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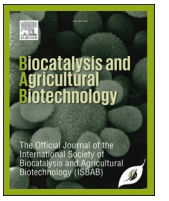

Biotechnological potential of medicinal plant *Erythrina velutina* Willd: A systematic review

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ABSTRACT

Plants have several biotechnological uses, such as for pharmaceuticals, food, fuel, insecticides, and as a source of gene sequences for genetic engineering. This study aimed to identify the biotechnological potential of *Erythrina velutina* Willd. a plant widely used in traditional medicine. Analyses were based on the prospecting of scientific data in recognized databases of scientific publications, patents, nucleotide sequences and products. The medicinal properties of the phytocomposites extracted from *Erythrina* spp. and *E. velutina* were evident in several studies, although the efficiency and safety of using these chemical compounds are still being tested. Potential for other chemical uses, such as for antibacterial and bioinsecticide functions, has also been reported. In the analysis of the molecular information, barcodes for phylogenetic studies are mentioned and in patents, *Erythrina* spp. plants are a source of polynucleotides and polypeptides. The number of patents and sequenced nucleotides for *E. velutina* is low (12 and 6, respectively). However, the scientific data establish that this species is prominent with high biotechnological potential.

1. Introduction

Plants are a historical source of compounds with medicinal properties, still being the primary resource of health treatment to most of the global population (Romanelli et al., 2015). Several pharmacological compounds have been isolated from plants, presenting medicinal properties used to treat and cure various diseases and leading to the development of clinically efficient drugs (Wangchuk, 2018).

The flora is rich in biodiversity and medicinal potential, largely accepted and used by local populations, as in Brazil. However, the number of herbal medicine products licensed by health agencies, especially ones composed of native plants, is still small compared to other countries (Cecília et al., 2018).

Beyond the medicinal aspects, another high biotechnological potential from Brazilian flora comes as a source of genetic material for the development or improvement of crops. Whether it is for the production of food (Andrade et al., 2016), biofuel (Hoang et al., 2015), or wood and cellulose (Silva et al., 2019), native and naturalized genetic material has been used in breeding programs and conserved as a valuable resource (Alves and Azevedo, 2018).

Plants from the Fabaceae family are amongst the most important plants due to their medicinal properties; 11.2% of the plants in this

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family - over 2,000 species - are part of traditional medicine. This family of plants has alkaloids as its key compound (Willis, 2017).

The genus *Erythrina*, from the Fabaceae family, comprises of over 120 species occurring in tropical and subtropical areas. The name of the genus comes from the Greek word "erythros", which means red, and relates to the pigment present in flowers and seeds. In Brazil, eight species are within the genus: *Erythrina crista-galli*, *E. falcata*, *E. fusca*, *E. mulungu*, *E. speciosa*, *E. poeppigiana*, *E. verna*, and *E. velutina* Willd. This genus has been studied for its medicinal properties, attributed to high bioproduction of alkaloids and phenolic compounds, such as flavonoids, flavons, isoflavonoids, and pterocarpans, produced in seeds, leaves, bark, and flowers (Soto-hernández et al., 1996; Hussain et al., 2016).

Erythrina velutina Willd. occurs in Antilles, Brazil, Colombia, Ecuador, Galapagos, and Venezuela. In Brazil, it occurs mainly in the Caatinga and Atlantic Forest biomes. Popular medicine has attributed calming, sedative, anesthetic, and analgesic properties to the bark and seeds of *E. velutina*, mainly due to the action of the erythrinan alkaloid (Palumbo et al., 2016). Studies have also found compounds such as aurones, chalcones, catechins, steroids, flavonols, flavones, flavanones, flavonoids, phenols, leucoanthocyanidins, saponins, tannins, triterpenoids, and xanthones in water extract from leaves and inflorescences from this species (Carvalho et al., 2009; Palumbo et al., 2016), and most of these components present medicinal value.

Therefore, this study aims to evaluate the biotechnological potential of *Erythrina velutina* through a systematic review of the scientific, patent, and molecular information.

