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## **Cladistic Analysis and Comparative Account of Different Invasive Weeds and their Dominance Using Various Bioinformatics Tools**

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### ABSTRACT

Cassia uniflora Mill. non Spreng. and Synedrella nodiflora (L.) Gaertn. are invasive alien weeds on Deccan plateau. Both the weeds are spreading on agricultural and fallow lands at an alarming rate replacing many native and exotic species. Along with the detail studies of their morpho-physiological, metabolomic and chemical attributes, an attempt was made to explore their ecological survival and dominance, which is responsible for development of huge monothickets. Their invasion success probably is due to containment of similar ecological behaviour and evolutionary relatedness to potential plant invaders. In the present study we have extensively employed different tools of bioinformatics such as BLAST, FASTA, servers like SWISSMODEL, CLUSTAL OMEGA and software like MEGA-X, and carried out phylo-genomics and evolutionary cladistic analyses for protein structures of important enzymes such as Rubisco and Maturase -K. The selected weeds were compared using molecular data from gene sequences with each other and other co-dominant native and exotic species. The results revealed that all the species under focus shared larger part (80%) of MSAs (Multiple Sequence Alignments). The data indicated that Cassia uniflora and Synedrella nodiflora exhibited parallel resistance to the environmental stresses, similar evolutionary patterns and highlighted their dominance amongst different species of Cassia and respective genera of Asteraceae. Based on further phylogenetic studies it can be proposed that C. auriculata and Lactuca indica would be the future successful invaders on Deccan plateau. The present investigation based on the results of MSA, deep view analyses and phylogenomics of weeds may predict the changes in weed flora of Deccan pleateau due to environmental changes.

KEY WORDS: INVASIVE WEEDS, MATURASE-K, MEGA-X, PHYLOGENY, RUBISCO.

### ARTICLE INFORMATION

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## **INTRODUCTION**

The alien species highly out-compete the native species or escape from adverse environmental conditions and dominate the community (MacDougall and Turkington 2005).Their diversity is controlled by population, ecosystem dynamics, disturbances, nutrient supply and climatic factors. The biotic restrictions also force them to skip from their previous habitat and start surviving in new habitats, helping in the process of invasion (Mack et al. 2000). Many a times these phyto-invasives become very aggressive due to production of some defensive chemicals (Carpenter and Cappuccino 2005). These invasions pose many ecological, economic and social problems. Because of this the studies on plant invasions and its mechanism and consequences of them on global biodiversity and ecosystem functioning are of urgent need. This is because slowly and gradually these invasives become aggressive and encroach cultivable lands and pose a great problem (Chauhan et al. 2017).

*Cassia uniflora* Mill. non Spreng. (family- Caesalpinaceae) is annual, erect herb with yellow flowers and clustered pods. It originated in tropical South America and now distributed worldwide. This invasive weed grows luxuriantly at many places (Almeida, 2003). *Synedrella nodiflora* (L.) Gaertn. (family- Asteraceae) originated in tropical America, is an annual, erect, dichotomously branched herb distributed all over India (Almeida, 2003). Their dominance is attributed to wide adaptability to diverse habitat, different morphophysiological characters and defensive allelo-chemicals (Ghayal et al.2007a,b; 2009; 2013).

Limited research has been done on the allelopathic effect or phyto-toxicity of *Cassia uniflora* to other plants. There is a general temper of agreement now-a-days that invasive plants displace the local biodiversity through their harmful effects including allelopathy (Cronk and Fuller, 1995). Allelopathic effects may due to the presence of allelochemicals in Cassia and Synedrella, like different types of phenolic compounds, alkaloids, triterpenoides, essential oils and flavonoids, biocides, juvenile hormones, growth hormones. They may be interacting with various physiological processes (Chatteriee et. al. 2012). From current literature review, it revealed that little research has been done on distribution, evolutionary studies and impact of Cassia uniflora and Synedrella nodiflora on cooccuring species by using various tools of bioinformatics. The work done till now on the metabolic compounds and various allelochemicals has been restricted only to the wet lab methods and very little is known about the gene level expression of all such compounds. Some advanced researches show the gene expression analysis on different weeds that indicate several compounds responsible for the invasion of weeds into new environments (Chen, 2013).

