REVIEW

Pharmaceutical, food potential, and molecular data of *Hancornia speciosa* Gomes: a systematic review

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Abstract *Hancornia speciosa* Gomes is a fruit and medicinal tree species native to South America, which in Brazil is considered of potential economic value and priority for research and development. We present a map of the state-of-art, including articles, patents, and molecular data of the species to identify perspectives for future research. The annual scientific production, intellectual, social, and conceptual structure were evaluated, along with the number of patent deposits, components of the plant used, countries of deposit, international classification and assignees, and the accessibility of available molecular data. Brazil has the most significant publications (306) between 1992 and 2020. Technological products (29) have been developed from different tissues of the plant. Most of the articles and patents were developed by researchers from public universities from different regions of Brazil. The molecular data are sequences of nucleotides (164) and proteins (236) of the chloroplast

genome and are described to identify the species as DNA barcodes and proteins involved in photosynthesis. The compilation and report of scientific, technological, and molecular information in the present review allowed the identification of new perspectives of research to be developed based on the gaps in knowledge regarding the species and perspectives for the definition of future research.

Keywords Mangaba · Biodiversity · Bioeconomy · Ethnopharmacology · Scientific mapping · Patents

Introduction

Fundamental concepts within Latin America have led to the adoption of bio-economy principles, which consists of the evolution to a new economic system based on the sustainable use of resources (Lewandowski 2018), with different levels of socio-economic impact. They highlight the valorization of biodiversity resources in medicine as one of the critical areas addressed (Sasson and Malpica 2018). Given economic limitations, there is a demand for low-cost, accessible, and effective medicines that can assist as an alternative or complementary medication for healing diseases, especially for middle-high, medium-low, and low-income citizens (Goyal and Ayeleso 2018).

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Since ancient times, plants are a source of essential products for human life, including food and medicines, especially in socio-economic vulnerability communities. *Hancornia speciosa* Gomes (Apocynaceae) is a fruit and medicinal tree species native of South America and is among the countless plants used by traditional communities. Its populations are widely distributed in neotropical biogeographic region, specifically Northwest and Midwest of Brazil, Paraguay, Peru, and Bolivia (GBIF 2021; Tropicos 2021). The species is a perennial, semideciduous, or deciduous plant, changing its leaves during the driest period of the year. The fruiting phase varies in different regions of Brazil, including on the coast of the Northeast. There are two fruiting phases (winter—May to July or July to October; and summer—January to April or December to April) (Oliveira and Alo-ufa 2020). However, in the Cerrado Biome, fruits can also be collected throughout the year (Campos et al. 2018); in the Midwest, only one collection per year is reported (from October to May) (Campos et al. 2018).

The fruits are harvested mainly by extractivist that chosen them from natural populations in local communities. *H. speciosa* research on domestication and agronomic techniques for sustainable and commercial cultivation is still in its early stages (Paula et al. 2019). There are indications that commercial plantations are being established in the Northeast and Midwest regions. However, in the literature, there is no data available (EMATER 2019). The fruits are commercialized *in nature* or industrialized as pulps for juices, ice creams, liqueurs, and jellies (Cardoso et al. 2014; Santos et al. 2017). There is great interest in *H. speciosa* fruits which are rich in potassium, iron, zinc, ascorbic acid, phenolic compounds, and carotenoids such as β -carotene, β -cryptoxanthin, α -tocopherol, and α -, β -, and γ -tocotrienols (Cardoso et al. 2014; De Lima et al. 2015a, b).

Furthermore, local communities traditionally use the plant to treat various diseases (Moraes et al. 2008; Cercato et al. 2015). Its latex has anti-inflammatory (Marinho et al. 2011), angiogenic (Almeida et al. 2014), and osteogenic (Floriano et al. 2016) properties. The leaves have anti-diabetic (Pereira et al. 2015) and antioxidant (Marques et al. 2015) effects, which provide wound healing and anti-inflammatory action (Geller et al. 2015). Ethnobotanical, pharmacological, and chemical reports highlight *H. speciosa* as the

most cited among the 78 species distributed in 27 genera in Brazil (Santos et al. 2013).

Popularly known as ‘mangaba’ (meaning, a good thing to eat in Tupi-Guarani indigenous dialect), was used last century for the extraction of latex as feedstock to produce rubber. However, such activity was further interrupted due to its low productivity compared to *Hevea brasiliensis* L. (rubber tree) (Vieira Neto et al. 2002; Bonete et al. 2020).

The species is conserved mainly through live plants in the field in Active Germplasm Banks in Brazil. There are 1,438 accessions distributed in eight banks maintained by public institutions, Embrapa Amapá (86 accessions), Embrapa Cerrados (15 accessions), Embrapa Meio Norte (39 accessions), Embrapa Tabuleiros Costeiros (271 accessions), State Agricultural Research Company of Paraíba (540 accessions), Federal University of Alagoas (20 accessions), Federal University of Goiás (57 accessions) and State University of Goiás (400 accessions) (Da Silva Júnior et al. 2018a).