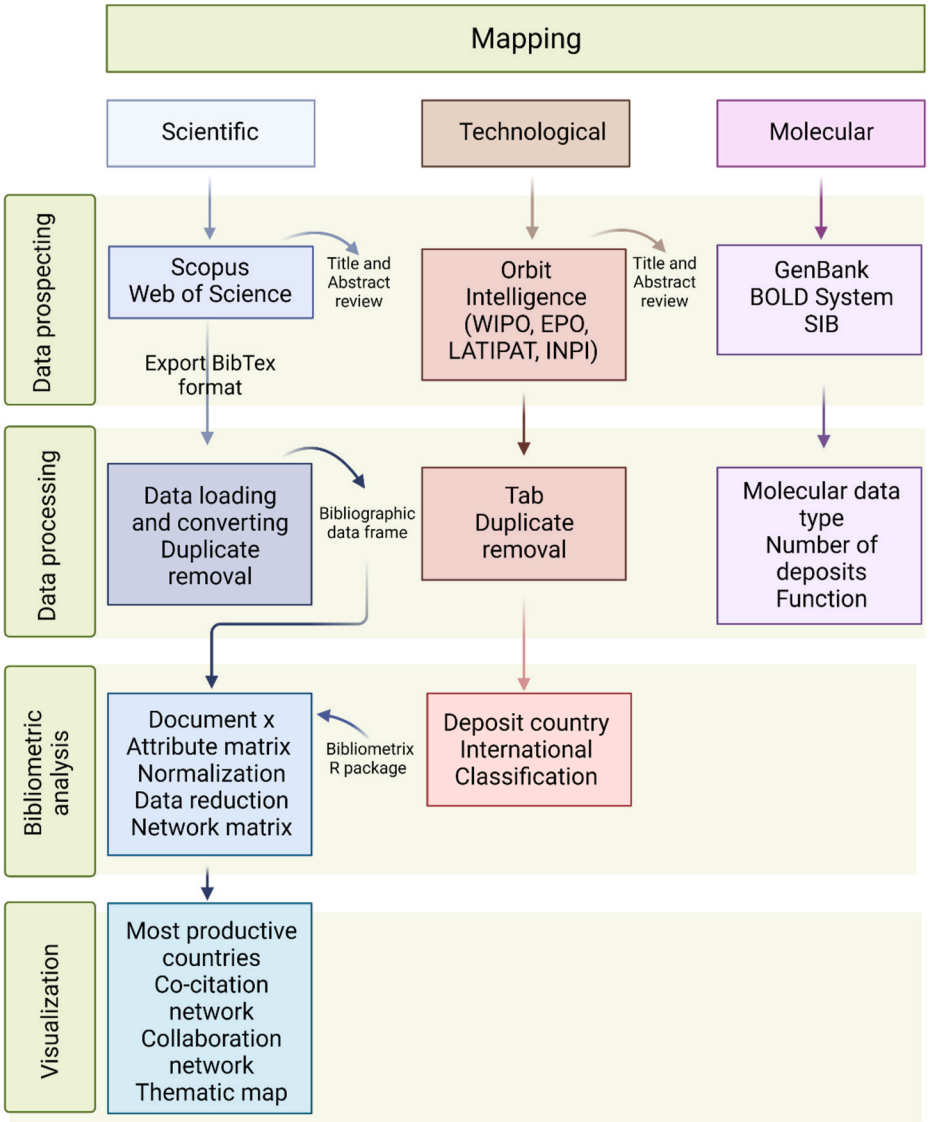


Fig. 1. Flow chart of the study stages for the scientific, technological, and molecular mapping for *Erythrina velutina* Willd.

2. Materials and methods

This study was based on the research of scientific articles, patents, and molecular data deposited in public databanks. It is composed of four stages: (1) Data prospecting, (2) Data processing, (3) Bibliometric analysis, and (4) Visualization (Fig. 1).

The analysis was conducted in April 2021 using the search terms "*Erythrina*", "*Erythrina* medicinal", "*Erythrina velutina*" and "*Erythrina velutina* medicinal" without limitations to timeframe to obtain a broad data set.

2.1. Scientific mapping

Scientific publications written in English, Spanish and Portuguese language were retrieved from the Web of Science (http://www.webofknowledge.com) and Scopus (http://www.scopus.com) databases. The search terms were screened in the title and abstract. The articles were revised to remove files not corresponding to the objective of this study. The data sets contained the metadata of the scientific publications obtained for each search term in both databases exported in BibTex format. The data sets were combined in a single set, duplicate files removed, and the meta-analysis was conducted with the Bibliometrix package at R software (R Core Team, 2021).

2.2. Technological mapping

The potential technological use was based on patent data obtained and analyzed using Orbit Intelligence software (Questel, 2021). The platform covers publications from 87 offices and databases, including the World Intellectual Property Organization (WIPO), European Patent Office (EPO), Patent Database in Spanish and Portuguese (LATIPAT), and the Brazilian National Institute of Industrial Property (INPI). Data from depositors, inventors, citations, international patent classifications, geographical and temporal distribution were processed. The search terms were considered in the advanced search option for documents that presented the information in the title, summary, and description.

2.2.1. Molecular data mapping

The nucleotide sequence databases Genetic Sequence Database (GenBank), of the National Center for Biotechnology Information (NCBI), and Barcode of Life Data System (BOLD) were used for gene, protein, or whole-genome sequence search. The three-dimensional structure of identified sequences was verified in the Swiss Institute of Bioinformatics (SIB) database. At this stage, only the terms "*Erythrina*" and "*Erythrina velutina*" were used without limitations to a timeframe.

3. Results and discussion

3.1. Scientific mapping

There was a higher number of scientific data for publications related to *Erythrina* spp. than *Erythrina velutina* species. This result is expected due to the high number of species within the genus, many of those with medicinal properties.

Most publications related to *Erythrina velutina* are from Brazil, where the species occurs natively, yet is not endemic (Fig. 2). Nevertheless, there are a few articles from Japan related to the elucidation of the species' chemical composition (Ozawa et al., 2008, 2009, 2011), emphasizing the international interest in Brazilian flora and its potential.

As for publication fields, scientific publications related to the genus are well distributed among agricultural and biological sciences,

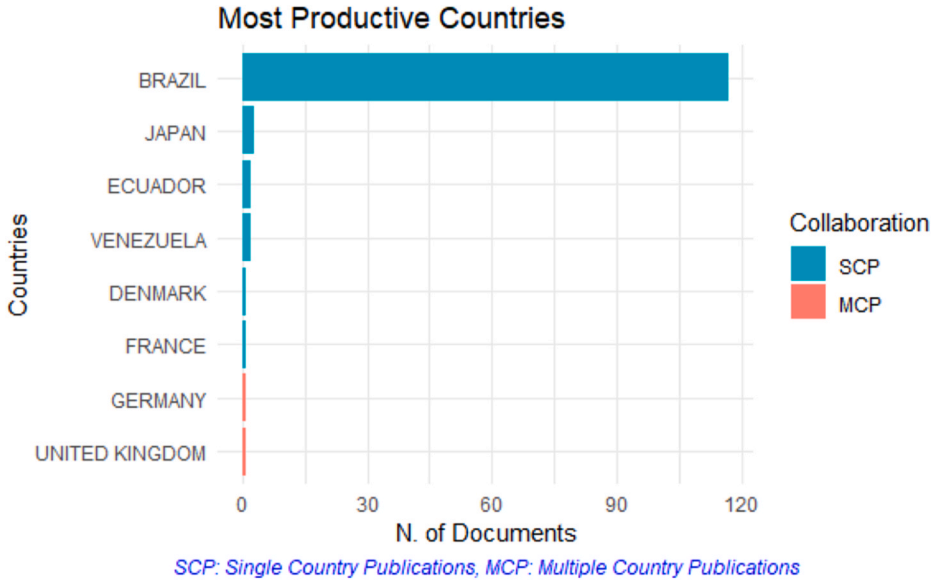


Fig. 2. Most productive countries for scientific publications about *Erythrina velutina* Willd.

molecular biology and chemistry, pharmacy, and pharmacology. Recent investigations are mostly related to restoration of natural forests (Soares and Rodrigues, 2008; Santos et al., 2012a), agroecosystems (Santos et al., 2013; Souza et al., 2014), carbon sequestration (Kumar and Nair, 2011), and climate change adaptation (Hell et al., 2019), when not related to medicinal chemical properties (Merlugo et al., 2015). The species *E. crista-galli* has been recommended for soil bioremediation due to its potential for germination and its root anatomy in soil contaminated with petroleum (Farias et al., 2009).

