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Genome-wide identification and analysis of the *SnRK2* gene family in cowpea (*Vigna unguiculata* (L.) Walp.) reveals potential stress-responsive roles

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Abstract

Plants, owing to their sessile nature, have evolved mechanisms to adapt and overcome various abiotic stresses by activating different signaling pathways triggering accumulation of stress-associate proteins. A key regulator in Abscisic acid (ABA) signaling pathway, sucrose non-fermenting-1-related protein kinase 2 (*SnRK2*), is a plant-specific serine/threonine kinase family involved in osmotic stress responses. While members of this protein family have been analyzed in some plant species, their characterization in cowpea (*Vigna unguiculata*), a tropical food grain legume cultivated in Africa and Southeast Asia, remains unexplored. Drought stress significantly hampers the growth and productivity of cowpea, highlighting the need for functional studies of stress-related genes. The genes encoding *SnRK2* in cowpea and their detailed characterization remain unexplored. The present study attempts to identify and characterize *SnRK2* gene families in cowpea using bioinformatics tools. Analysis of the draft genome of *Vigna unguiculata* in NCBI and Phytozome databases revealed sixteen *SnRK2* genes. *In silico* analysis were conducted to determine gene structure, transcript length and chromosomal mapping of the genes to *Vigna unguiculata* genome. Domain architectures of the SnRK2 proteins were predicted. Physico-chemical characterization revealed these proteins in sizes ranging 53 to 112 kDa with pI values of 4.99 to 9.59. All identified cowpea SnRK2 proteins are hydrophilic in nature. Analysis of the evolutionary relationship of *SnRK2* with other related families showed three clusters based on the relatedness to *Arabidopsis thaliana* and thirteen other crops. Findings of this study provide valuable insights into cowpea *SnRK2* gene family and its possible implications in plant stress tolerance.

Keywords

cowpea; genome wide; plant stress; *SnRK2*; *Vigna unguiculata*

Introduction

Cowpea (*Vigna unguiculata*), native from Africa, is widely cultivated in tropical and subtropical regions (1). It isa diploid member of the Fabaceae family with a chromosome number 2n = 22 and an estimated genome size of 613 Mb (2).Cowpea has gained more attention recently from consumers and researchers worldwide due to its various health beneficial, including anti-diabetic, anti-cancer, anti-hyperlipidemic, anti-inflammatory and antihypertensive properties (3). Wide adaptability of cowpea to low fertile soils, pH, high temperatures and drought makes this crop choicest for facing the changed climate scenario. Plants

responses to drought are complex and envisaged with different mechanisms to adapt and survive under drought stresses (4). Drought stressed plants various morphological, physiological, biochemical and molecular changes that adversely affect their growth, development and productivity (1).

Among these tolerance mechanisms, phosphorylation and dephosphorylation are key events modulated by protein families. In plants, major protein kinase groups include calcium-dependent protein kinases, mitogen-activated protein kinases and sucrose non-fermenting-related protein kinases (5). Abiotic stresses trigger a complex osmotic-stress and abscisic acid (ABA) signal transduction network. SNF1-related protein kinase2s (SnRK2s) are core ABA signaling components that are activated by ABA-triggered inhibition of type- 2C protein-phosphatases (6). Plant-specific *SnRK2* genes play crucial roles in the coordination of plant growth and development and responses to stress and are dubbed as equivalent of mammalian AMP-activated protein kinases and SNF-1 proteins 1 from yeast. SnRK (or SNF1-related protein kinase) family are specific types of serine/threonine protein kinases that exist widely in plants and function significantly in a host of processes, including growth and development, defense against various stresses and hormone-mediated signaling (7, 8). In higher plants, the SnRK family consists of three subfamilies *viz*., SnRKl, SnRK2 and SnRK3 based on their sequence similarity and C-terminal domain structure characteristics (5). The SnRK2 kinases phosphorylate and thus regulate the activity of downstream components including transcription factors and ion channels (6). Interaction of SnRK2 and protein phosphatase 2C (PP2C) in ABA-dependent signal transduction causes activation of stress-responsive genes (5).