H. speciosa is included in the list of species of Brazilian flora that have current or potential economic value. Therefore, it is considered a priority species for research and development (Coradin et al. 2018). Despite presenting bioeconomic importance, it is part of the list of underutilized species that provide food composition's Nutrition Indicators for Biodiversity (FAO 2021). Therefore, it is essential to map the studies and the gaps in relevant information to support and guide future research on the species. Accordingly, systematic reviews that use bibliometric analyses are helpful, as they provide objective and reliable information (Aria and Cuccurullo 2017).

One of the steps to carry out bibliometric studies is to obtain scientific metadata based on online databases of bibliographic information (Zupic and Čater 2015). Bibliometrics enable the measurement and evaluation of research results presented in a written form and the most diverse graphic representations (Ball 2017) and are also relevant for understanding the current scenarios of the points of interest.

Additionally, technical patent information can be accessed in databases from the World Intellectual Property Organization, the European Patent Office, Espacenet-Latipat, and the National Institute of Industrial Property. In increase, molecular tools may assist with complementary knowledge which can be used in assessing the level of domestication of the

species and are available in public databanks such as the Genetic Sequence Database, the European Molecular Biology Laboratory, the DNA Data Bank of Japan, the Universal Protein Resource, and the Barcode of Life Data System. This review proposes to map (1) the scientific studies, (2) the patented technological products, and (3) the molecular data in public banks for *H. speciosa* in order to contribute to the trend of future research.

Methods

The literature survey was conducted in November 2020 with the following keywords: “*Hancornia speciosa*” or “mangaba” or “mangaba tree.” The data was searched by title, abstract, and/or keywords of scientific articles; the title and patents abstract. The nucleotide and protein sequences were prospected in public banks using the term “*Hancornia speciosa*” for the molecular data. A time frame was not delimited to obtain as much information as possible (Fig. 1).

Scientific mapping

Articles were searched in the scientific bases of Scopus (<http://www.scopus.com>) and Web of Science (<http://www.webofknowledge.com>). The title and abstracts that did not match the research terms were excluded. The metadata referring to the scientific publications obtained for each term in the two databases was exported in BibTeX format, excluding the duplicate files. They were combined into a single data set and examined with the aid of the Bibliometrix R-package (Aria and Cuccurullo 2017). The annual scientific production was evaluated regarding the number of articles on the species published per year concomitantly with the H index, which measures the impact of the citations and considers the set of the most cited works and the number of citations they received (Aria et al. 2020).

The Intellectual Structure was assessed by the co-citation examination that uses co-citations to build similarity measures with documents, authors, or journals (McCain 1991; Kang et al. 2020). It is possible to measure the relationship between two articles based on the number of publications that are concurrently cited, estimating the impact and

influence of the different authors in the specific field (Aria et al. 2020).

The Social Structure was evaluated by the world map of collaborations for which at least one collaboration among the authors from different countries (Aria and Cuccurullo 2017). The Conceptual Framework was evaluated by thematic mapping, which allows the visualization of four different types of themes based on density, i.e., the strength of the internal links among all of the keywords used to describe the research topic, concurrently with the centrality and the strength of the external links with other themes, hence investigating the authors’ keyword field (Aria and Cuccurullo 2017; Mumu et al. 2020).

Technological mapping

The patents were prospected by the World Intellectual Property Organization—WIPO (<https://www.wipo.int/portal/en/index.html>), the European Patent Office—EPO (<https://www.epo.org/>), Espacenet-Latipat (https://lp.espacenet.com/?locale=pt_LP), and the National Institute of Industrial Property (Instituto Nacional da Propriedade Industrial)—INPI (<https://www.gov.br/inpi/pt-br>). The duplicated documents that did not match the research were reviewed and excluded. Data were evaluated for the tissues of the plant, the countries of the patent filed, the international code patent classification, and the assignees.

Molecular data mapping

The nucleic acid sequences were prospected in public molecular databanks as the Genetic Sequence Database—GenBank (<http://www.ncbi.nlm.nih.gov/genbank>), the Barcode of Life Data System—BOLD (<http://www.barcodinglife.org>) and the Swiss Institute of Bioinformatics—SIB (<https://www.sib.swiss>). The data were assessed for the nature of molecular information registered.