For *Erythrina velutina*, most publications were associated with agricultural and biological sciences, molecular biology, pharmacy and pharmacology, and biochemistry. *E. velutina* is a pioneer species highly recommended for reforestation due to its fast growth and plasticity to different climates and environments (Holanda et al., 2010). Besides, *E. velutina* has been established as a potential climate change indicator species in studying air moisture fluctuations. It was evaluated its phenological variations in response to water availability on a seasonal scale (Butz et al., 2016).

In addition, the natural occurrence of this species in both humid and dry biomes makes it interesting for studies of abiotic stress tolerance on biochemical and molecular levels (Ribeiro et al., 2014; Souza et al., 2020). The genetic diversity of the species is also a concern where natural occurrence and diversity are threatened by alternative land use (Azevedo et al., 2013; Gonçalves et al., 2014; Souza et al., 2014).

Information on pharmacy and pharmacology, biochemistry, and medicinal chemistry highlight bioactive compounds with medicinal properties on this species, currently being studied for safety and effectiveness. Catechins, steroids, flavanols, flavanonols, phenols, saponins, tannins, triterpenoids, and xanthones were detected in aqueous extracts of *E. velutina*, which presented medicinal properties (Carvalho et al., 2009). When tested in mice, hydroalcoholic extracts of *E. velutina* presented anxiolytic, antinociceptive, and anticonvulsant activity, supporting widespread use as a sedative analgesic and anesthetic (Vasconcelos et al., 2003, 2007; Raupp et al., 2008; Teixeira-Silva et al., 2008). Furthermore, from seed extracts of *E. velutina* were purified trypsin, Kunitz trypsin, and chymotrypsin inhibitors and identified its antitumor, anti-inflammatory, anticoagulant, antielastase, and gastroprotective properties (Machado et al., 2013; Oliveira et al., 2017).

The ethanolic extract of *E. velutina* had neuroprotective effects on mice for memory deficit due to ischemia (Sousa et al., 2017a). These effects were also evaluated in an in vitro study. The extract composed of hesperetin, homohesperetin, abyssinin, sigmoidin C, and rhizonic acid acted as an antioxidant, suggesting that these compounds have therapeutic potential against neurodegenerative diseases such as Alzheimer's and Parkinson's (Silva et al., 2016). Another in vitro analysis on the effect of aqueous, alkaloid-rich, and hexane extracts of *E. velutina* showed anticholinesterase properties valuable for treating Alzheimer's disease (Santos et al., 2012b; Almeida e Castro et al., 2016).

A neuroprotective action was observed using ethanolic extracts of the *E. velutina* barks in tests of induced neurotoxicity. The emphasis of the study was the action of rhizonic acid (2-hydroxy-4-methoxy-3,6-dimethylbenzoic acid), a phenolic acid whose biosynthesis has not been fully elucidated (Silva, 2012; Sousa et al., 2017b).

Phenolic compounds are characterized by a benzene ring, a carboxylic group, and one or more hydroxyl and/or methoxy groups in the molecule, thus having antioxidant properties (Soares, 2002). Several phenolic acids come from the shikimic acid pathway, which