For bioinformatics study, several soft-wares and tools were used to analyse the data present on both the weeds. Due to lack of research on the weed plants, it was difficult to retrieve the molecular data. Hence the common enzymes in Cassia uniflora Mill. non Spreng, and Synedrella nodiflora (L) Gaertn, were selected for further analysis. The enzymes or proteins that were studied in both the invasive weeds are - Maturase K [EC 2.7.10.2] and Ribulose-1,5-bisphosphate carboxylase / oxygenase(Rubisco/ rbcL)[EC 4.1.1.39]. Maturase K is a plant plastidial gene. The protein it encodes is an intron Maturase, a protein that splices introns. Mat-K is proposed as the only chloroplast-encoded group II intron Maturase, thus implicating Mat-K in chloroplast posttranscriptional processing. For a protein-coding gene, mat-K has an unusual evolutionary significance, including relatively high substitution rates at both the nucleotide and amino acids levels, (Barthet et. al.2015).

Table	Table 1. Phylogenetic trees of invasive species Cassia and Synedrella					
No.	Type of Phylogenetic tree	Enzyme	MSA %			
1.	Tree and herb species of <i>Cassia/ Senna</i>	Maturase-K	90%			
2.	Tree and herb species	Rubisco	Negligible - the authenticity of this			
	of Cassia/ Senna		clad was very low and hence was			
			not considered for comparison			
3.	Weed species of Cassia/ Senna	Maturase-K	95%			
4.	Weed species of Cassia/ Senna	Rubisco	90%			
5.	Synedrella nodiflora and	Maturase-K	60%			
	other weed species					
6.	Synedrella nodiflora and	Rubisco	90%			
	other weed species					
7.	Cassia/ Senna, Synedrella and	Maturase-K	80%			
	other related genera and species					
8.	Cassia/ Senna, Synedrella and	Rubisco	85-90%			
	other related genera and species					

The other enzyme that has been studied in both plants was ribulose-1,5-bisphosphate carboxylase/ oxygenase (Rubisco) is the major enzyme assimilating CO2 into the biosphere. At the same time Rubisco is an extremely inefficient catalyst and its carboxylase activity is compromised by an opposing oxygenase activity involving atmospheric O2. These enzymes were considered for checking the probable similarity in the protein sequences of these two weeds. The nucleotide research on these enzymes is done intensively since both the enzymes play crucial role in plant metabolism. The focus of the study was to acquire the common factor based on genomic data in both the weeds that is responsible for their dominance and to understand and interpret their ecological and evolutionary significance.

The present work was carried out for correlating different genes or proteins in Cassia uniflora Mill. non Spreng and Synedrella nodiflora (L) Gaertn. responsible for their invasiveness by using different bioinformatics tools. Scanty information is available on the molecular level work, gene identification and sequencing of the invasive weeds as compared to the crop plants. Therefore present attempt was made to fulfil this gap in above mentioned weeds. It has also helped to get the idea about the ecological corridor developed by current dominant invasive weeds. Not only that but it has also helped to predict the future changes in weed flora and their ecological status.

### MATERIAL AND METHODS

A) By performing Multiple Sequence Alignment (MSA): The Multiple Sequence Alignment of the 2 or more sequences was done to check whether the sequences align exactly similar to each other. Here, sequence homology is applied to assess if the sequences are sharing evolutionary origins. B) By using 'Deep-view software': This software was used for direct analysis of the similar or distant proteins. The proteins were modelled from the server 'SWISSMODEL' in PDB format to get the 3D structure. And then these proteins were analysed in the software. C) Preparation of phylogenetic tree: It was carried out to check the homology between the selected protein sequences. Cladistics analysis was performed by using software MEGA-X with the help of maximum likelihood method. Website used - www.ncbi.nlm.nih. gov

### **RESULTS AND DISCUSSION**

For tracking down the upshots on invasive species *Cassia* uniflora/ Senna uniflora and Synedrella nodiflora the efforts were carried out in the following manner –A) By performing Multiple Sequence Alignment (MSA) – For Maturase-K and Rubisco for *Cassia uniflora/Senna* uniflora and Synedrella nodiflora. B) By using 'Deepview software'- For protein structure of Maturase-K and Rubisco of *Cassia uniflora/Senna uniflora* and Synedrella nodiflora/Senna uniflora and Rubisco for *Cassia uniflora/Senna uniflora* and Rubisco for *Cassia uniflora*.