Results

Scientific mapping

Four hundred and seven (407) documents were accessed for *H. speciosa* species, which were indexed

Fig. 1 Flowchart of the scientific, technological, and molecular data mapping for *Hancornia speciosa* Gomes

in the Web of Science (189) and Scopus (218). After processing the data and excluding the duplicates, 303 documents (Supplementary data 1) remained for the study articles published from 1992 to 2020. The publications on *H. speciosa* showed an annual growth rate of 9.28%. There were 35 articles in 2009, whereas in subsequent years, publications ranged from 11 in 2013 to 28 in 2017. The documents were distributed in 129 sources (journals) from which one third of the total were published in seven journals, Revista

Brasileira de Fruticultura (30), Ciência e Agrotecnologia (18), Pesquisa Agropecuária Brasileira (16), Bioscience Journal (12), Ciência e Tecnologia de Alimentos (8), Ciência Florestal (8), and the Journal of Ethnopharmacology (8), which were among those with the highest H-index, i.e. H-9 for the Revista Brasileira de Fruticultura and for the Ciência e Agrotecnologia; H-8 for the Brazilian Agricultural Research and the Journal of Ethnopharmacology; H-5 for the Bioscience Journal; and H-4 for the Forest

Science and the Food Science and Technology journals.

Nine hundred seventy-one authors wrote the articles with an average value of 0.319 documents per author. Among the total, 99.69% of the documents had multiple authorship, and 0.31% had single authorship. Regarding the collaboration of authors, there were 3.13 authors per document, 5.09 co-authors per document, and a collaboration index equal to 3.16. The intellectual structure of the publications on *H. speciosa* was evaluated by the document co-citation network and presented in Fig. 2.

Three distinct groups were identified among the studies on *H. speciosa*, represented by blue, green, and red. The closely related articles had similar characteristics. Therefore, a group with solid co-citation relationships was considered a thematic area of research (Hjørland 2013).

The intellectual structure was the knowledge base of a theme or field of research. In studies with *H. speciosa*, three main fields of research were identified. The first has studies that characterize and investigate the biotechnological potential of latex (Marinho et al.

2011; Almeida et al. 2014; Floriano et al. 2016) (blue—Fig. 2) and leaves (Ferreira et al. 2007b, a; Silva et al. 2011; Pereira et al. 2015). The research field consisted of studies on the *H. speciosa* fruit (green—Fig. 2), which analyzed the composition and traits of the pulp (Cardoso et al. 2014; De Lima et al. 2015b), the bioactive compounds, and the antioxidant potential (Rufino et al. 2010; De Lima et al. 2015a). Finally, reports on the species morphological and genetic diversity studies in the third field of research (color red—Fig. 2). Some examples are studies carried out by Monachino (1945), which considered the morphological differences in the leaves, fruits, and flowers, indicating six botanical variations. There were studies on the morphological variability of the trees and fruits (Ganga et al. 2010), floral morphology (Darrault and Schlindwein 2005), diversity and the genetic structure of the natural populations (Collevatti et al. 2016), and the accessions of the Germplasm Banks (Santos et al. 2017).

The social structure of research on the species was evaluated by the world map of collaborations (Fig. 3), for which at least one collaboration between the

Fig. 2 The network of quotations of documents of *Hancornia speciosa* Gomes

Fig. 3 World collaboration map for the publications on *Hancornia speciosa* Gomes

authors from different countries was considered. Brazil figured as the country with the most significant number of publications, all developed by Brazilian researchers. There were also collaborations of Brazil and the United States of America (5), Canada (3), Germany (2), Portugal (2), Australia (2), Italy (1), Spain (1), and Colombia (1).

Although there were reports on the species that were developed by international collaboration, they were mainly produced by researchers from universities in Brazil, whereas the social structure of the reports was based on four central scientific communities, i.e. (1) the researchers from the Federal University of Goiás, the State University of Goiás, the Pontifical Catholic University of Goiás (PUC Goiás—private educational institution), and the Federal Institute of Education, Science, and Technology of Goiás (IFG); (2) the Federal University of Sergipe (UFS), which collaborates with the Embrapa Tabuleiros Costeiros, the Tiradentes University (private educational institution), and the Federal University of Minas Gerais (UFMG); (3) the researchers from two communities, who developed activities with the researchers from the State University of Campinas (Unicamp) and the São Paulo State University (UNESP); and (4) the Federal University of Lavras

(UFLA) and the Federal University of Paraíba (UFPB). Furthermore, a total of 250 keywords were examined to create the thematic map (Fig. 4) in which the minimum frequency of the group was five and the number of labels (for each group) was 1.

When considering the centrality and density parameters, the thematic map was divided into four quadrants, i.e. (1) the upper right quadrant (high centrality, high density), showing that the primer themes are well developed, with important themes for the structuring of a research field; (2) the upper left quadrant (high centrality, low density) demonstrating the specialized themes and peripheral character, with only marginal importance for the field; (3) the lower left quadrant (low centrality, low density) expressing that the emerging or decreasing themes are developed weakly and marginally; and (4) the lower right quadrant (low centrality, high density) depicting that the basic, transversal, and general themes are essential for a research field but that they are not well developed (Cobo et al. 2011).

