics and systematics, *Acta Hortic.*, pp. 71-84, (2009); Symons G.M., Chua Y.-J., Ross J.J., Quittenden L.J., Davies N.W., Reid J.B., Hormonal changes during non-climacteric ripening in strawberry, *J. Exp. Bot.*, 63, pp. 4741-4750, (2012); Tamura K., Stecher G., Kumar S., MEGA11: molecular evolutionary genetics analysis version 11, *Mol. Biol. Evol.*, 38, pp. 3022-3027, (2021); Ulrich D., Kecke S., Olbricht K., What do we know about the chemistry of strawberry aroma?, *J. Agric. Food Chem.*, 66, pp. 3291-3301, (2018); Ulrich D., Komes D., Olbricht K., Hoberg E., Diversity of aroma patterns in wild and cultivated *Fragaria* accessions, *Genet. Resour. Crop Evol.*, 54, pp. 1185-1196, (2007); Urrutia M., Rambla J.L., Alexiou K.G., Granell A., Monfort A., Genetic analysis of the wild strawberry (*Fragaria vesca*) volatile composition, *Plant Physiol. Biochem.*, 121, pp. 99-117, (2017); Valenzuela-Riffo F., Parra-Palma C., Ramos P., Morales-Quintana L., Molecular and structural insights into FaEXPA5, an alpha-expansin protein related with cell wall disassembly during ripening of strawberry fruit, *Plant Physiol. Biochem.*, 154, pp. 581-589, (2020); Vandesompele J., De Preter K., Pattyn F., Poppe B., Van Roy N., De Paepe A., Speleman F., Accurate normalization of real-time quantitative RT-PCR data by geometric averaging of multiple internal control genes, *Genome Biol.*, 3, (2002); Xu Y., Charles M.T., Luo Z., Roussel D., Rolland D., Potential link between fruit yield, quality parameters and phytohormonal changes in preharvest UV-C treated strawberry, *Plant Physiol. Biochem.*, 116, pp. 80-90, (2017); Yan J.W., Ban Z.-J., Lu H.-Y., Li D., Poverenov E., Luo Z.-S., Li L., The aroma volatile repertoire in strawberry fruit: a review, *J. Sci.*

Food Agric., 98, pp. 4395-4402, (2018)

Correspondence Address

L. Morales-Quintana; Multidisciplinary Agroindustry Research Laboratory, Instituto de Ciencias Biomédicas, Facultad de Ciencias de La Salud, Universidad Autónoma de Chile, Cinco Poniente #1670 Talca, Región Del Maule, Chile; email: luis.morales@uautonoma.cl; P. Ramos; Vicerrectoría de Investigación y Postgrado, Universidad Católica Del Maule, Talca, Chile; email: pramos@utalca.cl

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