Table 2: Showing details of two weeds used for MSA of Maturase-K enzyme						
Name of the Plant	Accession Number	Number of Base Pairs (Amino acids)	Included or Excluded	MSA percentage of Sequence Similarity		
Cassia uniflora	ARR68700.1	280	Included	All these species		
Synedrella nodiflora	AAR02837.1	508	Included	show about 70% sequence similarity		

Figure 2: Rubisco	Showing Multiple Sequence Alignment	for	Figure 1: Maturase	Showing Multiple Sequence Alignment	for
Rubisco			maturasc	-K CHZyme	
AQY09936.1 ADD48483.1 AYF60003.1 AFU54416.1	HERGYETERABYOFKADYKOVELTY YT FOVETEKT DI LAAFEV TEOROV FERADAAVAAE 	60 53 55 51	AAR02837.1 ARR68700.1	MEKFQSYLGLDRSHYFLYPLIFQEYIYVLAHDHGLNGSILLENAGYDNKSSLLIVKRLII	60 0
AKG25301.1 AFP23718.1 AZC11295.1 AAR11741.1		45 50 41 43	AAR02837.1 ARR68700.1	RMYQQNHLILSVNDSKQTPFLGHNKNFYSQVMSEVSSTIMEIPLSLRLISSLERKGVVKS	120 0
AQY09936.1 ADD48483.1 AYF60003.1	SSTOTWTTWTDGLTSLDRYKGRCYHIEPVTGEENQYIAYVAYPLDLFEEGSYTNWTSI SSTOTWTTWTDGLTSLDRYKGRCYHIEVYTGEENQYIAYVAYPLDFEEGSYTNWTSI SSTOTWTTWTDGLTSLDRYKGRCYHIEVYTGEENQYIAYVAYPLDFEEGSYTNWTSI	120 113 115	AAR02837.1 ARR68700.1	DNLRSIHSIFSFLEDNFSHLMYULDILIPYPAHLEILVQLEVWIKDASSLHILLRFIYE 	180 40
AF054416.1 AKG25301.1 AFF23718.1 AZC11295.1 AAR11741.1	BBTOTHTYWFDLITBLDHYKGRCYHLEVVACEBQCTAVVAVPLALFERGBYTHHFFBI STOTHTYWFDLITBLDHYKGRCYMCEVVACEBQCTAVVAVPLALFERGBYTHHFFBI STOTHTYWFDLITBLDHYKGRCYMEVVACEBQCTAVVAVPLALFERGBYTHHFFBI STOTHTYWFDLITBLDHYKGRCYMEVVACENQUFAU	111 105 110 101 103	AAR02837.1 ARR68700.1	CHNMDLITSNSKKVSSSTSKINHLFCFLYTSVVCEVESVFFFLNOSVHLESTSGAL YPNNHLITPRRISTSSSNPELFFLYNVVCEVESIFFLENSSVLLTSFOVL	240 98
AQY09936.1 ADD48483.1	VGNVF9FKAL#ALRLEDLRIFTSYTKTFQ9FPH9IQVERDKLNKYGRFLLGCTIKFKLGL VGNVF9FKAL#ALRLEDLRIFTSYTKTFQ9FPH9IQVERDKLNKYGRFLLGCTIKFKLGL	180 173	AAR02837.1 ARR68700.1	IERIYIYGKIEHLARVFARSFQANIWLIKDSFNHYVRYGKSILASKGFFLLMNKNKYYF FRIYFYAKIEHFVRVFNDFPSILMFKDDFTHYVRYGKSILASKNYFLMNKNKYYL	300 158
AF054416.1 AKG25301.1 AFF23718.1 AEC11295.1	VONVPOIPALIPALIRLEDLE I PENYSKTPGOPHIOLOVIRODELINKYOR PELOCT I PEKAD VONVPOIPALIPALIRLEDLE I PENYSKTPGOPHIOLOVIRODELINKYOR PELOCT I KPKAD VONVPOIPALIPALIRLEDLE I PENYSKTPGOPHIOLOVIRODELINKYOR PELOCT I KPKAD VONVPOIPALIPALIRLEDLE I PENYSKTPGOIPHIOLOVIRODELINKYOR PELOCT I KPKAD	171 165 170 161	AAR02837.1 ARR68700.1	VNLWKSYFYLWSHPGGIYININGLSNHSLDFLGYRSSVRLKPSNVRGQMLENFFLIDNAI Inlwgghfyuwsgpekihinglsenffylgyfsnyrlhpsvnsgallensflibnym	360 216
AAR11741.1	VONVFOFKALRALRLEDLRIFTAYIKTFDOPFHOLQVERDKLNKYGRFLLGGTIKFKLGL	163	AAR02837.1 ARR68700.1	KKFDSIVPIMPLVGSLAKSKFCNALGHPIGKAIWADLSDSDIIERFGRIYRNLSHYHSGS KRLDPIIPIIPLIRSLAKAKFCNILGHPISKPVWADSSDLDIIDRFLRRCRNLSHYYNGS	420 276
AQY09936.1 ADD48483.1 AYF60003.1 AFU54416.1 AKG25301.1 AFP23718.1	NARY GRAVYECLBGGLPFTKDDERVINGPTRIMERDELFCARALFFKAARTEGE IKGIYL BARNYGRAVYECLBGGLPFTKDERVINGPTRIMERDERFLACARTHFKAARTEGE IKGIYL BARNYGRAVYECLBGGLPFTKDERVINGPTRIMERDERFLACARALFFKAARTEGE IKGIYL BARNYGRAVYECLBGGLPFTKDERVINGPTRIMERDERFLACARALFFKAARTEGE IKGIYL BARNYGRAVYECLBGGLPFTKDERVINGPTRIMERDERFLACARATYKSAARTEGE IKGIYL BARNYGRAVYECLBGGLPFTKDERVINGPTRIMERDERFLACARATYKSAARTEGE IKGIYL	240 233 235 202 225 230	AAR02837.1 ARR68700.1	SKKKSLYRVKYILRLSCARTLARKHKSTVRAFLKRFGSQLLEEFFTEEEQVFSLTFPRVS STKK	480 280
AEC11295.1 AAR11741.1	SAKNYGRAYYECLEGGLDFTKDDENVNSQFFHEWRDRFLFCAEAIFKEGAETGEIKGHYL SAKNYGRACYECLRGGLDFTKDDENVNSQFFHEWRDRFLFCAEAIYKAQAETGEIKGHYL	221 223	AAR02837.1 ARR68700.1	SISRRLSRRRIWYLDIVCINDLANHE 506 280	