The most developed themes in the literature formed four groups of study on *H. speciosa* (Fig. 4), i.e., (1) Cerrado, which included the keywords related to the different studies on the species, such as different botanical variations, ethnobotanical studies,

Fig. 4 Thematic map of the publications on *Hancornia speciosa* Gomes

ethnopharmacology, and the studies on the molecular markers; (2) Post-harvest, meaning the food potential of *H. speciosa*; (3) Brazil, indicating the regions where the species occurrence, with its fruits, physicochemical properties, antioxidants, and vitamins; and 4) The advanced glycation end products, which combined terms, such as xanthine oxidase, hypoxanthine, methylglyoxal, glyoxal, and Reactive carbonyl species (RCS)-trapping.

The advanced glycation end products (AGEs) represented a set of substances that directly contribute to the triggering and/or aggravation of the pathologies that are associated with aging (Marques et al. 2018), and the terms grouped in this cluster were present in publications that investigated the potential of the *H. speciosa* extracts to inhibit the glycation process.

The specialized and peripheral themes (Fig. 4) formed the groups, i.e., (1) cytotoxicity; (2) l-(+)-bomnesitol; (3) enzymatic browning; and (4) biomaterial. The terms related to the photochemical studies, the biological activities, and the cytotoxic activities of the extracts, were grouped (Ribeiro et al. 2012; Santos et al. 2016) with the cytotoxic studies on latex (Almeida et al. 2014; Ribeiro et al. 2016) and fruits (Assumpção et al. 2014).

The studies on the methods used for the preservation of the nutritional compounds (freezing, drying, pasteurization, and lyophilization) were also grouped with the bioactive and antioxidant activities of the

pulp (Paula et al. 2019; Zitha et al. 2020) to short post-harvest longevity which is a characteristic that limits the commercialization of the fresh fruit. The potential of latex was also reported as a biomaterial for a biomembrane with angiogenic, anti-inflammatory, and antibacterial activities (Almeida et al. 2019), as well as anti-biofilm activities in the regeneration of skin wounds (Bonete et al. 2020).

In the lower-left quadrant are the groups such as an acceptance test, viscosity test, and native species, which display themes that were developed weakly and marginally (Fig. 4). The groups with acceptance and viscosity tests brought together the sensory analyses of food products, for example, dairy drinks (Da Silva et al. 2015; Moura et al. 2016), ice cream (Santos and Silva 2012), and jelly (Zitha et al. 2020). The native species group encompassed varied germination, recalcitrant seeds, tissue culture, *in vitro* conservation, and diversity conservation.

The clusters of nitric oxide, mangaba, tropical fruits, and *Hancornia speciosa* (Fig. 4) are important topics for research; however, they are not well developed. The nitric oxide research group was one of the studies investigating the vasodilatory effect of the ethanolic extract of the *H. speciosa* leaves by activating a mechanism dependent on nitric oxide production (Ferreira et al. 2007a, b; Silva et al. 2011, 2016). The other clusters included traditional populations, extraction, ethnopharmacology,

germination, conservation, genetic diversity, and other compounds present in the plant, such as rutin, quinic acid, chlorogenic acid, and anthocyanins. These findings are important because *H. speciosa* has many bioactive compounds (Table 1). Some of them have functional properties, with the potential use of the species to treat diseases and others that show the nutritional value as food.

Technological mapping

The prospection of patents based on *H. speciosa* returned 112 documents (WIPO—33, EPO—23, LATI-PAT—26, and INPI—30). With the refinement and the exclusion of duplicate files, 29 patents (Supplementary data 2) remained for review. The technological products had a geographic origin in Brazil. Some deposits were made in countries such as the United States of America, Japan, Argentina, Canada, China, and countries that make up the European Patent Organization and the World Intellectual Property Organization.

These patents were developed by using different tissues of the plant like seeds (Leite et al. 2018), leaves extract (Braga et al. 2009), latex (Neves et al. 2014; Barbosa et al. 2020), fruits (Santana et al. 2016; Barroso et al. 2018), and leaves tissues (Bitencourt et al. 2014; Droppa-Almeida et al. 2019). The technological products based on *H. speciosa* were divided into food products (55. 17%), reagents to produce chemical compounds (24.13%), medicines (17.24%), and cosmetics (3.44%). According to the International Patent Classification (WIPO 2020), these products are inserted in the areas of Human Needs, Operations, Transport, Separation, Mixing, Chemistry, and Metallurgy (Table 2).

Most of the patent assignment institutions on *H. speciosa* were public higher education institutions from different regions of Brazil. Most of them were located in the Northeast region, where Sergipe was the Brazilian State with the most significant number of patents that have been developed by researchers linked to the State Secretariat for Inclusion, Assistance, and Social Development (nine patents), the Federal University of Sergipe (four patents), and the Institute of Technology and Research of Tiradentes University (four patents). Other Northeastern states were also represented by the Federal University of Campina Grande and the Federal University of Paraíba (two

patents each), the Federal University of Rio Grande do Norte, the Federal University of Pernambuco, and the Federal University of Ceará UFRN (one patent each).