Genetic approaches have played a fundamental role in exploring key genes involved in osmotic stress and ABA signaling pathways. SnRK2 family members have been found in many plant species like Arabidopsis, maize, cotton, rice, wheat, soybean, Rapeseed, crabapple and grapevine (5). However, the SnRK2 family remains unexplored in cowpea. Therefore, the present study aims to identify and characterize the SnRK2 gene family in cowpea using bioinformatics tools.

Materials and Methods

Collection of datasets

The whole cowpea (*Vigna unguiculata*) proteome (assembly ASM411807v1) was downloaded from NCBI (https://www.ncbi.nlm.nih.gov/genome/). HMMER and keyword searches were performed in the Phytozome V12.1 database (https://phytozome.jgi.doe.gov/pz/portal.html) using the keywords SNF and SnRK2 in the “find genes by keyword” input tab. For reference search using heterologous sequences, *Arabidopsis thaliana* SnRK2 (AtSnRK2) protein sequences were obtained from The Arabidopsis Information Resource (TAIR) (https://www.arabidopsis.org/index.jsp).

Chromosomal Mapping of SnRK2 genes

Mapgene2chrom, a *tool* to draw gene physical map based on PERL and SVG languages. (http://mg2c.iask.in/mg2c_v2.0/) was used for chromosome mapping of cowpea SnRK2 genes. The obtained *SnRK2* sequences were mapped on the *Vigna unguiculata* chromosomes using MapGene2Chrom (9) with chromosome co-ordinates (gene id, gene start position, end position, chromosome id and size of chromosome).

Identification of sequence homologs using Hidden Markov models

The HMMER program version 3.3 (http://hmmer.org/), using hidden Markov models, was run to identify *SnRK2* sequences in the cowpea genome by using *AtSnRK2* sequences as bait sequence.

Identification of domain architecture in SnRK2 proteins

The domain and domain architecture of AtSnRK2s were obtained by Simple Modular Architecture Research Tool (SMART) (http://smart.embl-heidelberg.de).

Multiple Sequence Alignment

ClustalW, like other Clustal tools, is used for aligning multiple nucleotide or protein sequences in an efficient manner. Multiple sequence alignments (MSAs) of *AtSnRK2* genes were built using Clustal Omega to validate the results obtained. MSAs were built in MEGA X to confirm the presence of the conserved SnRK2 domain in identified cowpea SnRK2 proteins

Phylogenetic analysis

The evolutionary relationships of cowpea SnRK2 proteins were predicted by building a phylogenetic tree. SnRK2 protein sequences from fifteen different crops were aligned using ClustalW and the tree was constructed by MEGA X (https://www.megasoftware.net/) the neighbour joining method with 1000 bootstrap replications. Further analysis of the phylogenetic tree was performed by exporting this tree to MEGA X and was run by choosing default parameters such as gap penalty and gap extensions with default values

Physico-Chemical analysis of SnRK2 proteins

The theoretical isoelectric point and molecular weight of SnRK2 proteins were determined using ExPASy pI/Mw tool (https://web.expasy.org/compute_pi/).

Results

Whole genome characters of cowpea in NCBI

The results show the chromosome number, reference sequence ID, size of genome sequences, GC content, number of proteins, RNA and gene encoded (Table 1). Gene prediction showed 29,773 total loci containing 42,287 protein-coding transcripts and 12,514 total alternatively spliced transcripts in cowpea.

Characteristics feature of SNF protein in the cowpea genome

The SNF related proteins were characterized and found to be identical across the Cowpea genome. There are 12 protein identities of SnRK2 observed (Table 2).

