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Nutritional, Biochemical, and Pharmaceutical Potential of Proteins and Peptides from Jatropha: Review

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Increased bioenergy consciousness and high demand for animal products have propelled the search for alternative resources that could meet the dual demands. Jatropha seeds have potential to fit these roles in view of their multipurpose uses, broad climatic adaptability features, and high oil and protein contents. During the past five years many large-scale cultivation projects have been undertaken to produce jatropha seed oil as a feedstock for the biodiesel industry. The present review aims at providing biological significance of jatropha proteins and peptides along with their nutritional and therapeutic applications. The nutritional qualities of the kernel meal and protein concentrates or isolates prepared from seed cake are presented, enabling their efficient use in animal nutrition. In addition, (a) biologically active proteins involved in plant protection, for example, aquaporin and betaine aldehyde dehydrogenase, which have roles in drought resistance, and β-glucanase, which has antifungal activity, as well as those having pharmaceutical properties, and (b) cyclic peptides with various biological activities such as antiproliferative, immunomodulatory, antifungal, and antimalarial activity are discussed. It is expected that the information collated will open avenues for new applications of proteins present in jatropha plant, thereby contributing to enhance the financial viability and sustainability of a jatropha-based biodiesel industry.

KEYWORDS: ***Jatropha curcas*; proteins; cyclic peptides; animal nutrition**

INTRODUCTION

The oilseed proteins have a descriptive history in both nutrition and therapeutic applications. In plants, proteins are broadly classified as (a) storage proteins, which are devoid of functional activity but are used during germination, and (b) functional proteins such as enzymes, hormones, defense proteins, and structural proteins that have definite roles in the plant system (*1*).

From a nutritional perspective, seed storage proteins have always been major players in supplying global protein needs and food energy intake. In recent years, increased global industrialization and increased demand for livestock products for meeting human food demand have greatly increased the pressure on agricultural land and the environment (*2*, *3*). Higher need for proteins in the livestock sector has accentuated the search for new protein sources that do not conflict with human food security interests. In the current situation, nonedible oil seeds are the potential and preferred choice for protein and other nutrients for livestock, provided these could be made free of toxic and antinutritional factors. One promising oilseed plant is *Jatropha curcas* (Euphorbiaceae), which has advantages over other oilseed plants (e.g., *Pongamia pinnata*, *Simarouba glauca*, *Ricinus communis*, *Azadirachta indica*) because of its wide adaptability to grow under various agroclimatic conditions, for example, adverse soil conditions, drought areas, marginal lands, arid as well as higher rainfall conditions, and land with thin soil cover (*4*). More importantly, jatropha seed oil has gained tremendous interest as a feedstock for biodiesel industries.

Large-scale jatropha cultivation projects have been initiated in the past 5−10 years with a projected worldwide cultivation of 12.8 million hectares yielding 2 t/ha of oil by 2015 (Global Exchange for Social Investment market study (GEXSI) (*5*)). In the future this will result in the availability of high amounts of pressed seed cake or kernel meal as byproducts, which are rich in proteins of high quality. These byproducts can be utilized in animal nutrition after detoxification and could also be a source for various bioactive protein molecules having a wide range of activities. Approximately 60% of the antitumor and anti-infectious drugs that are already in the market or under clinical trials are of natural origin. A vast majority of these compounds cannot yet be synthesized economically, and their use relies on wild or cultivated plants (*6*). In pharmaceutical, industrial, or agricultural perspectives, similar to other oilseed plants, jatropha species are also rich sources of phytochemicals. Jatropha proteins and peptides have been studied for their roles in the plant's own metabolic activities and defense against predators as well as a therapeutic and industrial potential.

In the present review an attempt has been made to discuss (a) the nutritional quality of jatropha proteins and their potential for animal nutrition, and (b) the chemistry, biological role, and potential applications of biologically active jatropha proteins and peptides. The jatropha plant also contains an interesting

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class of bioactive compounds, phorbol esters (PEs), having a number of pharmaceutical and agricultural applications (*7*−*9*). These being diterpenes are not discussed in this review and are dealt elsewhere.

STORAGE PROTEINS AND NUTRITIONAL QUALITY

Protein-containing plant products are grouped as either complete or incomplete proteins. Complete proteins (most animal proteins) contain all nine essential amino acids, whereas most of the plant proteins, for example, from beans, peas, nuts, and seeds, are incomplete proteins lacking one or more essential amino acids. Soybean proteins are the only plant proteins considered to be a complete protein (*10*, *11*), but proteins from various plants can be combined to provide all of the essential amino acids to form complete proteins. However, the quality of proteins depends on the biological availability in the animal body and it varies with different protein sources. Generally, the protein quality is measured by biological value (BV), net protein utilization (NPU), nutritional index (NI), protein digestibility corrected amino acids score (PDCAAS), protein efficiency ratio (PER) methods, and ileal amino acid availability (*12*−*14*).

Jatropha Seeds and Kernel Meals. Jatropha is a genus of approximately 175 succulent plants, shrubs, and trees from the family Euphorbiaceae. All parts of the jatropha plant have been used traditionally as medicines, for both human and veterinary ailments, for a long time (*15*). The jatropha species that is most widely studied in a nutritional context is *J. curcas*. The seed contains kernel and shell with an average ratio of 62.2:37.7. The kernel has higher crude protein (22−28%) and oil contents (54−58%) compared to the shell (4−6% crude protein and 0.8−1.4% oil) (*16*). The seeds also contain antinutrients and toxic factors such as phytate, trypsin inhibitor, lectin, curcin, and phorbol esters (PEs) (*17*). In addition, Maciel et al. (*18*) have reported Jat C1, a heat stable 2S albumin (12 kDa) from *J. curcas* seeds that has allergenic properties. This protein binds IgE attached to rat mast cells, inducing histamine release. It has strong cross-reactivity with the major allergens from castor bean (Ric c 1 and Ric c 3).

The storage proteins in seeds are important for germination and are also of immense nutritional significance. The storage proteins in extracted protein fractions from defatted kernel meals of three genotypes of *J. curcas* (toxic and nontoxic genotypes from Mexico and a toxic genotype from Cape Verde) were studied by Selje-Assmann et al. (*19*). The total protein recovered using the method of Osborne (*20*) was 89.3%. The glutelins, globulins, and albumins shared a majority of the total recovered protein, contributing 56.9, 27.4, and 10.8%, respectively, whereas prolamins and nonextracted residues were present in minor quantities (0.6 and 4.3%, respectively). The polyacrylamide gel electrophoresis band patterns for each of the protein fractions were the same for the different genotypes of jatropha studied (both nontoxic and toxic genotypes). Although the amino acid profiles of the three meals were similar, the proportions of individual amino acids in albumins, globulins, and glutelins obtained from these three meals deviated. Gastric digestion of albumins and globulins by pepsin and pancreatin system had protein digestibilities of 64 and 61%, respectively, whereas a higher digestion (95%) was observed for glutelins (*19*). In ruminants, a higher glutelin fraction, which forms > 50% of the protein, leads to low solubility of jatropha protein (*19*), which in turn decreases protein degradation in rumen when compared to soybean protein. Thus, a high amount of rumen undegradable protein available postruminally can be utilized by gastric digestion. The higher ruminal and gastric protein digestion indicates the potential availability of jatropha proteins in both ruminants and monogastrics. However, the meal should be detoxified before it is incorporated into animal diets. In another study, Martinez Ayala et al. (*21*) have reported slightly lower (39.8%) glutelin and higher (44.4%) globulin contents in *J. curcas* meal compared to that reported by Selje-Assmann et al. (*19*). Furthermore, they reported that the albumin fraction was composed of four main components with molecular mass < 30 kDa, and the globulin fraction had six major bands: four between 30 and 70 kDa and two <20 kDa. The prolamins were fractionated in three bands, whereas glutelins constituted two bands of 33 and 27 kDa.