In the Southeast Region, there was the Federal University of Minas Gerais and the State University of Campinas (one patent each), and the company Pelenova Biotecnologia S.A., located in the State of São Paulo, with three patents.

Molecular data mapping

The search for *H. speciosa* sequences in the public molecular databases resulted in 164 nucleotides (Supplementary data 3) and 236 protein sequences (Supplementary data 4), obtained from the public Genetic Sequence Database (GenBank). This bank is part of the National Center for Biotechnology Information (NCBI—<http://www.ncbi.nlm.nih.gov>).

In the Barcode of Life Data System (BOLD), two nucleotide sequences were recovered from the Rubisco major subunit genes of ribulose-1,5-bisphosphate (*rbcL*) and Maturase k (*matK*) (Fig. 5).

The deposited sequences were obtained from the chloroplast genome, and they were related to the proteins that perform functions in photosynthesis, metabolism, transcription, ribosomal proteins, protein quality control and assembly, and membrane insertion. For some of them, three-dimensional structures were verified in the Swiss Institute of Bioinformatics (SIB) (Fig. 6).

Discussion

World governments face challenges such as feeding a growing population and mitigating environmental and social impacts while pursuing economic growth (Miranda et al. 2020). As part of the solution to these global challenges, a bioeconomy encompasses production from the biological basis and its conversion into food, feed, and bioenergy (Aguilar et al. 2018). Currently, in the world, there are different policies and strategies related to the bioeconomy. In South America, the strategies are more focused on using biodiversity as a source of medicines and functional foods through biotechnology and the production of biofuels (Sasson and Malpica 2018).

In Brazil, *H. speciosa* is an important asset for the bioeconomy as it enables the supply of food with

Table 1 Bioactive compounds identified in the different tissues of the *Hancornia speciosa* Gomes plants and their functional properties

Compounds	Property	Tissue	Reference
Rutin	Antidiabetic—inhibition of α -amylase and α -glucosidase, Anti-cancer Anti-inflammatory, AChE and BChE inhibition, Antihypertensive, Promising main protease inhibitor, and other SARS-CoV-2 protein targets	Leaves Shells Fruits	Silva et al. 2011; Perk et al. 2014; Pereira et al. 2015; Torres-Rêgo et al. 2016; Ghorbani 2017; Nikfarjam et al. 2017; Dos Santos et al. 2018; Al-Zahrani 2020; Das et al. 2020; Leite et al. 2020
L-(+)-Bornesitol	Angiotensin converting the enzyme inhibitors, Antihypertensive, Cancer chemopreventive agent	Leaves	Endringer et al. 2009, 2014; Silva et al. 2011; Moreira et al. 2019
Quinic acid	Anti-inflammatory—inhibition of NF- κ B and TNF- α production Inhibition of α -glucosidase, Chemopreventive, Antihypertensive	Leaves	Endringer et al. 2009; Pereira et al. 2011; Silva et al. 2011; Geller et al. 2015
Chlorogenic acid	Anti-inflammatory	Leaves Fruits Latex	Torres-Rêgo et al. 2016
Catechin	Anti-cancer, Antiobesity, Antidiabetic—inhibition of α -amylase and α -glucosidase, ATI cardiovascular, Anti-infective, Hepatoprotective, Neuroprotective, Antioxidant, AChE and BChE inhibition, Promising antiviral for preventing the formation of the SARS-ACE2 complex of SARS-CoV-2	Leaves Cascas Fruits Latex	Katalinić et al. 2004; Dos Santos et al. 2018; Isemura 2019; Leite et al. 2020; Jena et al. 2021
Isoquercetin	Antioxidant, Antidiabetic— inhibition of α -amylase and α -glucosidase	Leaves	Dos Santos et al. 2018; Leite et al. 2020
β -Carotene	Antioxidant, Antidiabetic, Anti-obesity	Leaves Fruits	Bailão et al. 2015; Dos Santos et al. 2018
Lupeol	Antidiabetic—inhibition of α -glucosidase and protein tyrosine phosphatase-1B	Leaves	Pereira et al. 2015

Table 1 continued

Compounds	Property	Tissue	Reference
α/β -amirin	Antidiabetic	Leaves	Pereira et al. 2015

Table 2 International Classification of the Patents developed with *Hancornia speciosa* Gomes