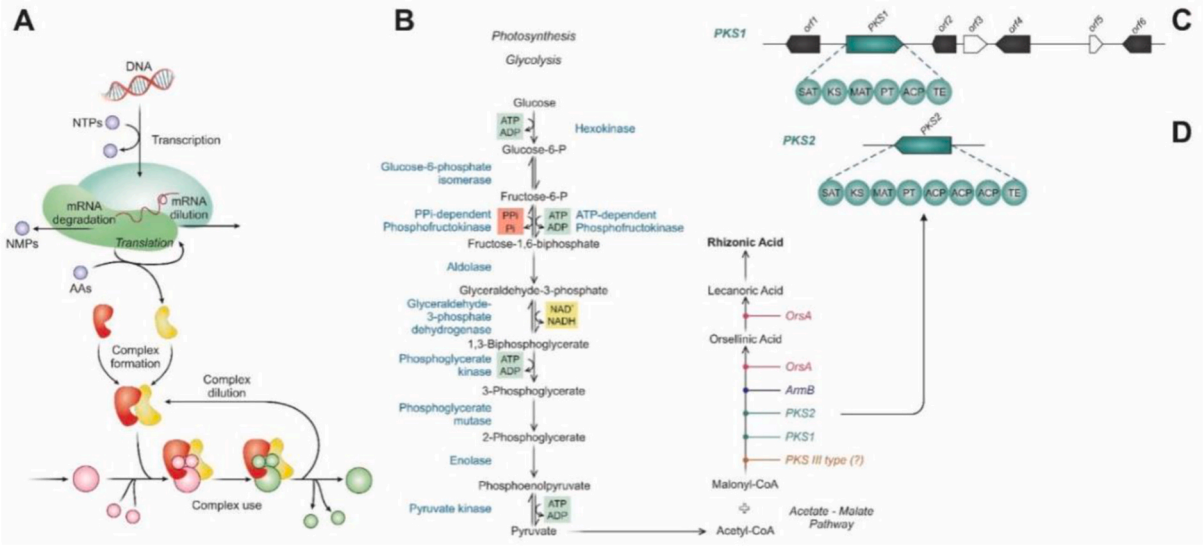


Fig. 3. Rhizonic acid biosynthesis. (A) Models of metabolism and expression explicitly account for the genotype-phenotype relationship with biochemical representations of transcriptional and translational processes. Source: Lerman et al. (2012). (B) Rhizonic acid biochemical pathway. Sources: Braesel et al. (2017); Lackner et al. (2013); Nielsen et al. (2011); Taiz et al. (2017); Taura et al. (2016) adapted. (C) and (D) Physical map of the genetic loci comprising *PKS1* and *PKS2* (green arrows). Putative products of adjacent genes (black): flavin-dependent monooxygenase (*orf1*), SAM-dependent methyltransferase (*orf2*, *orf4*, and *orf6*). Hypothetical proteins (*orf3* and *orf5*) are shown as white arrows. Below the *PKS* genes, the domain arrangement of polyketide synthases is shown. Domain abbreviations are SAT, starter unit: ACP transacylase; KS, ketosynthase; MAT: malonyl-CoA: ACP transacylase; PT, product template domain; ACP, acyl carrier protein; TE, thioesterase. Source: Braesel et al. (2017). (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

begins with the reaction of phosphoenolpyruvate and erythrose-4phosphate to form the central ring with a carboxyl substitute and three hydroxyls. However, other molecules with similar functions, such as the orsellinic, cannabidiolic, and 6-methylsalicylic acids are biosynthesized through the acetate pathway via intermediate polyketides (Khadem and Marles, 2010).

The synthesis of orsellinic acid is influenced by the action of genes *HXK2* (hexokinase), *PGIC* (glucose-6-phosphate isomerase), *PFK1* (ATP-dependent phosphofructokinase), *PFP-A1* (PPi-dependent phosphofructokinase), *AT4G26520* (aldolase superfamily), *GAPC1* (glyceraldehyde-3-phosphate), *PGK3* (phosphoglycerate kinase), *PGM1* (phosphoglycerate mutase), *ENO2* (enolase) and *AT5G6380* (pyruvate kinase) which synthesize enzymes essential to the biosynthetic pathway (Fig. 3).

In plants, opposite of lichens, it is conjectured that the formation of orsellinic acid occurs by the action of the type III polyketide synthases (Taura et al., 2016). The *PKS1* (polyketide synthase 1) and *PKS2* (polyketide synthase 2) (Braesel et al., 2017) and *ArmB* (Lackner et al., 2013) genes (Fig. 3), which have high similarity, had their action in the synthesis of orsellinic acid confirmed by cloning and vector transformation. *PKS1* and *PKS2* are also present in *Ostreococcus lucimarinus*, indicating the possibility of being evolutionarily conserved genes. The *orsA* gene has an action on synthesis of lecanoric acid, a compound derived from orsellinic acid (Nielsen et al., 2011). And rhizonic acid is derived from lecanoric acid (Venkateswarlu, 1947). Therefore, this is a potential pathway for the synthesis of this relevant acid in *E. velutina*.

Another phenolic compound present in the bark of de *E. velutina* is hesperidin (Silva, 2012). Despite being widely found in the Rutaceae family (*Citrus* genus) (Garg et al., 2001), it is also found in Asteraceae and Fabaceae families, the last being the family to which *Erythrina* spp. belongs. As observed with the ethanolic extract of *E. velutina*, this compound has medicinal properties, such as antioxidant. The biosynthesis of this compound has also not been fully elucidated, but the potential synthetic pathway has identified products and genes.

Unlike rhizonic acid, hesperidin comes from the flavonoid pathway (Fig. 4). In this route, the *4CL5*, *4CL3*, *4CL2*, and *4CL1* genes produce 4-coumarate coenzyme A ligases that act in the synthesis of 4-coumaroyl-CoA from 4-coumarate (Sun et al., 2013). Then, the product of the *GHS* gene, naringenin chalcone synthase, acts on the formation of naringenin chalcone, which is converted to (2S)-naringenin by the action of chalcone isomerases produced by the *CHI1*, *AT3g55120*, or *AT5g55120* genes (Castellarin et al., 2007; Wei et al., 2011).

From (2S)-naringenin, there is the biosynthesis of luteolin, a flavone. Flavones are compounds with antioxidant properties used medicinally to prevent cancer and coronary heart disease. The synthesis of this compound occurs through the action of the *AT5G07990* and *SHT12* genes that produce flavonoid 3′-hydroxylases, acting in the formation of (2S)-eriodyctiol, which in turn originates luteolin with the action of flavone synthase II produced by the *CYP93B2* gene (Martens and Mithöfer, 2005).