During biodiesel production the jatropha seeds are crushed in a mechanical press to obtain seed cake containing 7−10% residual oil and 22−24% crude protein (*22*). The seed cake could be sieved to remove shells, and the sieved material could be extracted with hexane or petroleum benzene to recover oil and to obtain the remaining defatted jatropha meal (JM). The defatted jatropha kernel meal (JKM), which is obtained after solvent extraction of kernels (free of shells), and JM have high protein content. The JKM contains higher protein content, varying among different genotypes, with 57.3, 61.9, 56.1, and 63.8% protein in the Cape Verde, Nicaragua, Ife-Nigeria, and nontoxic Mexican genotypes. These values are higher than those in commercial soybean meal (46.5%). The nonprotein nitrogen represented only 4.7−5.0% protein in JKM (*16*). Deshelling followed by extracting oil from kernels using organic solvent could be one of the options to obtain good-quality oil in high amounts for biodiesel production and to get protein-rich meal (JKM). The digestibility of JKM protein is high (90%), and the protein has good amino acid composition (*7*). The amino acid composition of proteins is often used to define their nutritional quality. The amino acid compositions of meals from nontoxic and toxic genotypes (Cape Verde, Nicaragua, and India) were similar. The levels of essential amino acids (EAA) except lysine were higher than that of the FAO reference protein and the EAA requirements for chicks and young pigs (*16*, *17*, *22*, *23*). Similarly, levels of EAA except isoleucine in the jatropha meals were higher or similar when compared to castor bean meal, and, except for lysine, the amino acid profile is comparable with that of soybeans (*16*). However, in JM and JKM, the presence of antinutritional factors and toxic factors restricts the utilization of the meal in animal nutrition (*7*, *23*).

Protein Isolate. Protein isolates, as the name suggests, are the concentrated forms of plant proteins, generally prepared by solubilizing proteins and in the process removing nonprotein ingredients. The nitrogen solubility profile of JKM, as a function of pH, was U-shaped, which is typical for oil seed proteins. Jatropha proteins had a minimum solubility in water at pH 5.5 and increased solubility at acidic and alkaline pH values, with maximum nitrogen solubility at pH 10.5. A similar trend of solubility pattern was observed for rice bran proteins, sunflower proteins, and groundnut proteins, with solubility minima between pH 5 and 6 (*23*, *24*). Makkar et al. (*22*) reported the preparation of protein isolate from jatropha screw-pressed cake (JC) prepared by pressing whole seeds and containing a high level of shells (approximately 50%). The residual oil content was 7%. They also prepared protein isolate from defatted jatropha screw-pressed cake (DJC) containing < 0.5% fat. The recovery of protein was highest (29.5 and 33%) when proteins were extracted at pH 11 (60 °C) and precipitated at pH 4 in cold for JC and DJC, respectively. The protein contents of the protein isolates were 76.0 and 87.0% for JC and DJC, respectively. The dry matter yield obtained for protein concentrate was 17.2%, and the protein digestibility was approximately 90%.

Devappa et al. (*23*) have reported the preparation of protein isolate from (a) jatropha meal (JM, fat 0.8% oil) obtained after

passing hexane-defatted jatropha seed cake (obtained after mechanical pressing), through a mesh to remove the majority of hulls, and (b) JKM (0.8% oil). In brief, both jatropha meal and JKM were extracted at alkaline pH (10.5) by injecting steam (92 ± 2 °C) for 10 min. The proteins in the cooled supernatant were precipitated at pH 5.5 to get wet protein isolate, which was neutralized and spray-dried to obtain jatropha protein isolates. These isolates had protein contents of 96−97% with a protein recovery of 70−77%. The protein digestibility of these isolates was also approximately 90%. The EAA content (except lysine) of the protein isolates was higher than those of the FAO/WHO reference protein for growing children aged 3−5 years, and the amino acid levels in the protein isolate were similar to those in the kernel meal (*16*, *23*).

The calculated nutritional indices such as computed protein efficiency ratio (C-PER), based on the essential amino acid profile and protein digestibility analysis, are excellent predictors of protein quality for animals. The C-PER values for JM (1.1), JKM (1.72), protein isolate from JM (1.85), and protein isolate from JKM (2.16) were comparable to or higher than the reported C-PER values for regular animal feed ingredients such as corn meal (1.1), wheat flour (0.8), soy flour (1.3), and quality protein maize (1.43) (*23*, *25*). This suggests that jatropha proteins have good quality, and these can supplement or replace the conventional protein sources in animal diets.

Constraints in the Utilization of Jatropha Meal and Isolate from Toxic Genotype. Toxic and nontoxic genotypes of *J. curcas* exist (*7*). The toxic genotype is prevalent throughout the world, and the nontoxic genotype exists only in Mexico. The use of jatropha meals and protein isolate prepared from the toxic genotype in animal nutrition is restricted due to the presence of antinutritional and toxic factors. The major antinutrients are (a) trypsin inhibitors, (b) lectin, and (c) phytate. The levels of trypsin inhibitor and lectin are similar to those in soybean meal, and the level of phytate (9.4%) is approximately 3 times higher. The main toxic factors present are PEs, present at levels of 2−4 mg/g (*7*, *17*). The force-feeding of jatropha meal containing PEs exhibited toxicity in mice, rats, and goats (*9*). Toxcity on feeding purified PEs has also been reported in fish (*26*) and mice (*27*). In all of these animal studies, the major organs affected were intestine, liver, and kidney. The LD_{50} in mice was found to be 27.34 mg/kg of body weight (*27*).

In the past two decades, several studies have been carried out for the complete detoxification of jatropha meals. In brief, trypsin inhibitor and lectin were completely inactivated by moist heat (*28*, *29*). However, toxic PEs could not be removed completely due to their stability to heat and chemical degradation (*30*−*32*). In addition, the residual toxicity of PEs is very high (toxic to carp even at 15 ppm in the diet (*26*)). Similarly, protein isolates prepared from the meal also contained PEs and high levels of phytate, trypsin inhibitor, and lectin (*22*).

Utilization of Jatropha Meal and Protein Isolate from Toxic Genotype in Animal Nutrition. Recently, in our laboratory jatropha kernel meal and protein isolate have successfully been detoxified. The detoxified jatropha kernel meal (DJKM) and detoxified protein isolate (DPI) prepared from screw-pressed cake have been added to fish diets at high levels with excellent growth performance and no toxic effects at blood and tissue levels. The DJKM and DPI have high protein contents (60 and 90%, respectively) and excellent amino acid composition, and these could replace at least 50% of the protein contributed by the high-quality fish meal (65% protein) in standard fish diet. Furthermore, at this level of DJKM or DPI incorporation, the growth response and nutrient utilization in common carp (*Cyprinus carpio*) and rainbow trout (*Oncorhynchus mykiss*) were better than those obtained using soybean meal at the same level of fish meal protein replacement (*33*−*35*). Feeding studies using DJKM and DPI in turkey, pigs, and broilers have been completed, and the growth response and nutrient utilization have been comparable to those obtained with concentrates prepared from conventional protein sources, and no signs of toxicity have been recorded (unpublished observations). Results so far obtained on fish and other animal species suggest that DJKM and DPI are ideal substitutes for fish meal or soybean meal for livestock diets (*36*).

Potential of Jatropha Meal from Nontoxic Genotype in Animal Nutrition. Similar to the toxic genotype, the nontoxic *J. curcas* kernels are rich in oil (55−58%) and protein (26−29%) (*7*). The EAA composition of the meal, except lysine, is similar to that of the toxic genotype, and levels of other EAA are comparable to that of the FAO reference protein (*16*). The meal from the nontoxic genotype is free of PEs, but it contains trypsin inhibitor, lectin, and phytate at the same levels as the meal from the toxic genotype. The nutritional quality of the nontoxic jatropha meal, after heat treatment (to inactivate trypsin inhibitor and lectin), evaluated in fish (carp) and rat models was found to be very high (*37*).The meal or the protein isolate obtained from the nontoxic genotype, after heat treatment, could be an excellent protein-rich ingredient in feeds of ruminant and monogastric animals including fish.