***Chromosomal Mapping*:** The identified SnRK2 genes were mapped on six chromosomes (chromosomes 1,3,4,8,9 and 11). Four genes, namely 114192996 and 114181284, were predicted

Table 1. Whole Genomic information of cowpea (*Vigna unguiculata*)

Type	Name	RefSeq	INSDC	Size (Mb)	GC%	Protein	Rrna	tRNA	Other RNA	Gene	Pseudogene
Chr	1	NC_040279.1	CM014066.1	42.13	32.8	3,567	-	79	489	2,849	120
Chr	2	NC_040280.1	CM014067.1	33.91	33.3	2,987	10	73	390	2,299	40
Chr	3	NC_040281.1	CM014068.1	65.29	32.0	6,200	-	146	777	4,804	112
Chr	4	NC_040282.1	CM014069.1	42.73	32.9	2,869	3	77	589	2,424	121
Chr	5	NC_040283.1	CM014070.1	48.75	32.7	4,192	-	78	754	3,285	100
Chr	6	NC_040284.1	CM014071.1	34.46	32.8	3,282	-	81	565	2,694	107
Chr	7	NC_040285.1	CM014072.1	40.88	32.0	4,243	-	105	490	3,182	72
Chr	8	NC_040286.1	CM014073.1	38.36	32.9	3,187	-	79	357	2,563	83
Chr	9	NC_040287.1	CM014074.1	43.93	32.7	4,019	32	84	516	3,072	68
Chr	10	NC_040288.1	CM014075.1	41.33	33.2	2,888	282	92	542	2,696	113
Chr	11	NC_040289.1	CM014076.1	41.68	33.2	3,079	123	109	538	2,694	130
	Pltd	NC_018051.1	-	0.15	35.2	84	8	38	-	131	1
Un	-	.	-	45.46	36.6	576	828	94	236	1,690	147

Table 2. SNF related protein families in cowpea

Name	Accession	Start	Stop	Std	Gene ID	Locus	Protein product	Length
VuSnRK2.1	NC_040279.1	18482681	18484506	+	114192996	LOC114192996	XP_027938484.1	471
VuSnRK2.2	NC_040279.1	27455241	27459193	-	114181284	LOC114181284	XP_027923498.1	832
VuSnRK2.3	NC_040289.1	37980286	37985690	+	114168947	LOC114168947	XP_027909735.1	1036
VuSnRK2.4	NC_040281.1	50643408	50646050	+	114178934	LOC114178934	XP_027920886.1	511
VuSnRK2.5	NC_040281.1	61287418	61298513	+	114179887	LOC114179887	XP_027922179.1	703
VuSnRK2.6	NC_040282.1	11541389	11543515	-	114181894	LOC114181894	XP_027924343.1	547
VuSnRK2.7	NC_040286.1	13343970	13349236	-	114194176	LOC114194176	XP_027940068.1	777
VuSnRK2.8	NC_040287.1	32398570	32403138	+	114164083	LOC114164083	XP_027904391.1	537
VuSnRK2.9	NC_040287.1	33057516	33064380	-	114162893	LOC114162893	XP_027902685.1	785
VuSnRK2.10	NC_040287.1	42775720	42778372	-	114164364	LOC114164364	XP_027904808.1	499
VuSnRK2.11	NC_040287.1	17565838	17567763	+	114162141	LOC114162141	XP_027901727.1	528
VuSnRK2.12	NC_040287.1	42901634	42905741	+	114163745	LOC114163745	XP_027903839.1	510

to be located on chromosome 7, whereas 114178934 and 114179887 had predicted locations on chromosomes 3 and 114181894, 114168947 and 114194176 are located chromosome 4, 8 and 11, respectively. 114162141,114162893, 114163745 and 114164364 are located onchromosome 9 (Fig.1).

Identification of SnRK2 proteins in the *Arabidopsis thaliana* database (TAIR) using gene name, GenBank accession and description about SnRK2 protein matched with 17 proteins belonging to SnRK2 protein family.