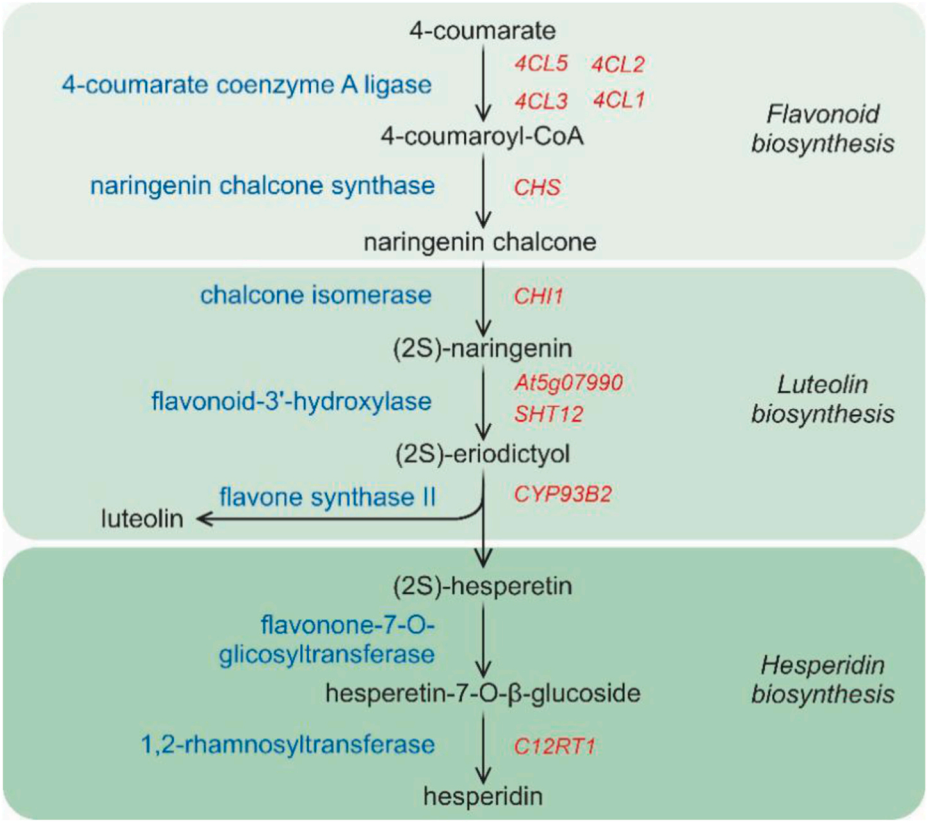
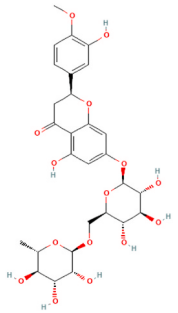
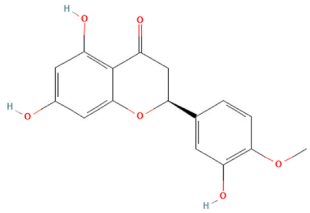
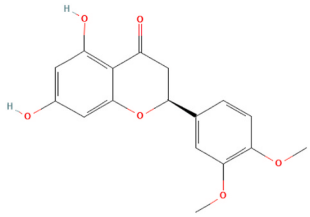
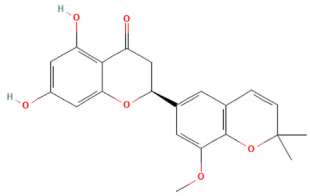
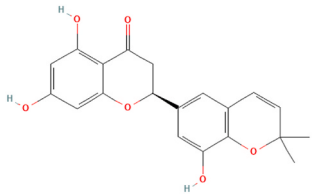
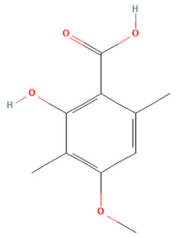


Fig. 4. Biosynthetic pathway of hesperidin. Source: Plant Metabolic Network (plantcyc.org) adapted.

Table 1
Bioactive compounds identified in different tissues of *Erythrina velutina* Willd. and their functional properties.

Compounds	Property	Tissue	Reference
Hesperidin 	Antioxidant activity	Bark	Silva (2012)
Hesperetin 	Antioxidant activity	Bark	Silva et al. (2016)
Homohesperetin 	Antioxidant activity	Bark	Rabelo et al. (2001); Silva et al., (2016)
Abyssinin 	Antioxidant activity	Bark	Silva et al. (2016)
Sigmoidin C 	Antioxidant activity	Bark	Silva et al. (2016)
Rhizonic acid 	Antioxidant activity; neuroprotective	Bark	Silva et al., (2016); Silva (2012); Sousa et al., (2017b)
	Sleep-inducing activity; selective apoptosis of cancer cells	Seeds	Ozawa et al., (2008), 2011

(*continued on next page*)

Table 1 (*continued*)

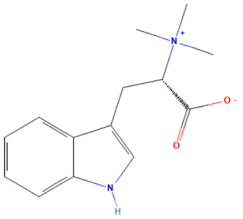
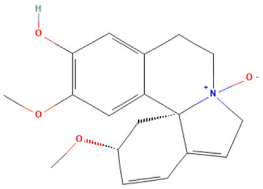
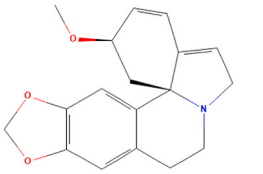
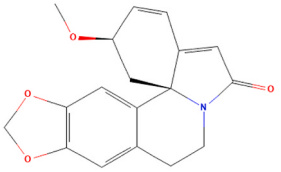
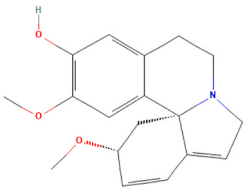
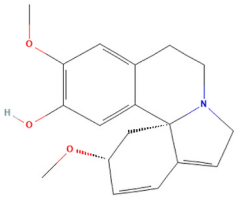
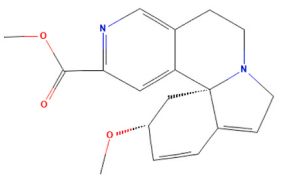
Compounds	Property	Tissue	Reference
Hypaphorine 			
Erysodine N-oxide 	Selective apoptosis of cancer cells	Seeds	Ozawa et al. (2009)
Erythraline 	Selective apoptosis of cancer cells	Seeds	Ozawa et al. (2009)
8-oxo-erythrinaline 	Selective apoptosis of cancer cells	Seeds	Ozawa et al. (2009)
Erysodine 	Selective apoptosis of cancer cells	Seeds	Ozawa et al. (2009)
Erysovine 	Selective apoptosis of cancer cells	Seeds	Ozawa et al. (2009)
Erymelanthine 	Selective apoptosis of cancer cells	Seeds	Rabelo et al., (2001); Ozawa et al., (2009)
	Antioxidant activity	Bark	Rabelo et al. (2001); Emmanuel et al. (2016)

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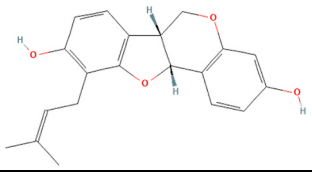
Table 1 (*continued*)

Compounds	Property	Tissue	Reference
Phaseollidin 			

The (2S)-hesperetin compound, from the (2S)-eriodyctiol of the luteolin pathway, originates hesperetin-7-*O*-β-glucoside, a precursor to hesperidin. The synthesis of hesperidin occurs with the action of 1,2 rahmonosyl transferase, an enzyme produced by the *C12RT1* gene, present in *Citrus* (Frydman et al., 2004).