FUNCTIONAL PROTEINS

The enzymes or higher molecular weight proteins having different biological activities are produced by plants for various metabolic activities. In this section jatropha proteins having specific biological roles with respect to metabolic, physiological, or defensive activities are discussed (**Table 1**).

Aquaporin. Aquaporins are membrane proteins or major intrinsic proteins (MIP) that form water channels or pores in biological cell membranes, controlling the water content of the cells. These channels are widely distributed in all kingdoms of life including bacteria, plants, and mammals (*38*). In plants, aquaporins are present in multiple isoforms. The sequence relationship between all plant MIP like cDNAs (126) indicates that the encoded proteins fall into four sequence subclasses: (1) tonoplast intrinsic proteins (TIP) localized in tonoplast; (2) plasma membrane intrinsic proteins (PIP) that localize in vacuolar/plasma membrane; (3) nodulin-26, which is expressed in the peribacteroid membrane of root symbiotic nodules; and (4) small basic intrinsic protein (SIP). PIPs are further classified on the basis of their amino acid sequence into PIP1 and PIP2 subgroups. Compared to PIP1, PIP2 proteins possess a shorter N-terminal extension and a longer C-terminal end containing a putative phosphorylation site (*39*−*42*). Aquaporins are thought to be involved in plant adaptation to drought stress, controlling transmembrane water movement in plants. The presence of aquaporins is considered to play an important role in the rapid growth of *J. curcas* in dry weather conditions.

In jatropha, PIP type proteins (JcPIP2) have been reported from the seedlings of *J. curcas*. The encoding gene has an 843 bp open reading frame encoding a protein of 280 amino acids. The amino acid sequence showed 94% identity with *R. communis* PIP. The injection of JcPIP2 cRNA into a *Xenopus* oocyte system showed 10-fold higher swelling than the oocytes injected with water, indicating water transport ability of JcPIP2. JcPIP2 are present in most plant tissues of jatropha. The abundance of JcPIP2 in the seedlings of drought-resistant populations increases when compared with drought-sensitive populations under water deficit. The abundance of JcPIP2 was increased by heavy drought stress, indicating its role in the drought resistance of *J. curcas* (*43*).

Table 1. Biological Activity of Jatropha Proteins

	biological activity	source	reference
functional proteins			
aquaporins	drought resistance	*J. curcas*	*43*
betaine aldehyde dehydrogenase	drought resistance	*J. curcas*	*46*
esterase and lipase	hydrolysis of triglycerides	*J. curcas*	*52*−*56*
curcain	wound-healing property	*J. curcas*	*58*−*62*
curcin	inhibits protein synthesis, immunotoxins	*J. curcas*	*66*−*68*
β-glucanase	antifungal activity	*J. curcas*	*82*, *83*
cyclic peptides			
mahafacyclin	anitmalarial activity	*J. mahafalensis*	*89*, *94*
labditin and biobollein	immunomodulatory activity	*J. multifida*	*95*−*97*
jatrophidin	antifungal activity	*J. curcas*	*95*
chevalierins	antimalarial activity	*J. chevalieri*	*98*
cycloglossine	no biological activity reported	*J. gossypifolia*	*99*, *100*
podacyclin	no biological activity reported	*J. podagrica*	*101*
pohlianins	antimalarial activity	*J. pohliana*	*93*
curcacycline	antimalarial activity, inhibits cell proliferation and inhibits classical pathway of human complement	*J. curcas*	*94*, *100*, *102*
integerrimides	antiproliferative activity against tumor cells	*J. integerrima*	*87*

Betaine Aldehyde Dehydrogenase (BADH). In the biological systems (plants, animals, bacteria, etc.), many organic osmolytes (e.g., betaine) or other substances are synthesized by cells for protection against osmotic stress, drought, high salinity, or high temperature (*44*). Intracellular accumulation of betaines (nonperturbing to enzyme function, protein structure, and membrane integrity) permits water retention in the cells and, thus, protects against the effects of dehydration. The betaine also maintains protein and membrane conformations under various stress conditions including high salt concentration by maintaining turgor pressure. BADH is an enzyme belonging to the family of oxidoreductases, which catalyzes the chemical reaction

$$\text{betaine aldehyde} + NAD^+ + H_2O \rightleftharpoons \text{betaine} + NADH + 2H^+$$

Thus, BADH indirectly controls the biological activity of cells under stress (*45*).

In jatropha, BADH gene (*JcBD1*) has been cloned. The cDNA of *JcBD1* has 1769 bp with a complete open reading frame of 1509, a 44 bp 5′ noncoding region and 214 bp 3′ noncoding region. The open reading frame encoded 503 amino acids with a predicted molecular mass of 54.58 and a p*I* of 5.32. *JcBD1* showed high identities with BADH of other organisms such as *Gossypium hirsutum* (85%), *Panax ginseng* (84%), *Medicago truncatula* (82%), *Amaranthus hypochondriacus* (83%), *Arabidopsis thaliana* (80%), *Brassica napus* (80%), *Avicennia marina* (79%), and *Spinacia oleracea* (79%). The deduced amino acids of *JcBD1* protein contained a decapeptide motif VSMELGGKSP and the cysteine residue at a distance of 28 amino acids from the decapeptide motif, which are strongly conserved among the general aldehyde dehydrogenase. The *JcBD1* gene belongs to a multigene family and is expressed in roots, flowers, and young seeds, but the expression level was highest in leaves and stems. Under stress conditions such as drought, heat, and salt, the leaves showed increased expression of the *JcBD1* gene, conferring a resistance to abiotic stress (*46*).

Esterase and Lipase. Esterases are widespread in nature and are found in mammals, microorganisms, and plants. Esterases, as well as lipases, catalyze the hydrolysis of triglycerides to fatty acids and glycerol or the synthesis of an ester bond between an alcohol and a carboxylic acid (*47*). Esterases catalyze the hydrolysis and synthesis of short-chain fatty acid esters, whereas lipases act mostly on long-chain acylglycerols (*48*). Currently they find use in various processes such as stereospecific hydrolysis of drugs, ester synthesis for food ingredients, and other organic biosynthetic reactions. Their applications are mainly in food processing, beverages, perfume industries, cosmetics, leather, paper, degradation of synthetic materials, agriculture, and pharmaceutical and chemical industries. Many of the applications in industry have a demand for enzymes that are highly stable against high temperatures and pressure and have broad specificity for substrates and organic solvents (*49*−*51*).

From the *J. curcas* seeds two esterases (JEA and JEB) have been isolated, and both of the enzymes are most active at around pH 8 and are stable at high temperatures (50−55 °C). The molecular masses were found to be 21.6−23.5 kDa (JEA) and 30.2 kDa (JEB) with isoelectric points of 5.7−6.1 (JEA) and 9.0 (JEB). Both of the esterases had high stability over a broad pH range with half-lives of 61 and 52 days for JEA (at 30 °C, pH 3 and 9, respectively) and half-lives of 16 and 5 days for JEB (at 30 °C, pH 3 and 9, respectively). Addition of 20% ethanol (v/v) increased the enzyme activity of JEA (201%) and JEB (170%), and addition of 10 mM $BaCO_3$ enhanced JEB enzyme activity by 142%, whereas diethyl pyrocarbonate, bis(4-nitrophenyl) phosphate hydrate, significantly reduced the activity of both enzymes. The kinetic parameters using *p*-nitrophenyl butyrate as a substrate had a K_m of 0.02 mM and a V_{max} of 0.26 μmol/mg/min for JEA and a K_m of 0.07 mM and a V_{max} of 0.24 μmol/mg/min for JEB. Both of the enzymes (JEA/JEB) hydrolyzed tributyrin, nitrophenyl esters up to a chain length of C4 and naphthyl esters up to a chain length of C6 (*52*).