Sequence homologs and domain architecture of cowpea SnRK2 genes

By using the HMMER program, the domain architectures of cowpea SnRK2s were studied. Search predicted the protein kinase domain belonging to PF00069 super family. SMART detects domains from sequences with relatively high selectivity and specificity. The *Vigna unguiculata* protein SnRK2 is predicted by SMART to contain the

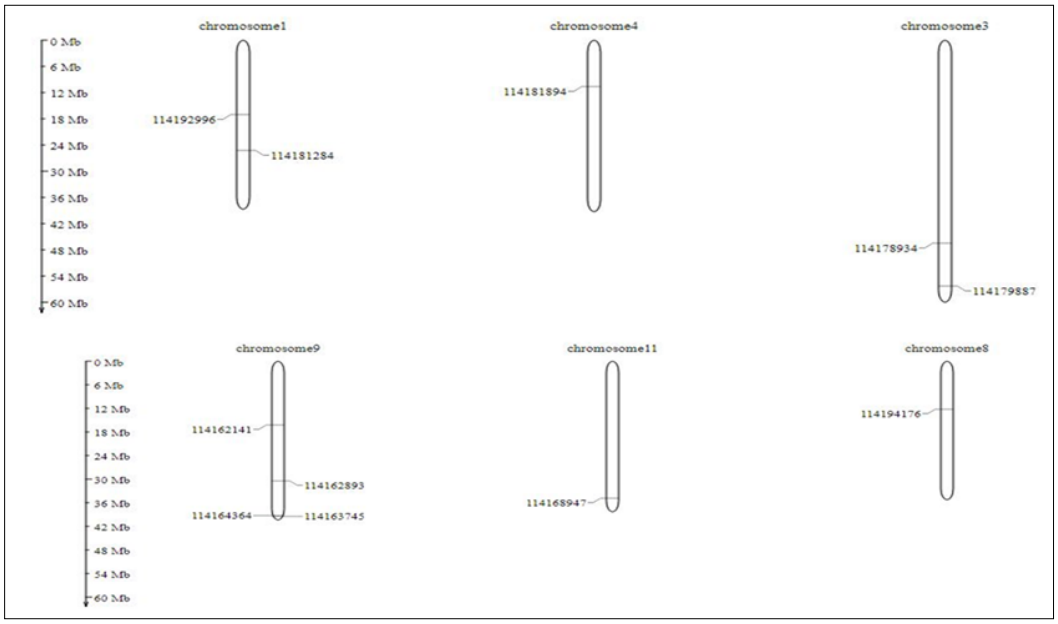

Fig. 1. Chromosomal mapping of cowpea *SnRK2* genes.