*Synedrella nodiflora*. C) Preparation of phylogenetic tree / Cladistic analyses

**A) Results of Multiple Sequence Alignment (MSA):** Multiple sequence alignment showed that the sequence of enzyme 'Maturase-K' is exactly similar in plants *Cassia uniflora* and *Synedrella nodiflora*. This result revealed the sequences with almost homologous regions showing '\*'symbol as exactly matching sequences (Fig.1, Table 2). Similar MSA was carried out on Rubisco for the same two plants *Cassia uniflora* and *Synedrella nodiflora* and equivalent similarity was observed. The figure and table for this are not included to avoid repetition of the sets.

When similar MSA (Multiple sequence alignment/s) was carried out for Rubisco enzyme, *Cassia auriculata* had to beexcepted because it has different base pairs than all other plants which was affecting the comparison among the selected plants. The comparison of remaining

Figure 3: Circled portion indicates common sequence coding similar structure of enzyme MATURSE-K in *Cassia uniflora* and *Synedrella nodiflora* 



plants showed almost similar sequences in all the species related to the weed species under consideration i.e. *Cassia uniflora* and *Synedrella* (Fig. 2, Table 3). Similar comparison is done for Maturase-K enzyme and it shows similar results except the inclusion of *Cassia auriculata*. Hence it can be predicted that these invasive species could have evolved in similar way for the enzymes like 'Maturase-K' and Rubisco.