Lipases isolated from *J. curcas* are active at neutral pH and have an optimal temperature of 37 °C, similar to that of lipases from potato tuber (pH 7.5), rice bran (pH 7.5), and peanut (pH 8.5) (*53*). Partial purification of the *J. curcas* lipase by 80% ammonium sulfate precipitation increased lipase relative activity by 28-fold in the supernatant, and subsequent ultrafiltration of this fraction resulted in an additional 3-fold increase in its relative activity. Jatropha lipase increased its activity in the presence of calcium and magnesium ions (130 and 30%), whereas ferric and zinc ions inhibited the activity by 100 and 92%, respectively (*54*).

J. curcas lipase activity was observed in both dormant and germinating seeds. This enzyme hydrolyzed (a) palm kernel, coconut, and olive oils at comparable rates, (b) *Raphia hookeri* and *J. curcas* seed oils at twice the rate of the former oils, and (c) palm and fish oils at a higher rate than all other oils (*54*). The lipase hydrolyzed long-chain triacylglycerol (TAG) at a faster rate than medium-chain TAG. The lipase also showed preference for partial acylglycerol hydrolysis wherein it hydrolyzed

monoolein at a much faster rate than triolein and was slightly faster for diolein. The study with palm, *R. hookeri*, and *J. curcas* seed oils resulted in a high rate of hydrolysis by the lipase from *J. curcas* seeds, as all have palmitic acid as one of their major fatty acids (*54*−*56*). Staubmann et al. (*52*) have also reported that the amount of water required for maximal enzyme-catalyzed transesterification reactions was lower (0.2) than for other commercial enzymes (lipozyme). Owusu and Cowan (*57*) have reported that the thermostability is correlated with the resistance to denaturation in the organic solvents, suggesting that thermostable enzymes such as jatropha esterases are likely to have advantages for many industrial applications.

Curcain. Curcain is a proteolytic enzyme extracted from the latex of *J. curcas* shoots. The molecular mass of curcain was found to be 22 kDa with an isoelectric pH between 5.6 and 6.0 (*58*). It showed different proteolytic activities with different substrates with an optimum temperature between 45 and 50 °C and with optimum pH 5.0 when casein, hemoglobin, gelatin, and azoalbumin were used as substrates. Sodium sulfide is a potent inhibitor of curcain activity. A complete inactivation of the enzyme occurred at >80 °C (*58*). The K_m and V_{max} (maximum attainable reaction velocity) of curcain were 20% (w/v) and 0.67 units min^{-1}, respectively, when azoalbumin was used as substrate and 0.28% (w/v) and 0.052 units/min, respectively, when the substrate was hemoglobin. A higher enzyme−substrate affinity was observed for hemoglobin as compared with azoalbumin.

Curcain has an oral LD_{50} of 3 g/kg of body weight and intraperitoneal LD_{50} of 0.96 g/kg of body weight in mice, indicating lower toxicity (*61*). The curcain was found to have a wound-healing property, and this activity was checked in mice at two different enzyme concentrations (curcain powder at 0.5 and 1.0% (w/w), which is mixed with washable ointment base). Healing of wounds by the curcain ointments was better compared to the control ointments (0.2% w/w) nitrofurazone (furcin ointment, SK&F) and 0.15% (w/w) propamidine isoethionate (antiseptic cream, M&B). The wound tissue collected after application of curcain ointment (10th day) from the mice showed complete healing of wound with abundant collagen deposition and formation of epidermis/keratin; on 15th day, mice had normal skin, whereas the control ointments on the 15th day had only progressive healing and the structures of healed skin were observed only on the 29th day thus indicating the high potential of curcain in pharmaceutical applications (*59*−*62*).

Curcin. Curcin, a plant toxin, belongs to a group of proteins called ribosome-inactivating proteins (RIPs), which inactivate ribosomes and finally halt protein synthesis. RIPs are classified into three groups on the basis of their physical properties. Type 1 RIPs are single-chain (~30 kDa) with the enzymatic activity and can inhibit cell-free protein synthesis, but are relatively nontoxic to cells and animals. Type 2 RIPs are highly toxic heterodimeric proteins (~60 kDa) consisting of an A chain (which has similar function as type 1 RIP) attached to a sugar-binding B chain by a disulfide linkage. The lectin chain can bind to galactosyl moieties of glycoproteins and or glycolipids found on the surface of the eukaryotic cells and mediate retrograde transport of the A chain to the cytosol (*63*). Type 3 RIPs are synthesized as inactive precursors, which require further proteolytic processing to become active. The main enzymatic activity of RIPs is an N-glycosidation that removes a specific adenine corresponding to residue A_{4324} in rat 28S rRNA. This adenine lies within a 14-nucleotide region that is known as the α-sarcin loop and is conserved in large rRNAs from bacteria to humans (*64*, *65*). Curcin is a toxalbumin, a type I RIP (28.2 kDa, isoelectric point of 8.54) and affects protein translation activity. It was first purified from the seeds of *J. curcas* (*66*, *67*). Studies showed that arginine is important for conformation of curcin molecule and that modification of arginine, lysine, and tryptophan residues in the active site resulted in loss of inhibitor activity (*68*). The curcin exhibited RNA *N*-glycosidase activity like other type 1 RIPs. A comparison of amino acid sequences of curcin with other RIPs, for example, ricin A chain and trichosanthin (from *Trichosanthes kirilowii*) revealed that they have high similarity to each other with 54% (156/287) and 57% (138/241) identity, respectively. All amino acid residues forming the active sites of the A chain of ricin and trichosanthin were also found in curcin at corresponding positions with the exception of one residue, Gln-173 in ricin and trichosanthin, which was replaced by Glu-163 in curcin (*69*). Jing-ping et al. (*70*) have reported that there are two subfamilies in the curcin gene family expressed either (a) by stress conditions and microbes or (b) in the endosperm of the seeds. In the leaves, a curcin-related RIP (curcin-L) is induced by infection (*Pestalotia funerea*, *Gibberelle zeae*), and its expression could be activated by abscisic acid, salicylic acid, polyethylene glycol, temperatures of 4 and 45 °C, and ultraviolet light (*71*). Curcin-L has antifungal and antiviral activities. Similarly, Wei et al. (*72*) and Huang et al. (*73*) have also reported that under stress, drought, or fungal infection conditions, *J. curcas* plant expresses another protein similar to curcin, called curcin 2 (32 kDa).

In jatropha, purified curcin inhibited cell-free translation in the reticulocyte lysate system with an IC_{50} (95% confidence limits) of 0.19 (0.11−0.27) nmol/L (*65*). Curcin has cell-free translation inhibitory activity higher than most RIPs, such as saporin (0.5 nmol/L), luffin A (1 nmol/L), luffin B (4 nmol/L), and trichosanthin (0.32 nmol/L) (*63*). On feeding 200 μg of raw curcin fluid, 94.4% of *Gambusia* (fish) died within 99 h, and the LD_{100} for mice was at 1.6 mg/kg of body weight on subcutaneous injection after 9 days (*74*). Water extracts from *J. curcas* seed displayed a low poisoning effect on snail and schistosome larva. In the water extract solutions, snail heartbeating stopped at 48 h and schistosome larva stopped moving within 2 h. The LD_{50} values were 1 and 5 g/kg, respectively. This is believed to be associated with saponin and curcin (*74*). At 5 μg/mL, curcin inhibited hyphal growth and spore formation in the bacteria *Pyriclarimoryzae Cav.*, *P. funerea*, and *Sclerotinia sclerotiorum* (Lib.) de bary, thus exhibiting the potential of being a biological bacteriocide and pesticide. Crude curcin and purified curcin (curcin I) caused acute toxicity (9.11 and 6.48 mg/mouse) and delayed toxicity (5.83 and 2.21 mg/mouse) in mice (*66*).