International patent classification		Symbol
Human necessities	Agriculture; forestry; animal husbandry; hunting; trapping; fishing	A01N65/08, A01P1/00
	Baking; equipment for making or processing doughs; doughs for baking	A21D 13/08
	Foods or foodstuffs; their treatment, not covered by other classes	A23G 3/48, A23G3/54, A23B7/024, A23L 2/00, A23L 3/00, A23L 19/00, A23L 1/064, A23B 7/00, 23B7/0205
	Medical or veterinary science; hygiene	A61L 27/00, A61K 36/24, A61K, 36/00, A61K127/00, A61K131/00, A61K 135/00, A61K7/48, A61K38/16, A61P31/04, A61P31/04, A61L 27/54, A61P 19/08
Performing operations; transporting; separating; mixing	Physical or chemical processes, or apparatus in general	B01D 71/24
	Spraying or atomizing in general; applying liquids or other fluent materials to surfaces in general	B05D 5/00
	Disposal of solid waste; reclamation of contaminated soil	B09B 3/00
	Working of plastics; working of substances in a plastic state in general	B29C 35/00
Chemistry; metallurgy	Treatment of water, wastewater, sewage, or sludge	C02F 1/00, C02F 101/00
	Organic chemistry	C07K14/00
	Organic macromolecular compounds; their preparation or chemical working-up; compositions based thereon	C08B 30/14, C08K 5/053, C08L 3/02
	Biochemistry; beer; spirits; wine; vinegar; microbiology; enzymology; mutation or genetic engineering	C12P 1/00, C12R 1/00, C12N 9/00, C12C 5/00, C12C 12/00, C12G 3/04

Fig. 5 DNA barcodes *rbcL* (A) and *matK* (B) of the species *Hancornia speciosa* Gomes, deposited in the Barcode of Life Data System. Fonte: BOLD System, 2020

nutritional quality and bioactive compounds for medicines, in addition to developing in sandy or sandy clay soils, acidic, poor in nutrients and organic matter, with low retention of water, rough and rocky, considered unwanted for agricultural purposes (Pereira et al. 2016; Da Silva Júnior et al. 2018a).

The number of scientific publications on *H. speciosa* has been growing, and the tendency is to continue considering that the species contributes to the Nutrition Indicators for Biodiversity, according to the International Network of Food Data Systems (FAO/INFOODS), while it is also a Brazilian flora, with current or potential economic value (Coradin et al. 2018; FAO 2021).

The publications on *H. speciosa* were developed by research institutions in Brazil distributed in different regions. A reflection on the wide occurrence of the species in the country presented different biomes and phytophysiognomies. In the Northeast region, it occurs naturally in sandbank areas on the coast of

Fig. 6 Three-dimensional structure of the proteins that were modeled by homology of *Hancornia speciosa* Gomes. A. Photosystem I assembly protein; B. ATP synthase subunit. C. Subunit 9 of the photosystem I reaction center; D. Protein

Z of the reaction center; E. Iron-sulfur center of photosystem I; F. Protein T from the photosystem II reaction center; G. Cytochrome b6-f subunit 6; H. Protein D of photosystem II. Fonte: SIB, 2020

the States of Sergipe, Alagoas, Pernambuco, Paraíba, Rio Grande do Norte, and Ceará (Martins et al. 2012; Santos et al. 2017; Silva et al. 2017a). In the Southeast, Center-West, Tocantins, and the Southern Bahia regions, it occurs in the Cerrado biome under the phytophysognomies of Cerradão, Cerrado restricted sense, dirty field, or rupestrian field (Ganga et al. 2010; Nascimento et al. 2014).

Some universities collaborate among the institutions and also are assignees of the patents. This fact is a way to transfer scientific knowledge of these institutions in technological products that generate, albeit infrequently, which considers the discrepancy between the number of articles developed and the patents generated. The conversion of scientific knowledge into technological products is a positive aspect, and this needs to be encouraged when innovation and the obtainment of technological products are important factors for the country's development.

Studies of genetic diversity that were estimated by the molecular markers were also among the most developed themes. Numerous studies that used molecular markers, such as RAPD (Silva et al. 2013), ISSR (Da Costa et al. 2015), and SSR (Silva et al. 2019), to assess the natural populations (Silva et al. 2017b) and variability in germplasm banks (Silva et al. 2019). The significant themes focused on the use as food and as a medicinal plant, and studies of natural populations in different regions, where the plant is known and is used mainly by extractive communities to treat diseases and as food has been carried out. Technological products based on the species also followed this trend, and most of them were direct to the potential as food, from the processing of fruits and the development of products, such as liqueurs, cakes, and jellies. It is noteworthy that the studies of the widely distributed populations in the country that investigated the molecular differences among them, and botanical varieties of the species were less frequent (Collevatti et al. 2016, 2018; Chaves et al. 2020).