**Results of using 'Deep-View' software:** When the models of protein structures for both the enzymes 'Maturase-K' and 'Rubisco' were run in Deep view software, models exhibited similar sequences of both the enzymes that implied the similar structures and hence all the models tracked in the software were able to get merged. Results of deep view analysis (Fig. 3 & t 4) showed that the enzymes studied had identical structures and the highlighted portion in both the images showed shared structures of the same protein but in two different plants

Figure 4: Circled portion indicates common sequence coding similar structure of enzyme RUBISCO in *Cassia* uniflora and Synedrella nodiflora



Table 3: Showing details of nine plants used for MSA of Rubisco enzyme

Name of the Plant	Accession Number	Number of Base Pairs (Amino acids)	Included or Excluded	MSA percentage of Sequence Similarity
Cassia uniflora	AQY09936.1	249	Included	
Cassia obtusifolia	ADD48483.1	234	Included	
Cassia tora	AYF60003.1	238	Included	All these species
Cassia auriculata	AII33731.1	290	Excluded	together show
Cassia occidentalis	AZC11295.1	416	Included	about 80 %
Cassia sophera	AFU54416.1	202	Included	sequence
Synedrella nodiflora	ARR11741.1	468	Included	similarity
Tridax procumbens	AFP23718.1	461	Included	
Pulicaria dysenterica	AKG25301.1	439	Included	

*Cassia / Senna uniflora* and *Synedrella*. This probable further confirms *simultaneous* evolution of these invasive species and their imperative enzymes.

**Preparation of phylogenetic trees / Cladistic analyses:** The construction of phylogenetic trees was carried out with the interest of searching the evolutionary associations of Cassia/ *Senna uniflora* with the other native, weedy and less dominant species of *Cassia*. In case of *Synedrella* searching was attempted with the same approach but due to very much insubstantial outcomes, the cladograms were developed based on few weedy, local and fairly prevailing genera and species from the same family Asteraceae, as this family is well known to contain globally distributed, highly dominant invasive weed genera other than *Synedrella*.







automatical by applying the photo-ion and fold appetrim to a material particle dataces estimated using a 77 model, and then seeding the topology with upper top likelihood usite. The two is dataces estimated using a 77 model, and then seeding the topology with upper to plikelihood usite. The two is dataces and topology using the topology with upper of both dataces and topology and topology with upper of both dataces and topology an

The Cladistic analysis (Fig. 5, Table 4) performed on different herb and tree species of *Cassia* revealed that *Cassia uniflora* had a distant phylogeny and did not share any recent ancestry with any of the other Cassia species for Maturase-K enzyme.As against that when the phylogenetic comparison of different weed species of *Cassia*/ Senna was carried out for these two enzymes, it was observed that *Cassia uniflora* and *Cassia auriculata* might have progressed in the most parallel way and from very recent common ancestor in due course of evolution

(Figures 6, 7; Tables 5,6). It can also be confirmed by the habitat of both the species of *Cassia*. Both Cassia uniflora and *Cassia* auriculata grow intensively in semiarid conditions.

The similar phylogeny here, in both the enzymes, Maturase-K and Rubisco, suggests that these two plants must have acquired similar properties that help them survive under the unfavourable conditions and this could be the key to their dominance over other native plants. The results showed that the evolution of *Cassia uniflora* and *Cassia auriculata* is relatively similar to each other over other species of *Cassia. Cassia uniflora* is the most dominant species of the genus Cassia presently and *Cassia auriculata* might evolve further as dominant species in subsequent situations of environment, as *Cassia uniflora* is today.

The other species of *Cassia* such as *Cassia* occidentalis and *Cassia* tora have shown distant phylogeny. Both Cassia uniflora and Cassia auriculata are distantly evolved from other species of Cassia and hence show significantly different habitat and possibly also the chemical properties than other members of genus Cassia. The comparison of *Synedrella* in cladogram with the other genera of asteraceae for Maturase-K showed that, number of base pairs varies greatly among genera and hence the MSA percentage has fallen (60%) but the matching base pairs show completely identical sequences for all the plants. Synedrella nodiflora indicated distant phylogeny from Tridax procumbens and Pulicaria dysenterica but is relatively nearer to Lactuca indica (Fig. 8, Table 7). These three genera of Asteraceae show their frequent but less dominant occurrence than Synedrella.For the same members of asteraceae, the building up of phylogenetic tree for Rubisco was performed excluding *Lactuca indica* as its protein sequence was unavailable. Here, it was observed that Tridax procumbens and Pulicaria dysenterica had the closest phylogeny showing Synedrella nodiflora distantly placed (Fig. 9, Table 8).