RIP has gained interest in the development of antitumor drugs that selectively target tumor cells. Antitumor activity is related to *N*-glycosidase action, which cleaves the N-glycosidic bond of adenine, making ribosome unable to bind elongation factors 1 or 2, consequently arresting protein synthesis. Although there are many reported RIPs from different plant sources, but the effects of these proteins in vitro are different on ribosomes isolated from different organisms (*75*). Recently, type 1 RIPs have gained interest as immunotoxins (type of hybrid molecule consisting of a toxic peptide chain linked to an antibody). Immunotoxins can be promisingly used to eliminate targets such as harmful cells, neoplastic, immunocompetent, and parasitic cells. At present, there is a search for new RIPs with the highest antitumor activity to a variety of tumor cells and to overcome the immune response that follows clinically oriented administration of RIP conjugates (*66*, *69*). Curcin could be the most preferred choice.

Most type I RIPs do not have any free cysteine residues, which are needed for the modification of both antibody and RIP with chemical agents to produce the disulfide bond during the preparation of immunotoxins. However, curcin contains one cysteine residue, and it may directly form a disulfide bond with an active antibody thiol group via a disulfide exchange reaction (*68*).

Curcin inhibited protein synthesis in SGC-7901 (gastric cancer cell line), Sp2/0 (mouse myeloma cell line), and human hepatoma cells with IC_{50} values of 0.23 (0.15−0.32) mg/L, 0.66 (0.35−0.97) mg/L, and 3.16 (2.74−3.58) mg/L, respectively. However, curcin was nontoxic to HeLa cells (carcinoma cell line) and normal cells (human embryo lung diploid cell line) (*68*). Overall, being nontoxic to normal cells, curcin is a cysteine-containing RIP and can form disulfide bonds with an active antibody, thus indicating a potential for the preparation of immunoconjugates with the aim of using it as a chemotherapeutic agent for the treatment of cancers.

Trypsin Inhibitors (TIs) and Lectin. TIs are proteins that inhibit proteolytic enzymes (trypsin and chymotrypsin) during digestion, and lectins are glycoproteins, which generally agglutinate red blood cells and affect absorption of nutrients by binding intestinal membrane. From a nutritional perspective, both are considered to be antinutritional factors. The TI content in JKM ranges from 18.5 to 27.5 TIU (trypsin inhibition/mg of sample), and its concentrations are similar in both toxic and nontoxic genotypes (*16*, *17*). On the other hand, lectin content of JKM is higher in the nontoxic genotype than in toxic genotype (51 vs 102 U; 1 U = minimum amount of sample in mg/mL assay producing agglutination; the lower the number of units, the higher the activity) (*16*). Generally, both TIs and lectins are prone to heat and could be inactivated by heat treatment. Nevertheless, some plant lectins (e.g., black bean and kidney bean lectins) and trypsin inhibitors (Bowman−Birk inhibitors) are not heat labile (*76*). In jatropha, both TIs and lectins could be completely inactived by autoclaving the kernel meal at 121 °C for 30 min (*7*, *28*, *29*).

Despite the negative nutritional effects of TIs and lectins, they have been widely studied for pharmacological benefits. Many plant lectins have been to shown to possess anticancer properties in in vitro, in vivo, and human studies. Lectin causes cytotoxicity, inhibits tumor cell growth by binding selectively to the receptors present on the cell membrane, inhibits protein synthesis by binding to ribosomes, down-regulates telomerase activity, and reduces angiogenesis (*77*, *78*). Similarly, TIs (such as soy TI, Kunitz type) have anticancerous properties such as suppression of ovarian cancer cell invasion by blocking urokinase upregulation (*79*). However, no information is available on the biochemical and pharmaceutical properties of TIs and lectins from jatropha. Studies are required to elucidate the potential of these molecules as therapeutic agents.

***β*-Glucanase.** β-1,3-Glucanases are enzymes that hydrolyze glucans present in many higher plants. The cell wall of various fungi including plant pathogens consists of chitin and β-1,3/1,6-glucans. Many chitinases and β-1,3-glucanases produced by plants can inhibit fungal growth by hydrolyzing the glucans present in the tips of germ tubes and hyphae. It is known that a combination of chitinase and β-1,3-glucanase shows stronger antifungal activity to a wider range of fungi than when each of them act separately (*80*).

β-Glucanase also helps in the breakdown of plant walls (cellulose), digests fiber, and increases the overall efficiency of binding excess cholesterol and toxins in the intestines for removal. It is used in animal healthcare as a feed supplement for increasing the feed conversion ratio in poultry and for enhancing milk yield in cattle. It is also used in commercial food processing industries, for example, the coffee industry, the brewing industry, and the textile industry, as a fading agent (http://www.enzymeindia.com/enzymes/beta-glucanase.asp). It also exhibits a broad defense mechanism againt pathogen attack (*81*).

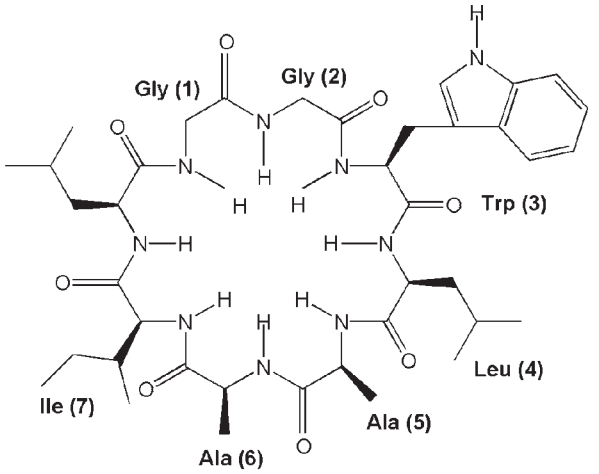
A β-1,3-glucanase isolated from *J. curcas* seeds has a molecular mass of 65−66 kDa and consists of three subunits with a noncovalent bond conjugate. The optimal temperature and pH of the β-1,3-glucanase activity were 40−50 °C and pH 7, respectively. The enzyme was stable at pH 6−8 and at temperatures between 30 and 55 °C. The protein had an isoelectric point of 8.3. It exhibited in vitro antifungal activity against *Rhizoctonia solani* Kuha (IC_{50} = 12.6 nM) and *G. zeae* (Schw.) Petch. by hydrolyzing cell walls of fungi. It was slightly toxic to mice with an LD_{50} of 2.22 g/kg. The author suggested that this protein could be beneficial as a biological fungicide in agriculture (*82*, *83*).

CYCLIC PEPTIDES

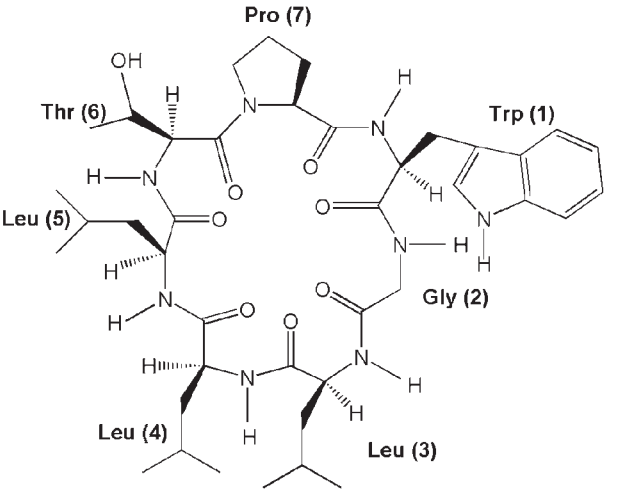
Recently, cyclopolypeptides and related congeners have been shown to have potential pharmacological applications (*84*−*86*). Cyclic peptides isolated from latex, seeds, and roots of many plants possess various biological activities such as cytotoxic activity (*87*), immunosuppressive activity (*88*), antimalarial activity (*89*), vasorelaxant activity (*90*), and cyclooxygenase, acetylcholine esterase, and tyrosinase inhibitory activities (*91*, *92*). Conformational determination of such cyclic pcptides is an important step to exhibit local interactions, which could initiate the folding of native proteins. In addition, as biological activities are known to be related to the three-dimensional structure, it is of importance to determine their solution conformational preference (*93*). *Jatropha* species have been shown to be a rich source of bioactive cyclic peptides, which contain 7−10 residues with a high proportion of hydrophobic amino acids (**Figure 1**). There is a need to exploit the potential and role of cyclic peptides from jatropha for pharmacological applications. In the following section we discuss the literature available on jatropha cyclic peptides (**Table 1**) emphasizing chemistry and its potential toward agricultural/pharmaceutical properties.