In addition to gene expression, genetic regulation of the biosynthesis of cellular compounds can occur through the action of transcription factors and RNA interference (RNAi). The silencing of *CHS* by the action of RNAi affects the synthesis of flavonoids such as hesperidin but favors the production of other phenolic compounds, such as phenolic acids (Schijlen et al., 2007; Zhang et al., 2015).

Erythrinan alkaloids, compounds characteristic of this genus, have a unique tetracyclic spiro-amine framework presenting various biological properties (Maertens et al., 2015). These compounds have a strong interest as targets for total synthetic synthesis for the industry (Mostowicz, 2015). The indole alkaloid hypaphorine and 4 erythrinan alkaloids (Ozawa et al., 2011) and hypaphorine purified from *Erythrina velutina* have presented industrial potential with sleep-inducing activity confirmed on mice (Ozawa et al., 2008). Besides, *Erythrina mulungu* is already commercially used as a sleep-inducing and anxiolytic medicine (Rech et al., 2017).

Other erythrinan alkaloids, erysodine N-oxide, eythraline, 8-oxo-eryhraline, erysodine, erysovine, glycoerysodine, and erymelanthine were also isolated from seeds of *E. velutina*. These compounds, together with hypaphorine, were tested as tools for cancer therapy working synergistically with Tumor Necrosis Factor (TNF)-related Apoptosis-Inducing Ligand (TRAIL) for the induction of selective apoptosis on cancerous cells (Ozawa et al., 2009). Another compound purified from *E. velutina* was phaseollidin (Table 1), which was identified as a radical scavenging component from *E. droogmansiana* extracts presenting antioxidant properties (Rabelo et al., 2001; Emmanuel et al., 2016). This compound also occurs on *E. burana*, *E. crista-galli*, *E. sandwicensis*, *E. sigmoidea*, and *E. variegata*.

Erythrina speciosa has presented antiviral activity in vitro mainly due to the vitexin isolated (Fahmy et al., 2020). These properties were tested against the herpes simplex virus type 1 (HSV-1) and could be further analyzed for other viruses, such as the SARS-CoV-2, in natural treatments (Bhuiyan et al., 2020).

Other chemical uses are being studied for the compounds extracted from *Erythrina* spp. plants. The alkaloids found in *Erythrina* spp. inhibited plant protein and DNA synthesis (Parsons and Williams, 2000) and had genotoxic action on onion roots (*Allium cepa*) forming cell abnormalities (Silva et al., 2011). The allelopathic action of extracts from seeds of *E. velutina* influenced germination and development of lettuce (*Lactuca sativa* L.) (Centenaro et al., 2009; Oliveira et al., 2012). And it was found evidence of antibacterial activity of components from the bark of *E. velutina* against *Staphylococcus aureus* and *Streptococcus pyogenes* (Virtuoso et al., 2005). Bioinsecticide properties were observed on vicilin extracted from seeds of *E. velutina* against *Plodia interpunctella* and *Ceratitis capitata* (Wied) (Amorim et al., 2008; Macedo et al., 2008).

4. Technological mapping

Patent results were higher for the *Erythrina* genus, as observed for the number of scientific publications (Fig. 5). Other deposits, on a much lower number, are related to the medicinal properties of the genus, to *Erythrina velutina*, and *E. velutina* associated with its

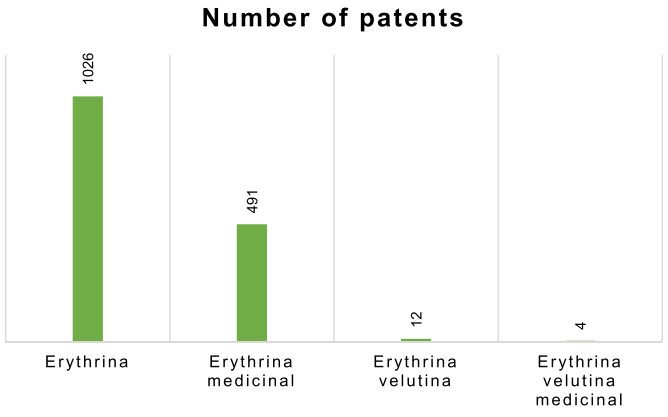


Fig. 5. Number of patents related to *Erythrina* spp. and *Erythrina velutina* Willd.

medicinal properties.

Most patents related to the *Erythrina* spp. are from Israel, Belgium, the United States, and Japan (Fig. 6) and for *E. velutina*, patents are from American and Brazilian research projects. However, there is a low number of published papers studying this species from the United States. Contrarily, the number of patents from Brazil is much lower than published papers, presenting a strong contrast. This demonstrates the lack of linkage between scientific research and economically valuable by-products in Brazil that originated from its native flora.

In Japan, for instance, the scientific publications and patents for *Erythrina* spp. are better closely related, indicating more product-driven research. This highlights the international concern in developing products using compounds from native Brazilian flora, as most patent holders for pharmaceutical products are international companies (Stevens and Huys, 2017).

Several patents concerning *E. velutina* are related to protocols and potential medicinal use. However, applying compounds extracted from this species on commercial medicines for humans is a long process due to the necessity of extensive tests for its safety and efficiency. There is a patent and several variations using *E. velutina* related to lectin compositions and methods for modulating an immune response to an antigen (Segal and Young, 2018). In contrast, the others were directly related to the plant extract with medicinal properties. For example, a patent for medicine for anxiety and depression treatment by Brazilian researchers and an expired patent for a sleep-inducing product using hypaphorine, of the same researchers from the previously mentioned study (Osaki and Honda, 2008; Ozawa et al., 2008) (Table 2).