The species of the Apocynaceae family are reported as a source of secondary metabolites used for therapeutic purposes, with an anticarcinogenic, cardiac stimulant, antihypertensive potential. However, *H. speciosa* is not among the species studied, and the phytochemical profile and the constituents responsible for its bioactivity have not been fully elucidated (Süntar 2020). Studies that characterize the bioactive compounds present in latex, leaves, peels and fruits of

the species and the functional activities of these compounds are considered specialized and peripheral themes. Among the main bioactive compounds identified in the species are rutin, 1—(+)—bornesitol, quinic acid, chlorogenic acid, catechins, isoquercetins, β -carotene, lupeol, and α/β -amirin. Rutin is a flavonol abundant in plants (Ganeshpurkar and Saluja 2017), and it is present in the leaves, bark, and fruits of *H. speciosa* (Leite et al. 2020). It has several pharmacological applications, such as antidiabetic (Ghorbani 2017), anti-cancer (Perk et al. 2014), and anti-inflammatory effects (Nikfarjam et al. 2017), and more recently expressed as a promising inhibitor of the main protease and other protein targets of SARS-CoV-2 (Al-Zahrani 2020; Das et al. 2020). Quinic acid is a cyclitol that is present in several plant species. It is also one of the main constituents of the *H. speciosa* leaves, and it displays an anti-inflammatory activity by inhibiting the pro-inflammatory transcription factor (NF- κ B) and the production of tumor necrosis factor- α (TNF- α) (Geller et al. 2015).

The 1—(+)—bornesitol is the main constituent of *H. speciosa* leaves extract (Endringer et al. 2014) and is a potent inhibitor of the angiotensin-converting enzyme (Moreira et al. 2020). Therefore, it is associated with an antihypertensive effect on the species (Moreira et al. 2019). This cyclitol has also been cited as a chemopreventive agent for cancer treatment (Endringer et al. 2009). Chlorogenic acid is associated with antioxidant activity, and it is present in the leaves, fruits, and latex (Torres-Rêgo et al. 2016). Catechins are present in the leaves, fruits, latex, and bark, and they have numerous pharmacological applications, in addition to being a promising antiviral for preventing the formation of the SARS-CoV-2 S Protein-ACE2 complex (Katalinić et al. 2004; Dos Santos et al. 2018; Isemura 2019; Leite et al. 2020; Jena et al. 2021).

Isoquercetins, lupeol, and α/β -amyirin have been reported for the leaves related to antidiabetic properties (Pereira et al. 2015). B-carotene is mentioned mainly for the fruits, while it is also present in the leaves and has been associated with antioxidant, antidiabetic, and anti-obesity properties (Bailão et al. 2015; Dos Santos et al. 2018). The presence of these bioactive compounds was also considered for the development of the patents aimed for pharmacological use and the production of chemical and cosmetic reagents, based mainly on the properties of latex and leaves extracts.

The literature studies are vast and point to the biotechnological potential of the latex of *H. speciosa*. However, the constituents that confer these functional effects are not yet fully elucidated and not well developed, although they are among the important topics for research. Some latex constituents identified chlorogenic acid, naringenin-7-O-glucoside, catechin, and procyanidin (Neves et al. 2016). The same is true for the other compounds present in the other unknown tissues of the plant.

Fruit processing, propagation, and conservation of the species have been little explored. In Brazil, the processing of fruits is handily carried out by extractive communities that use the pulp to produce candies, jellies, and pulps, and a minor use by agribusiness to juice pulp and ice cream in the Midwest and Northeast regions of the country. The presence of toxic substances in fruits has not been reported. These are considered functional foods and the results obtained by Araújo (2019) suggest benefits from the consumption of the *Hancornia speciosa* fruit by women at risk for breast cancer.

Propagation for *H. speciosa* occurs mainly by the recalcitrant seeds, which have low longevity and quickly lose their viability. For this reason, it is necessary that sowing for the production of seedlings takes place immediately after the processing of the fruits. The propagation of this species can also occur *in vitro* from explants, such as the internodal segments (Prudente et al. 2016). However, this form of propagation is usually only in active germplasm banks.

H. speciosa recalcitrant seeds lead to conserving germplasm collections in the natural populations present in conservation units. Researchers seek to develop protocols for exploring cryopreservation (Prudente et al. 2017). More information on how to conserve and produce the species at a forestry level is relevant to take advantage of the potential of its cultivation.

The species are in the domestication phase and breeding programs are still under development. Although there are established morphological descriptors for *H. speciosa* (Da Silva Júnior et al. 2018b), there are no registered cultivars (*sui generis* protection), nor have technologies been verified based on the genetically modified plants or the engineered and patented genes of the species. In the public databases of molecular data, information about the nuclear genome is not available so far.

Only nucleotide and protein sequences belonging to the chloroplast genome (cpDNA) are available in the public banks. Among these are the nucleotide sequences of the *rbcL* and *matK* genes that function as DNA barcodes. The DNA barcodes are a taxonomic method for identifying the species, and they aim to use the diversity within the DNA of living beings to discriminate the species by using a short sequence of DNA (400–800 bp), a universal sequence (present in all plant species), or a variable sequence (with enough differentiation between the species to be able to distinguish them), which are easily isolated (Hebert et al. 2003).