Mahafacyclin. Mahafacyclin was purified from a CH_2Cl_2/MeOH extract of dried *Jatropha mahafalensis* latex as one major component (mahafacyclin A) and one minor component (mahafacyclin B). The amino acid composition of mahafacyclin A cyclo-($C_{34}H_{54}N_7O_8$; calcd MW 688.40) was determined to be cyclo-(Gly^1-Thr^2-Ile^3-Leu^4-Gly^5-Val^6-Phe^7), whereas the sequence of amino acid in mahafacyclin B ($C_{44}H_{50}N_7O_8$; calcd MW 804.37) was determined to be cyclo-(Gly^1-Thr^2-Phe^3-Phe^4-Gly^5-Phe^6-Phe^7). The absolute configuration of the chiral amino acids from both heptapeptides showed "L". The cyclic heptapeptides usually possess a stable and rigid backbone conformation in solution, forming a typical motif termed β-bulge. This motif is defined by two β-turns with a mixed hydrogen bond. Such a structure is generally observed for cycloheptapeptides containing at least one proline residue. Mahafacyclin A showed two β-turns at Gly^1-Thr^2 and Leu^4-Gly^5 and a H-bonding pattern involving Phe^7-NH and Ile^3-CO, which is consistent with a β-bulge. Mahafacyclin B also shows the presence of two β-turns around (type 1) Phe^4 -Gly^5 and (type 2) Phe^7 -Gly^1. These β-turns are stabilized by 4→1 hydrogen bonds between CO-Phe^3 and NH-Phe^6 for type I β-turn and a type II β-turn stabilized by a hydrogen bond between CO-Phe^6 and NH-Thr^2. Computer modeling also showed a third intramolecular hydrogen bond (5→1) between CO-Phe^6 and NH-Phe^3, thus supporting the β-bulge motif in mahafacyclin B. Both mahafacyclin A and mahafacyclin B exhibited antimalarial activity against *Plasmodium falciparum* with IC_{50} values of 16 and 2.2 μM, respectively (*89*, *94*).

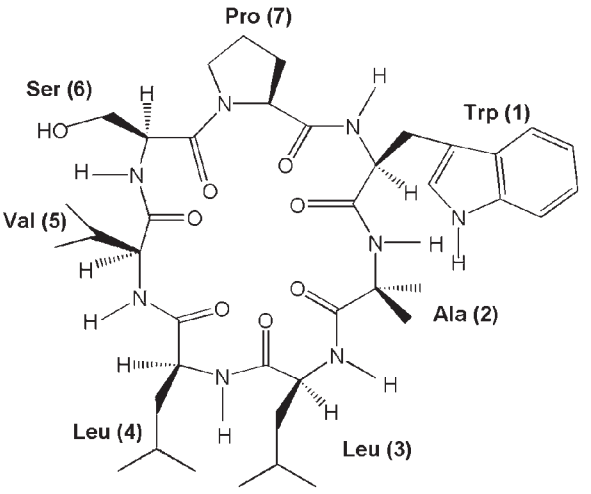
Labaditin and Biobollein. Labaditin and biobollein are cyclic peptides isolated from *Jatropha multifida*. Labaditin is a decapeptide with an amino acid sequence of cyclo-(Ala^1-Gly^7-Val^8-Trp^2-Thr^{10}-Val^5-Trp^6-Gly^9-Thr^3-Ile^4), with a structural formula of $C_{53}H_{74}N_{12}O_{12}$ (calcd MW 1071.2). Labditin selectively inhibited



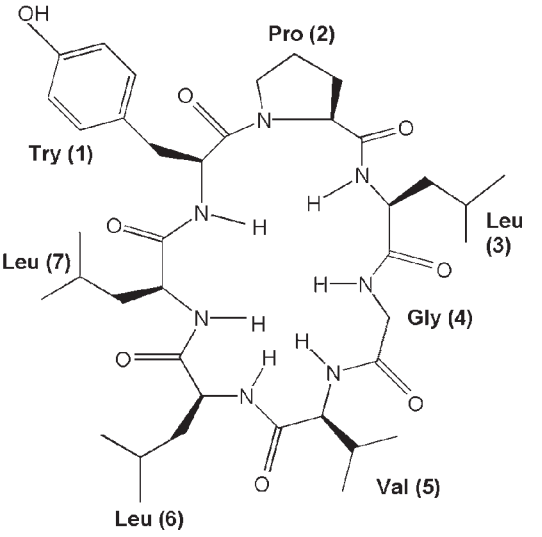
Cyclogossine B



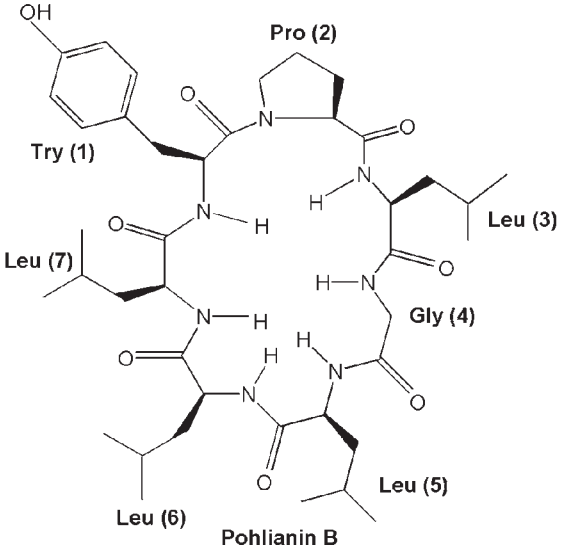
Integerrimide A



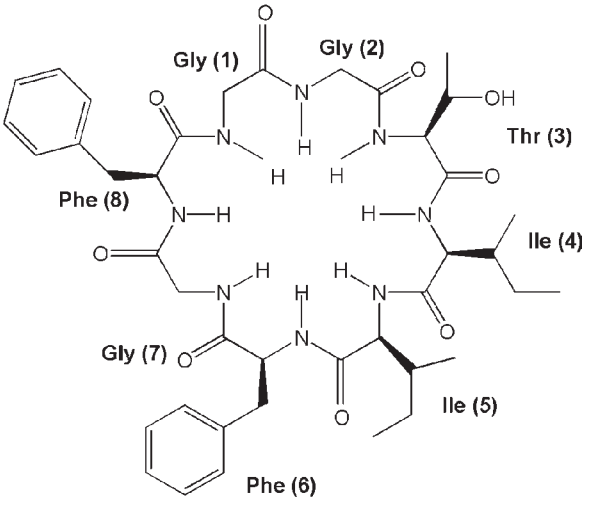
Integerrimide B



Pohlianin A



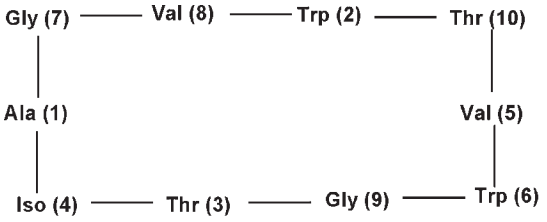
Pohlianin B



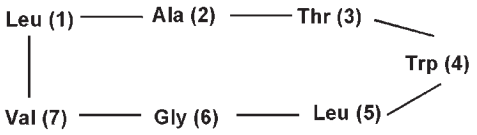
Pohlianin C

Figure 1. Continued

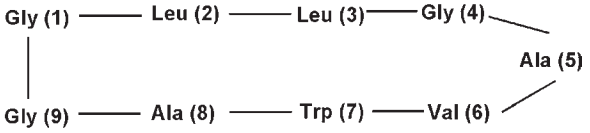
the classical pathway of human complement activation in vitro, whereas Biobollein is a cyclic nonapeptide, with an amino acid sequence of cyclo-(Ala[1]-Ser[2]-Ile[3]-Leu[4]-Gly[5]-Leu[6]-Gly[7]-Trp[8]-Ala[9]). The activity of both cyclic peptides was suggested to