The comparison of both *Cassia uniflora* and *Synedrella* nodiflora for Maturase-K showed very distant origin. Cassia uniflora showed quite distant phylogeny from other Cassia species (Fig. 10, Table 9) whereas; Synedrella nodiflora shares similar phylogeny with Lactuca indica. In contrast the comparison for Rubisco showed common ancestry for Cassia uniflora and Synedrella nodiflora as they are placed very close to each other (Fig. 11, Table 10). This shows that both the plants might have developed different evolutionary patterns than all the other plants under consideration which resulted in distant phylogeny of both. In this clad, Lactuca indica was not considered for the comparison as its protein sequence for Rubisco was unavailable (Fig. 11, Table 10). The importance of genomic tactics for understanding the weedy and invasive behaviours of plants, their evolution and resistant response to environmental fluctuations is better realised now as a part of weed biology (Stewart et al. 2009).

BIOSCIENCE BIOTECHNOLOGY RESEARCH COMMUNICATIONS

### Ghayal & Deodhar

It further opens a new research route for perception of reckless growth and evolution of phyto-invasives and their functioning under harsh stress conditions. It also shares knowledge about weed management, herbicide resistance mechanism of allelopathy and evolution of invasiveness of such plant species (Thomas and Klaper, 2004). Such phylogenetic studies using various methods help to better understand causes of invasion success, ecosystem disturbance and alterations in biodiversity (Forest et al., 2007; Proches et al., 2008; Winter et al., 2009; Dawson et al., 2009). Some studies have also claimed that phylogenetic and functional attributes of alien species readdress different aspects of ecosystem functioning and variations produced at the level of organisms (Chen, 2013; Ricotta et al. 2009, 2010; Cadotte et al. 2009).

According to some researchers unusual characters and ancestral relations with natives probably are promoting the aliens to become invasive very swiftly in non-native ranges of global vegetation (Clements and Ditommaso, 2011).Bezeng et al. (2013) have claimed that phylogenomic studies of invasive species with reference to their native co-survivors are the most important drivers of ecosystem change, which can alter the vegetational set up of a particular area. Similar studies on Maturase-K and Rubisco of island flora have been carried out by them to understand the causes of invasion on Robben island. South Africa. The results recorded in the figures 1 and 2 and Tables 2 and 3 showed that multiple sequence alignments are shared for Maturase-K and Rubisco of Cassia uniflora and Synedrella. Deep view analysis (Figures 3 and 4) also revealed major portions identical for both the enzyme proteins for C. uniflora and Synedrella. This further indicates that these two enzymes might be the drivers in the invasion success of C. uniflora and *Synedrella*(Bezeng et al., 2013), since these enzymes have prime importance in the plant metabolism.

When evaluation of different species of *Cassia* for Maturase-K was carried out (Fig. 5, Table 4), it exhibited minor likelihood of *C. uniflora* from others. Further, when

Table 4: Showing details of different species of Cassia for Maturase-K         enzyme						
Name of the Plant	Accession Number	Number of Base Pairs (Amino acids)	Included or Excluded	MSA percentage of Sequence Similarity		
Cassia uniflora	ARR68700.1	280	Included			
Cassia roxburghii	AFU54442.1	278	Included	All these species		
Cassia javanica	AFU54432.1	278	Included	show about		
Cassia leptophylla	APZ80402.1	499	Included	90 % sequence		
Cassia javanica var.	AFC38374.1	501	Included	similarity		
indochinensis Cassia fistula	AR084601.1	501	Included			

Table 5: Showing details of four weed species of Cassia used for MSA of Maturase-K enzyme