There has also been a new industrial interest in using native medicinal plants in patents of advanced molecular protocols, in consonance with published articles (Wilson and Roberts, 2014; Hao and Xiao, 2015; Harvey et al., 2015). Genomic analyses can elucidate important characteristics of plants, such as genes involved in the biochemical pathways of active phytocompounds.

Despite the exponential increase in plant DNA sequencing, medicinal plants compose less than 2% of these studies (Chaudhary and Sharma, 2016; Willis, 2017). Sequencing these species could contribute to yield and field survival in advanced breeding programs using genomic selection or gene editing. *Erythrina* spp. plants are among the recommended species used on patented protocols (Evogene, 2018) as sources of polynucleotides and polypeptides for increasing nitrogen use efficiency, yield, growth rate, vigor,

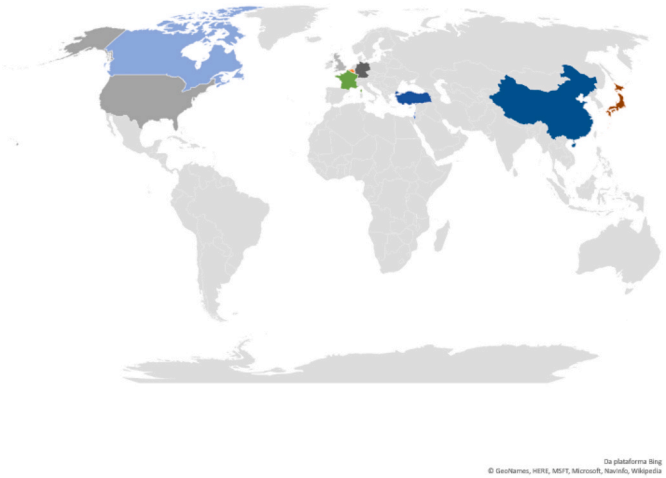


Fig. 6. Worldwide distribution of patents related to *Erythrina* spp.

Table 2
International Classification of the patents developed using *Erythrina velutina* Willd.

International patent classification		Symbol
Human necessities	Biocides, e.g. as disinfectants, as pesticides, or as herbicides pest repellants or attractants; plant growth regulators	A01N
	Preparations for medical, dental, or toilet purposes	A61K
	Specific therapeutic activity of chemical compounds or medicinal preparations	A61P
Chemistry	Sugars; derivatives thereof; nucleosides, nucleotides; nucleic acids	C07H
	Peptides (peptides containing β-lactam rings C07D; cyclic dipeptides not having in their molecule any other peptide link than those which form their ring, e.g. piperazine-2,5-diones, C07D; ergot alkaloids of the cyclic peptide type C07D 519/02; single-cell proteins, enzymes C12N; genetic engineering processes for obtaining peptides C12N 15/00)	C07K
	Mutation or genetic engineering; culture media	C12N
	Measuring or testing processes involving enzymes, nucleic acids, or microorganisms (immunoassay G01N 33/53); compositions or test papers thereof; processes or preparing such compositions; condition-responsive control in microbiological or enzymological processes	C12Q
	Investigating or analyzing materials by determining their chemical or physical properties (measuring or testing processes other than immunoassay, involving enzymes or microorganisms C12M, C12Q)	G01N

biomass, oil content, and/or abiotic stress tolerance (Fig. 7).

Consequently, genomic studies can improve production and minimize the impact of increased demand for plant medicinal compounds on natural populations, while attending to industrial needs.

4.1. Molecular mapping

BOLD is an online workbench and database that supports the assembly and use of DNA barcode data to identify species based on nucleotide similarity to samples of known taxonomy. On its Public Data Portal were found 59 records mentioning the term *Erythrina* spp. and 6 for *E. velutina*. For the genus, all results are distributed among 11 countries, most from Costa Rica, and specifically for *E. gibbosa* and *E. lanceolata*. While for *E. velutina*, half of the results are from Brazil and the others from unspecified regions.

The data for *Erythrina* spp. is mainly related to DNA barcoding in phylogeny studies (De Luca et al., 2018), such as the relations among phaseoloid legumes - based on nucleotide sequences from chloroplast regions (cpDNA) (Pfeil et al., 2009), and the efficacy of the core DNA barcodes in identifying processed and poorly conserved plant materials commonly used in South African traditional medicine (Mankga et al., 2013).

All results related *to E. velutina* are for the sequencing of Maturase K and Ribulose-1,5-Biophosphate Carboxylase/Oxygenase (Rubisco) Large Subunits (*rbcL*) of different base pair lengths (Fig. 8). Rubisco's genome is of extrachromosomal inheritance, non-recombinant, and structurally stable, it is one of the best genes for plant DNA barcoding (Ganie et al., 2015).

The GenBank database from NCBI provides access to biomedical and genomic information. At this database, for *Erythrina* spp. it was found 2,945 nucleotide results, 155 popsets, 293 identical protein groups, 1,467 proteins, and 51 protein structures. Species of this genus are part of 3 BioProjects for genome-wide sequencing and bioassays for medicinal properties. For *E. velutina* results were 47 nucleotides, 14 popsets, 8 identical protein groups, and 14 proteins. No country distinctions were made for this database. Most nucleotide sequences from *E. velutina* are from chloroplast genome and popset data and are related to phylogenetic studies, such as barcode research (Tripathi et al., 2013).