Table 3. Domain information of VuSnRK proteins analyzed using SMART tool

SnRK2 proteins	Position	E-value	Sequence
VuSnRK2.1	84 to 232	1.00e-20	KKPRQNEKQLPEKASAILPQSALYTQLLDVEARVDAALTRKKVDIQEAMRNPPCIQKTLRIFV FNTFANQSGDSSAPTWTLKIVGRILEDGEEAEQPGVLAHRMPPLYPKFSAFFKRVTISLDKRL YPDNNVITWENSRSSATHEGFE
VuSnRK2.2	361 to 409	1.995e-13	NGGKWTDQETLLLLEALELYKENWNEIAEHVGTKTKAQCISYFVQMPIE
VuSnRK2.3	120 to 273	3.00e-22	PPRKKRSFPEKLIPDKVAKLVPESAIYAKLLELETHIDSVLVRKKIDVQENLRNPRCVRRTLRIY VYNTFSKQVKVEPGKIDVEELSWVLRITGRVLEDGKDSVADGVLSKENRRFSAFFKKITVYLDQ GFYPDNHVVVWDSARSTAQRDGFE
VuSnRK2.4	152 to 308	1.00e-21	SRRKKQKLPEKQLQDKVAAILPESALYTQLLEFESRVDAALARKKADIQEALKNPPCIQKTLRI YVFNTFANQIRTIPKKPTAEPPTWTLKIVGRILEDGVDPDQPGVVQKSTPLYPKFSAFFKRVTI SLDQRLYPDNHIIMWENARSPAPHEGFE
VuSnRK2.5	152 to 308	1.00e-21	SRRKKQKLPEKQLQDKVAAILPESALYTQLLEFESRVDAALARKKADIQEALKNPPCIQKTLRI YVFNTFANQIRTIPKKPTAEPPTWTLKIVGRILEDGVDPDQPGVVQKSTPLYPKFSAFFKRVTI SLDQRLYPDNHIIMWENARSPAPHEGFE
VuSnRK2.6	324 to 368	6.00e-19	LSENYCHYCSRSLPVVYYQSQKEVDILLCTDCFHDGRFVAGHSS
VuSnRK2.7	86 to 220	1.00e-13	LPESALYTQLLDFEAQVDTALARRKFDIQEARLPPHVQKTLRVYVFNTFSNHAKMDSENKKA NESSWSLRITGRILEDGMDSMSGISQRSSPSYPKFSAFFKKITIHLDQSIYPDNHVIVWDSARS PAQQDGFE
VuSnRK2.8	156 to 290	2.00e-13	LPESALYTQLLDFEAQVDTALARRKFDIQEARLPPHVQKTLRVYVFNTFSNHAKMDSENKKA NESSWSLRITGRILEDGMDSMSGISQRSSPSYPKFSAFFKKITIHLDQSIYPDNHVIVWDSARS PAQQDGFE
VuSnRK2.9	192 to 229	2.00e-07	NCGLCGGKYSSGHYRCTQDNFIICANCFKSGNYGEKR
VuSnRK2.10	334 to 378	1.00e-21	LSDNHCIYCSRPLPVVYYQSQKEVDILLCTDCFHDGRFVIGHSS
VuSnRK2.11	238 to 286	4.152946138265 37e-11	TKTDWSEKETTNLLEALTHYGDDWKRVSQHVAGRTEKECVAHFLKLPFA
VuSnRK2.12	171 to 219	0.029e-12	SGGKWTDQETLLLHEALELYKENWNEISEHVAAKSKSSITLFQMPIEDA

domain sequence as depicted in Table 3.

***Multiple Sequence Alignments*:** Multiple Sequence Alignments were performed using Clustal Omega to validate the conservation of VuSnRK2 protein sequences and presented (Fig. 2).

***Phylogenetic Analysis*:** The evolutionary relationship of cowpea SnRK2 proteins was predicted by building a phylogenetic tree. cowpea SnRK2 and AtSnRK2 protein sequences were aligned by Mega X and tree was built by the neighbor joining method with 1000 bootstrap replications (Fig. 3). The phylogenetic relationship was done among the 12*VuSnRK2* and 14 different crops SnRK2 protein were determined by constructing a phylogenetic tree by using complete protein sequences of AtSnRK2 and cowpea SnRK2. Based on similarity with AtSnRK2, the identified cowpea SnRK2 were placed into four different groups (I, II, III and IV).

***Physico-Chemical Analysis*:** The theoretical isoelectric point and molecular weight of VuSnRK2 proteins were determined by ExPASy pI/Mw tool. The isoelectric point of proteins ranged from 4.99 to 9.59 and the molecular mass ranged from 53259.04 to 112344.7 Da.

Discussion

Plants cope with changing climatic conditions and evolve self defense mechanism against various stresses. These mechanisms trigger expression of key genes that regulate important metabolic responses (10). Among these inducers, the plant hormone ABA regulates genes involved in growth and development as well as stress responsiveness (11-13). *SnRK2*, a plant-specific serine/threonine kinase has been reported to activate genes in response to biotic and abiotic stress signals (14, 15). Although these genes have been reported in several crop species, only a few have been validated.