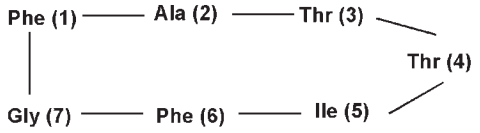
Labaditin



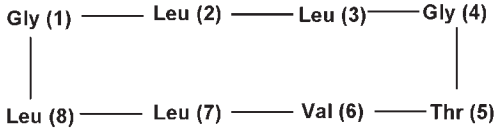
Cyclogossine A



Podacyclin A



Podacyclin B



Curcacycline A

Figure 1. Continued

be based on interaction with C-1 of the human complement system. Both peptides bind to aggregated and antigen-bound IgG and, most probably, block the antibody Clq acceptor site. This property is restricted to IgG subclass IgG1. The immunomodulatory activity of these peptides could be of pharmaceutical importance (*95*−*97*).

Jatrophidin. Jatrophidin is an octapeptide isolated from the latex of *J. curcas*. The latex was partitioned with ethyl acetate, fractionated on Sephadex G15, eluted in solid phase extraction, and purified by HPLC to obtain jatrophidin I. The amino acid analysis, mass spectroscopy, and 1D/2D nuclear magnetic resonance (NMR) studies demonstrated that jatrophidin I exists as two conformers of a cyclic structure (Gly-Trp-Leu-Asn-Leu-Leu-Gly-Pro) with the conformational equilibrium of proline residues between cis and trans forms, indicating that this peptide has more than one conformational state in solution. The isolates of jatrophidin I had weak antifungal effect against the strains of *Candida albicans*, *Candida krusei*, *Candida parapsilosis*, and *Cryptococcus neoformans* and moderate activity as an acetylcholinesterase inhibitor, when compared with the standard galanthamine (*95*).

Chevalierins. Chevalierins are cyclic peptides isolated from the latex of *Jatropha chevalieri*. To date, three types of chevalierin peptides have been isolated. Chevalierins A ($C_{39}H_{69}N_8O_8S$; calcd MW 809.49) and B ($C_{39}H_{69}N_8O_9S$; calcd MW 825.49) are cyclo-octapeptides and chevalierin C ($C_{52}H_{69}N_9O_{13}$; calcd MW 1028.51) is a nonapeptide. The amino acid compostion showed the presence of one Ala, one Gly, three Ile, one Leu, and one Pro for both A and B. The differences between A and B arose from the presence of one methionine in A and one methionine sulfoxide in B. The amino acid sequence of chevalierin A is cyclo-(Gly^1-Ile^2-Pro^3-Ile^4-Leu^5-Ala^6-Ile^7-Met^8). Chevalierin A possesses antimalaraial activity with an IC_{50} of 8.9 μM. The amino acid sequence of chevalierin C is cyclo-(Tyr^1-Thr^2-Ile^3-Phe^4-Asp^5-Ile^6-Phe^7-Gly^8-Ala^9). The absolute configuration of the chiral amino acids was shown to be "L" (*98*).

Cyclogossine. Cyclogossine peptides (A and B) have been isolated from the alcoholic extract of latex of *Jatrohpa gossypifolia*. Cyclogossine A is a cyclic heptapeptide with an amino acid sequence of cyclo-(Leu^1-Ala^2-Thr^3-Trp^4-Leu^5-Gly^6-Val^7). The absolute stereochemistry of the residues was shown to be "L". Cycloglossine B ($C_{39}H_{59}N_9O_8$; calcd MW 782.45) is an octapeptide and has two Ala, two Gly, one Ile, two Leu, and one Trp. The absolute stereochemistry of the residues was shown to be "L". The amino acid sequence of cycloglossine B is cyclo-(Gly^1-Gly^2-Trp^3-Leu^4-Ala^5-Ala^6-Ile^7-Leu^8) (*99*, *100*). The biological activities of these peptides have not been reported.

Podacyclin. Podacyclin peptides (A and B) are isolated from the latex of *Jatropha podagrica* Hook. Podacyclin A ($C_{40}H_{60}N_{10}O_9$; MW 824.97) is a cyclic nonapeptide with the amino acid sequence cyclo-(Gly^1-Leu^2-Leu^3-Gly^4-Ala^5-Val^6-Trp^7-Ala^8-Gly^9), whereas podacyclin B is a heptapeptide ($C_{35}H_{47}N_7O_8$; MW 693.79) and the amino acid sequence is cyclo-(Phe^1-Ala^2-Gly^3-Thr^4-Ile^5-Phe^6-Gly^7). The amino acid residues of both compounds have the "L" configuration (*101*). The biological activities of these peptides have not been reported.

Pohlianins. Pohlianins were isolated from the ethanolic extract of *Jatropha pohliana* latex. Pohlianins A (I) and B (2) are two cyclic heptapeptides, and pohlianin C (3) is a cyclic octapeptide. The amino acid sequence of pohlianin A ($C_{39}H_{62}N_70_8$; calcd MW 756.46) is cyclo-(Tyr^1-Pro^2-Leu^3-Gly^4-Val^5-Leu^6-Leu^7). The mean structure adopts a type I β-turn at Val^5-Leu^6 stabilized by a 4→1 hydrogen bond between Leu^7-NH and Gly^4-CO. The proposed solution conformation also showed a turn at $Tyro^1$-Pro^2 stabilized by a 4→1 hydrogen bond between Leu^3-NH and Leu^7-CO and a third hydrogen bond between Gly^4-NH and Leu^7-CO, consistent with the low-temperature coefficient of the Gly^4-NH, exhibiting a β-bulge motif. Pohlianin B ($C_{40}H_{64}N_7O_8$; calcd MW 770.48) differs from A by 14 Da. Both A and B have one Gly, three Leu, one Pro, and one Tyr, and the distinction between A and B arose from the presence of one $valine^5$ in A instead of one $leucine^5$ in B. Pohlianin C has an amino acid sequence of cyclo-(Gly^1-Gly^2-Thr^3-Ile^4-Ile^5-Phe^6-Gly^7-Phe^8), with a structural formula of $C_{40}H_{57}N_8O_9$ (calcd MW 793.42). The absolute configuration of the chiral amino acids was shown to be "L". Temperature-dependence studies