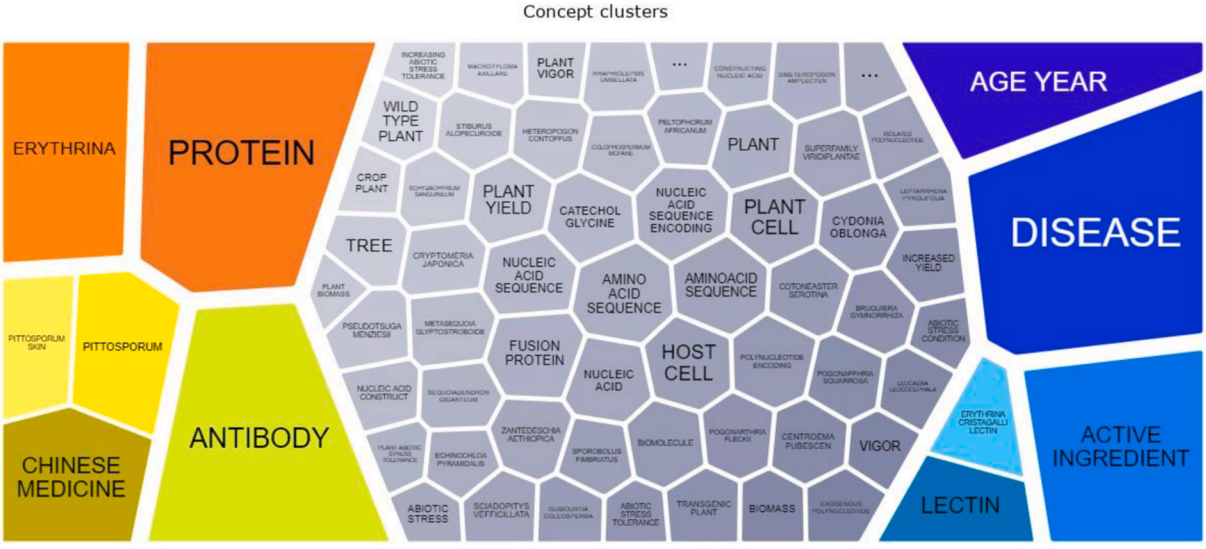


Fig. 7. Concept clusters for the most mentioned terms in patents related to *Erythrina* spp. plants.

Fig. 8. *Erythrina velutina* Willd. DNA barcodes deposits for *matK* (A) and *rbcL* (B) at the Barcode of Life Data System. Source: BOLD System, 2021.

The three-dimensional structures were built by homology (>95% sequence identity) at the SIB database for three sequences related to *rbcL* genes (Fig. 9). Based on the alignment of structural similarities, this is a valid method for predicting the unknown structure and understanding protein function, especially for understudied species such as *E. velutina*.

The structural model of proteins is key to understanding biological processes at the molecular level (Satyanarayana et al., 2018). These models provide valuable information about their function and can contribute to a wide spectrum of science (Waterhouse et al., 2018), especially when available for native species, for which there is little information available and which usually does not have information on X-ray crystallographic structure in the literature.

Modeling proteins by homology is also frequently applied in drug and molecule discovery research (Cavasotto and Phatak, 2009). However, the application of this technique in the investigation of erythrinan alkaloids has not been verified, although they are of interest to the industry.

Considering the amplitude of species within the *Erythrina* genus, information on sequences of cpDNA is highly relevant for evolution and phylogenetic studies. However, considering the economic potential of *E. velutina* and its chemical components, molecular data for its genome would be imperative for conservation and sustainable use strategies.

5. Conclusion

Erythrina velutina has high biotechnological potential proven by several studies identifying bioactive compounds with human therapy properties. However, medicines resulting from these studies are still in a developmental phase. Considering the number of patents for the genus and the scientific data, this is a prominent species for pharmaceutical use. There is also potential as a source of bioactive compounds for antibacterial or insecticide solutions. Furthermore, despite incipient, patents and molecular information including the genus and the species also present a substantial potential for using these plants in highly developed genetic programs.

Author Contributions

JLS conducted the research and wrote the text, RSM guided the research, revised the text, and contributed to the writing of the manuscript, VVN and CCC contributed to obtaining the research data, in the writing and revision of the text. All authors contributed to the article and approved the submitted version.

Ethical approval

The study was performed under a code A077941 from the Genetic Heritage Management Council (CGEN). This article does not contain any studies with human participants or animals performed by any of the authors.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

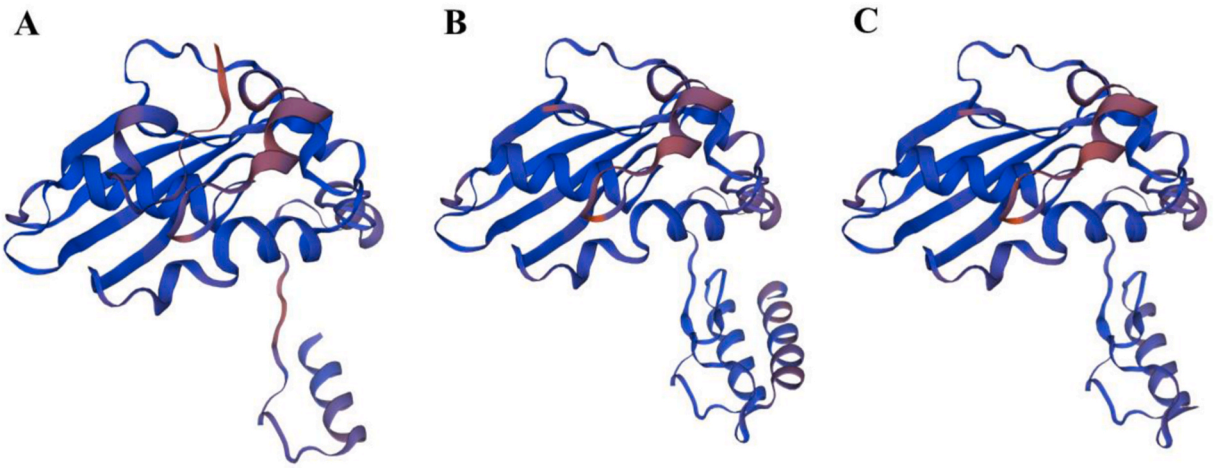


Fig. 9. Three-dimensional structure of the homology modeled proteins of *Erythrina velutina* Willd. A. Ribulose Biphosphate Carboxylase Large Chain; B. Ribulose Biphosphate Carboxylase Large Chain; C. Ribulose Biphosphate Carboxylase Large Chain. Source: SIB, 2021.

Data availability

Data will be made available on request.

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