Comprehensive analysis of such genes in Vigna family is limited thus demands attention to explore the family in cowpea. In this study, 16 *VuSnRK2* genes were identified from the genome database and designated as*VuSnRK2.1-VuSnRK2.12* (Table 2). Chromosome distribution and physico-chemical property analysis revealed that these*VuSnRK2* genes were unevenly distributed. Gene family expansion could be attributed to tandem duplication, segmental duplication and whole genome duplication which drives genetic variation and

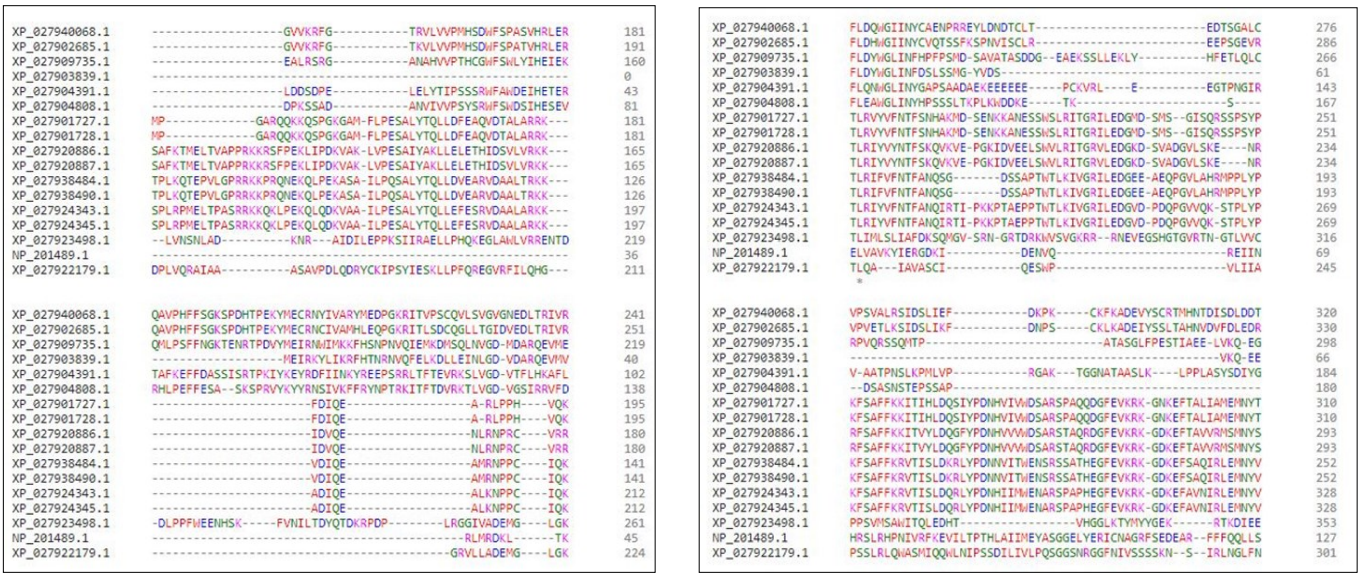

Fig. 2. Multiple Sequence Alignment results of *VuSnRK2* proteins.