Name of the Plant	Accession Number	Number of Base Pairs (Amino acids)	Included or Excluded	MSA percentage of Sequence Similarity
Cassia uniflora	ARR68700.1	280	Included	All these species
Cassia	ASU41854.1	276	Included	show about 95
obtusifolia				0/0
Cassia tora	AJM88385.1	248	Included	sequence
Cassia	ARR68699.1	261	Included	similarity
auriculata				

we examined the cladistics patterns of different species of Cassia for both the enzymes (Figures 6, 7 and Tables 5, 6), it was observed that C. auriculata is lineally related to C. uniflora, indicating similar or parallel functional traits which are essential for invasion. Martyniuk et al. (2009) have phyletically compared members of Amaranthaceae in the same way for pollen structures based on these two enzymes. The evaluation of different asteraceae members along with the invasive alien species Synedrella nodiflora suggested its racial link with Lactuca indica for Maturase-K (Fig.8, Table 7). When Synedrella nodiflora was (Fig. 9, Table 8) compared with same herb species from asteraceae for Rubisco revealed distant phylogeny. The consideration for phyletic relatedness when was performed for Maturase-K (Fig. 10, Table 9), showed totally separate placement of C. uniflora but indicating probable common ancestry. This clad suggested coevolution of Synedrella nodiflora and Lactuca indica. The same set of plants was used to prepare clad for Rubisco revealed (Fig. 11, Table 10) the diversification from the common inherited line. The studies on evolutionary population genomics in the Asteraceae family have been carried out by Stevens (2007), Barker et al. (2008), Broz et al. (2007) and Mandel et al. (2017).

Figure 9: Showing Phylogenetic tree of herb species of members of Asteraceae for Rubisco enzyme

AFP23718.1 rbulose-15-bisphosphate carboxylase/oxygenase large subunit partial (plastid) Tridax procumbens

AKG25301.1 ribulose-15-bisphosphate carboxylase/oxygenase large subunit partial (plastid) Pulicaria dysenterica

MR11741.1 ribulose-15-bisphosphate carboxylase/oxygenase large subunit partial (chloroplast) Synedrella nodiflora

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#### Evolutionary analysis by Maximum Likelihood method

The relationship is a set of processing of the set of t

Figure 10: Showing Phylogenetic tree of all 9 species for Maturase-K enzyme

6. Cladistics analysis for weed related species of both Cassia uniflora and Synedrella

nodiflora for Maturase-K enzyme -

ARR02837.1 maturase K (chloroplast) Synedrella nodifiora ACV1114.1 maturase K (chloroplast) Lactuca indica AZC11030.1 maturase K partial (chloroplast) Senna coticentalis ARR08700.1 maturase K partial (chloroplast) Senna coticentalis AFUE4430.1 maturase K partial (chloroplast) Senna software ARR08700.1 maturase K partial (chloroplast) Senna software ARR0800.1 maturase K partial (chloroplast) Senna suriculati AIMBB385.1 maturase K partial (chloroplast) Senna tora

Evolutionary analysis by Maximum Likelihood method
The existence of the second of the

# Figure 7: Showing phylogenetic tree of weedspecies for Rubisco enzyme

CAQY09936.1 ribulose-15-bisphosphate carboxylase/oxygenase large subunit partial (chloroplast) Senna uniflora

- All33731.1 ribulose-15-bisphosphate carboxylase/oxygenase large subunit partial (chloroplast) Senna auriculata

ADD48483.1 ribulose-15-bisphosphate carboxylase/oxygenase large subunit partial (chloroplast) Senna obtusifolia

AYF60003.1 ribulose-15-bisphosphate carboxylase large subunit partial (chloroplast) Senna tora

H 10

### Evolutionary analysis by Maximum Likelihood method

The excitationsy haitsy was refered by using the Maximum Likelation method and JTT matrix-search more (1). The two with the industrial planitodes (2011-1) is proven, that there) for the twent obtained submatch by applying Neglitors and Bolt apportions is a main of particle database standard area (1). There is a bolt of 200 positions in the fault database (1) and the selection of the participant of the selection of the selection

# Figure 8: Showing Phylogenetic tree of herb species of members of Asteraceae for Maturase-K enzyme



interviewel provide an elementary super elementary burrely elementary of a set of the se