For most terrestrial plants, cpDNA is conserved, with the coding regions containing two groups of genes. The first group comprises components for the photosynthetic machinery, specifically for photosystems I and II, the cytochrome b6f complex, and the ATP synthase complex. The second group includes the genes needed for the plastid genetic system, the subunits of RNA polymerase, the rRNAs and the tRNAs, and the ribosomal proteins, with enough 16S, 23S, 5S, and 27–31 tRNA genes, which are sufficient to translate all of the amino acids, including the three genes for the RNA subunits (Green 2011; Huang et al. 2013).

Chloroplast DNA (cpDNA) is recommended for phylogenetic studies because it has regions with a low evolution rate; consequently, more significant conservation is observed among the known genomes in evolution. These sequences help elucidate the phylogenetic issues between the higher families and the taxa. At the same time, it has non-coding regions that have evolved enough for phylogenetic resolution at the species level. In addition to the characteristics mentioned, cpDNA has a uniparental (haploid) inheritance. That is, for most species of this genome, it is inherited from one of the parents. This fact allows for the generation of inferences about the contributions related to the flow of seeds and pollen to the genetic structure of the natural populations when comparing the nuclear and plastid markers, in addition to the phylogenetic inferences that can be made at the intraspecific level (Delplancke et al. 2012; Khadivi-Khub et al. 2014). Maternal inheritance is more widespread for most species than paternal inheritance (Hagemann 2002), with rare biparental or paternal inheritance (Zhang and Sodmergen 2010).

Another relevant aspect is the size of the cpDNA, which is considered small when compared to the nuclear genome; depending on the species, it is 120–200 kbp in length, has a contour length of about 30–60 μm , and a mass of about 80–130 million Daltons (Shaw et al. 2007). Its structure is simple, as previously highlighted. These characteristics facilitate studies and genome sequencing development, which may justify the significant deposits in the public molecular data banks.

On the molecular data available for *H. speciosa*, the three-dimensional structure of the cpDNA proteins obtained from molecular modeling by homology has been verified, which is a successful tool for predicting the three-dimensional structures based on proteins molecular evolution assuming the similarity between the primary structures of this protein and the homologous proteins of the known three-dimensional structures (template proteins). The homology implies a structural similarity (Muhammed and Aki-Yalcin 2019). Among its steps is the alignment of the target sequence, or the problem sequence (unknown protein to be modeled), with the template or mold sequence (homologous proteins of the known three-dimensional structures) (Santos Filho and Alencastro 2003).

Predicting the structure and function of the proteins is fundamental to determine their contribution to an organism's vital process. Furthermore, as a valuable tool, significantly to improve the understanding of the mechanisms of the chemical reactions, structure, and function, mainly of the proteins that are difficult to be purified on a large scale, or of species for which there is a smaller volume of studies and information available, for example, *H. speciosa*.

It is worth mentioning that the availability of molecular data from public banks allows this to be used for the development of *in silico* studies (Bezerra et al. 2018). Additionally, for the prospecting of disease resistance genes (Debibakas et al. 2014), pests (Joukhadar et al. 2013), and tolerance to different abiotic stresses (Das et al. 2019; Abhayawickrama et al. 2020; Tripathi et al. 2020). Moreover, it is relevant for phylogenetic analysis (Karakulah and Pavlopoulou 2018; Bauwens et al. 2018), primer design for diversity studies (Feng et al. 2016; Thatikunta et al. 2016), and gene expression (Bustin and Huggett 2017; Alonso et al. 2018).

Conclusion

H. speciosa appears as an important food source with high nutritional quality and displays compounds for biotechnological applications while having a relevant bioeconomic role. However, there are knowledge gaps that limit its best use and endanger the conservation of the species. Specifically, studies that focus on the propagation methods, the definition of adequate spacing for planting, fertilization, and the evaluation of fruit production, are all necessary. In addition, research into the development of management plans, domestication, and genetic improvement in the initial stadiums of development is needed.

Despite the vast amount of literature on the anti-inflammatory, angiogenic, osteogenic, antidiabetic effects, and antioxidant properties reported for different plant tissues, additional studies are needed to know the constituents that confer these functional activities actions. There is also a need for studies on the genes and metabolic pathways that produce the bioactive compounds found in *H. speciosa*.

Although the number of publications is increasing, there are few technological products based on the species, and these are limited to food, pharmacological products, chemical reagents, and cosmetics. There are no innovations based on biotechnology.

Inadequate information is available about this species in the public databases of molecular data. This valuable information could contribute to the elucidation of the genes and the metabolic routes related to the bioactive compounds.

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Data availability The datasets generated during and/or analyzed during the current study are available from the corresponding author on reasonable request.

Declarations

Conflict of interest All the authors of this manuscript declare that they have no conflict of interest.

Ethical approval This article does not contain any studies with human participants or animals performed by any of the authors.

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