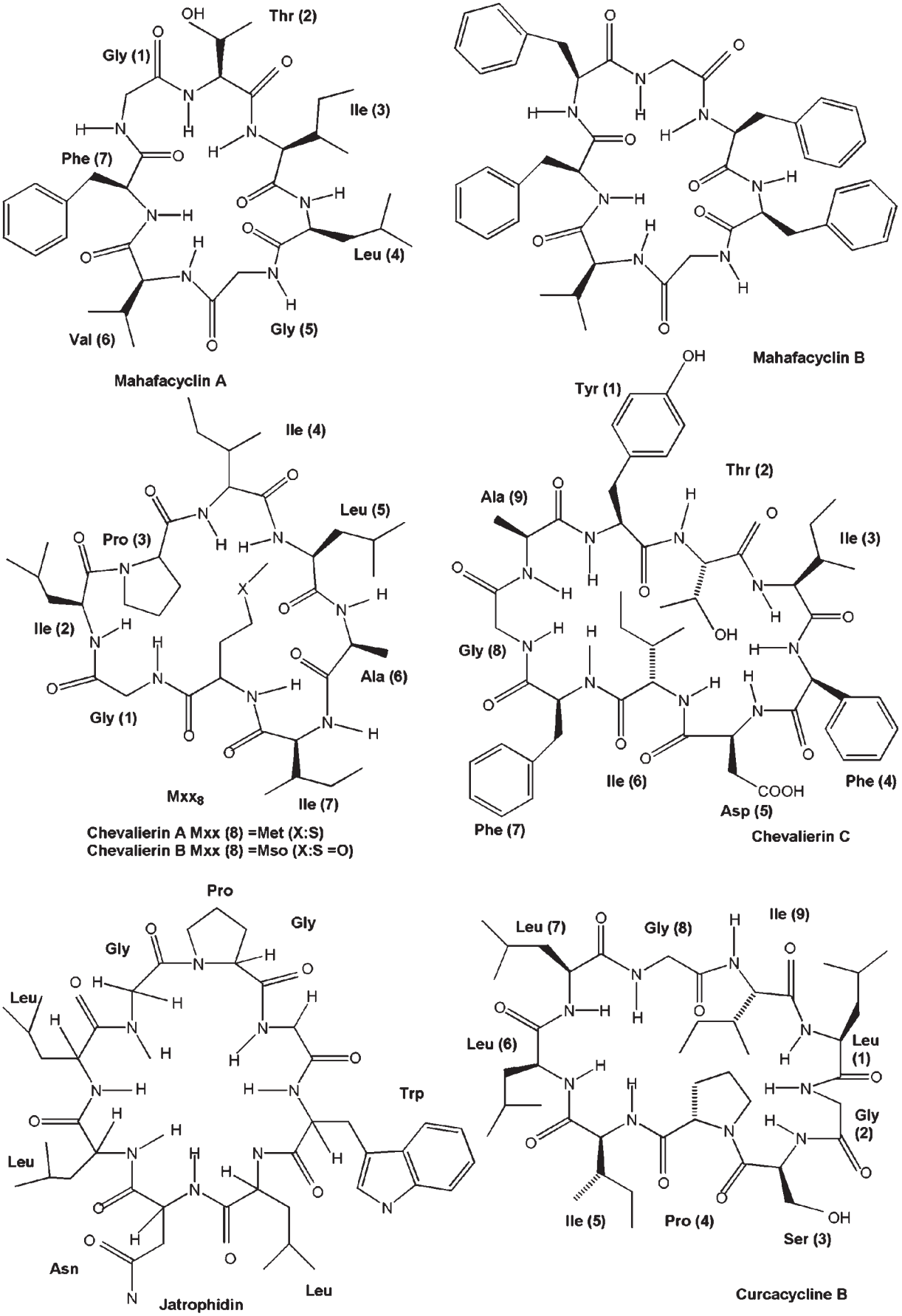


Figure 1. Structures of cyclic peptides.

suggested Gly^1, Gly^2, Ile^5, Phe^6, and Gly^7 are solvent exposed, whereas Thr^3 and Ile^4 are involved in intramolecular hydrogen bonds or buried in a hydrophobic pocket. All of the peptides (pohlianins A−C) have antimalarial activity with IC_{50} values

of 57, 25, and 16 μM, pohlianin C being the more potent among them (*93*).

Curcacyclines A and B. Curcacycline A was isolated from the ethanolic extract of *J. curcas* latex. It is a cyclic octapeptide ($C_{37}H_{66}N_8O_9$; calcd MW 766.97). The amino acid sequence was determined to be cyclo-(Gly[1]-Leu[2]-Leu[3]-Gly[4]-Thr[5]-Val[6]-Leu[7]-Leu[8]). Curcacycline A displayed a moderate inhibition of (i) the classical pathway activity of human complement and (ii) the proliferation of human T-cells (*102*).

Curcacycline B is a cyclic nonapeptide ($C_{42}H_{73}N_9O_{10}$; MW 863) isolated from the latex of *J. curcas*. The amino acid sequence was found to be cyclo-(Leu[1]-Gly[2]-Ser[3]-Pro[4]-Ile[5]-Leu[6]-Leu[7]-Gly[8]-Ile[9]). The absolute stereochemistry of the amino acids was shown to be "L" configuration. It contains mostly hydrophobic residues and one proline, thus differing from the previously cyclic peptides isolated from jatropha species latex, which do not contain proline. The structure of curcacycline B was suggested to be a substrate for peptidyl-prolyl cis−trans isomerase (PPIase), as it has some structural features in common with cyclosporin A (inhibitor of cyclophilins A and B). Curcacycline B enhances PPIase activity by 60% at 30 μM based on α-chymotrypsin rotamase coupled enzymatic experiment using human cyclophillin B, whereas no modification of cyclophilin B activity was observed in the presence of curcacycline A (*100*). Curcacycline B from *J. curcas* possesses antimalarial activity (IC_{50} < 10 mM) against *P. falciparum* (*94*).

Integerrimides. Integerrimides A (1) and B (2) were isolated from *Jatropha integerrima* leaf stalk latex. The amino acid sequence of intgerrimide A ($C_{40}H_{60}N_8O_8$; calcd MW 781.46) was found to be cyclo-(Trp[1]-Gly[2]-Leu[3]-Leu[4]-Leu[5]-Thr[6]-Pro[7]), and integerrimide B ($C_{39}H_{58}N_8O_8$; calcd MW 767.45) has an amino acid sequence of cyclo-(Trp[1]-Ala[2]-Leu[3]-Leu[4]-Val[5]-Ser[6]-Pro[7]). Peptides A and B significantly inhibited neurite outgrowth at 50 μM when assessed by culturing E7 chicken spinal cord neurons for 2 days. Similarly, blebbistatin-induced neurite sprouting was also completely abolished in the presence of 50 μM A. Both peptides A and B had significantly lower (up to 40% at 50 μM) cell densities when treated with cultured human melanoma cells (IPC-298) for 2 days. The authors (*87*) observed that cell debris and apoptotic cell nuclei were absent in the treated cell cultures, suggesting both peptides have an antiproliferation but no cytotoxic activity. Both peptides (A and B at 50 μM) exhibited cell migration activity in confluent human Capan II pancreatic carcinoma cells by 30 and 20%, respectively. Thus, the peptides have potency to inhibit basic cytoskeleton-dependent cellular processes such as neurite outgrowth, cell proliferation, and cell migration (*87*).

CONCLUSION

The increased global demand to meet the protein requirement in animal nutrition and future energy needs has given impetus to the search for alternative plant sources that do not compete with human nutrition and at the same time have high oil content. Jatropha seeds may be a good alternative with respect to their multipurpose features such as high adaptability for cultivation, applicability of seed oil for biofuel production, and generation of productive value-added coproducts. The plant has potential to enhance both food and energy security as well as contribute to land reclamation and prevention of land degradation.

Jatropha proteins have interesting nutritional and biochemical properties. From a nutritional perspective, they seem to be at least comparable to if not better than soybean proteins. High protein content and their digestibility and good amino acid composition make jatropha proteins a promising source for incorporation into the diets of ruminant and monogastric animals including fish. A major drawback for poor utilization of jatropha proteins in animal nutrition has been the presence of antinutritional factors and particularly of phorbol esters. However, a detoxification process developed recently in our laboratory will pave the way for using jatropha kernel meal and protein isolates in livestock nutrition. The plant expresses proteins (such as aquaporins and betaine aldehyde) necessary to sustain environmental pressures such as drought and arid conditions. The bioactive protein, particularly, curcin has potential to be used as a successful immunoconjugate in chemotherapy. Furthermore, several cyclic peptides present in jatropha seeds are of clinical significance and show their potential in pharmacy (**Table 1**). The immediate benefits of research on jatropha proteins and peptides would be in the area of nutrition and clinical diagnostics. The information provided in this review could form a basis for (a) using synthetic chemistry and genetic engineering approaches for chemical modification of the bioactive molecules to modulate their activities and (b) formulating strategies for using them in practical situations, benefitting human and animal health and making agriculture efficient, sustainable, and environmentally friendly.

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