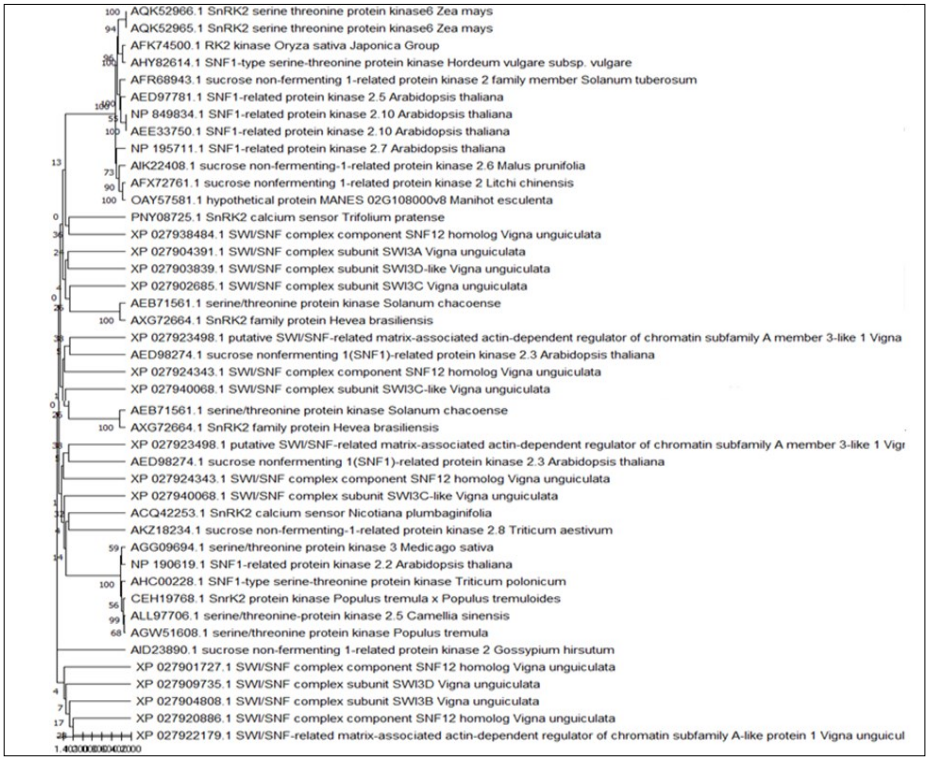

Fig. 3.Evolutionary relationship of cowpea SnRK2 proteins- Phylogenetic tree constructed using MEGA X tool.

adaptation under natural selection (16, 17).

The evolutionary relationship between *VrSnRK2* and *AtSnRK2* was examined through a comprehensive phylogenetic analysis performed by constructing a phylogenetic tree. The result showed that *VrSnRK2* genes were clustered into four groups (I, II, III and IV) (18, 19).

The Group I comprised of *Zea mays, Oryza sativa* (Japonica group), *Hordeum vulgare, Solanum tuberosum, Arabidopsis thaliana, Malus prunifolia, Litchi chinensis* and *Manihot esculenta.* Group II included *Trifolium pratense, Solanum chacoense, Heaveabrasilensis, Vigna unguiculata* (VuSnRK 2.1, 2.8, 2.9 and 2.12). Group III consisted of *Arabidopsis thaliana* 2.3, VuSnRK2.2,2.6 and 2.7, *Nicotiana plumbaginifolia, Triticum aestivum, Medicago sativa, Populus tremuloides, Camellia sinensis, Populus tremula, Gossypium hirsutum* whereas Group IV included *Vigna unguiculata* (VuSnRK 2.3, 2.4, 2.5, 2.10 and 2.11).

These groupings align with previously reported classifications as in Arabidopsis (20), wheat (21), cotton (19), sugarcane (*Saccharum officinarum* L.) and maize (22), where*SnRK2* genes have been categorized. These results suggest that *VuSnRK2* might have been evolved from a common ancestor and has been later diverged after the segregation of monocots and dicots.

Furthermore, gene descriptions obtained from the TAIR database search has shown the possible role of these genes in abiotic stress signaling. These findings corroborates with previous reports and adds value of information that SnRK2s are indeed involved in signaling pathways related to drought-stress (23, 24). Future research of these identified proteins could demonstrate the possible role of VuSnRK2 proteins in the stress responses.

Conclusion

In the present study, twelve*SnRK2* genes in *Vigna unguiculata* were identified and *in silico* analysis has determined the gene structure, transcript length, chromosomal location and evolutionary relationships of this *SnRK2* gene family in *Vigna unguiculata* with other crop species with similar functions. These findings shed light on the possible role of *SnRK2* genes in *Vigna unguiculata* and provide a foundation for further functional validation studies.

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Authors' contributions

The manuscript was developed through a collaborative effort among the authors. RS and RSV conceptualized the research, wrote the original draft. RS involved in overall supervision of the work. KS involved in use of methodology, data curation and formal analysis using softwares. NS, RS, RT and AT involved in review, editing and proof reading. All authors read and approved the final version of the manuscript, ensured its readiness for submission.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interests to declare.

Ethical issues: None

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