# Figure 11: Showing Phylogenetic tree of all 9 species for Rubisco enzyme

7. Cladistics analysis for weed related species of both Cassia uniflora and Synedrella

nodiflora for Rubisco enzyme -



Table 6: Showing details of weedspecies for Rubisco enzyme						
Name of the Plant	Accession Number (Amino acids)	Number of Base Pairs	Included or Excluded	MSA percentage of Sequence Similarity		
Cassia uniflora	AQY09936.1	249	Included	All these		
Cassia obtusifolia	ADD48483.1	234	Included	species show		
Cassia tora	AYF60003.1	238	Included	about 90 %		
Cassia auriculata	AII33731.1	290	Excluded	sequence similarity		

Table 7: Showing details of asteraceae members herb species for Maturase-K enzyme

Name of the Plant	Accession Number	Number of Base Pairs (Amino acids)	Included or Excluded	MSA percentage of Sequence Similarity
Synedrella nodiflora	AAR02837.1	506	Included	All these species
Tridax procumbens	AZC11634.1	254	Included	show about
Lactuca indica	ACY71114.1	506	Included	60 %
Pulicaria dysenterica	AFC83880.1	324	Included	sequence similarity

Table 8: Showing details of herb species of members of Asteraceae for Rubisco enzyme

Name of the Plant	Accession Number	Number of Base Pairs (Amino acids)	Included or Excluded	MSA percentage of Sequence Similarity
Synedrella nodiflora	AAR11741.1	468	Included	All these species
Tridax procumbens	AFP23718.1	461	Included	show about 90
Lactuca indica	-	-	Excluded	% sequence
Pulicaria dysenterica	AKG25301.1	439	Included	similarity

Thus the present study has facilitated to establish the correlations of the invasive species *Cassia uniflora* and *Synedrella nodiflora* with the other innate and aggressive species either of the same genus or family. The phylogenomic studies using bio-computing tools enabled to understand the protein nature of Maturase-K

and Rubisco of these two weeds mainly and also of other species. There could be generated various clades giving insights into the evolutionary connections of these aliens developing monothickets with each other along with the other plants. Further it will help to know the changing and dominating weed flora in the same area.

Table 9. Showing details of weedspecies for Maturase-K enzyme						
Name of the Plant	Accession Number	Number of Base Pairs (Amino acids)	Included or Excluded	MSA percentage of Sequence Similarity		
Cassia uniflora	ARR68700.1	280	Included			
Cassia obtusifolia	ASU41854.1	276	Included			
Cassia tora	AJM88385.1	248	Included			
Cassia auriculata	ARR68699.1	261	Included	All these species		
Cassia occidentalis	AZC11603.1	269	Included	together show		
Cassia sophera	AFU54436.1	278	Included	about 80 %		
Synedrella nodiflora	AAR02837.1	506	Included	sequence		
Tridax procumbens	AZC11634.1	254	Included	similarity		
Lactuca indica	ACY71114.1	506	Included			
Pulicaria dysenterica	AFC83880.1	324	Included			

Table 10. Showing details of weed species for Rubisco enzyme						
Name of the Plant	Accession Number	Number of Base Pairs (Amino acids)	Included or Excluded	MSA percentage of Sequence Similarity		
Cassia uniflora	AQY09936.1	249	Included			
Cassia obtusifolia	ADD48483.1	234	Included			
Cassia tora	AYF60003.1	238	Included			
Cassia auriculata	AII33731.1	290	Included	All these species		
Cassia occidentalis	AZC11295.1	416	Included	together show		
Cassia sophera	AFU54416.1	202	Included	about 90 %		
Synedrella nodiflora	AAR11741.1	468	Included	sequence		
Tridax procumbens	AFP23718.1	461	Included	similarity		
Lactuca indica	-	-	Excluded			
Pulicaria dysenterica	AKG25301.1	439	Included			

### CONCLUSION

Overall this research work points out to the protein based phylogenetic similarities and distinctiveness of alien taxa with respect to the other genera as significant details deciding their invasion success (Ordonez, 2014). This enhances to the idea of phylogenetic and metabolic patterns of successfully invaded species. Further these studies have focussed light on the future invasive followers of them on Deccan plateau through different probability patterns.

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