

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 plateau due to environmental changes.

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

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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 morpho-physiological 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 (Chatterjee 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 co-occurring 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 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 of <i>Cassia/ Senna</i>	Rubisco	Negligible - the authenticity of this clad was very low and hence was not considered for comparison
3.	Weed species of <i>Cassia/ Senna</i>	Maturase-K	95%
4.	Weed species of <i>Cassia/ Senna</i>	Rubisco	90%
5.	<i>Synedrella nodiflora</i> and other weed species	Maturase-K	60%
6.	<i>Synedrella nodiflora</i> and other weed species	Rubisco	90%
7.	<i>Cassia/ Senna, Synedrella</i> and other related genera and species	Maturase-K	80%
8.	<i>Cassia/ Senna, Synedrella</i> and other related genera and species	Rubisco	85-90%

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

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

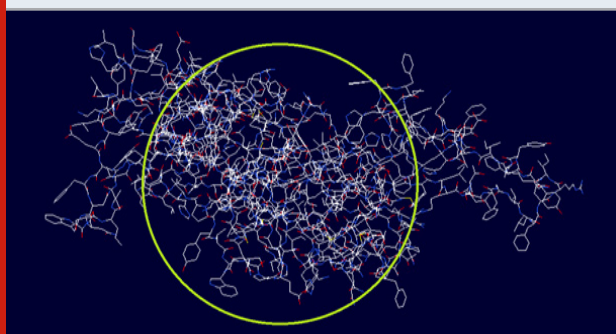


Figure 4: Circled portion indicates common sequence coding similar structure of enzyme RUBISCO in *Cassia uniflora* and *Synedrella nodiflora*

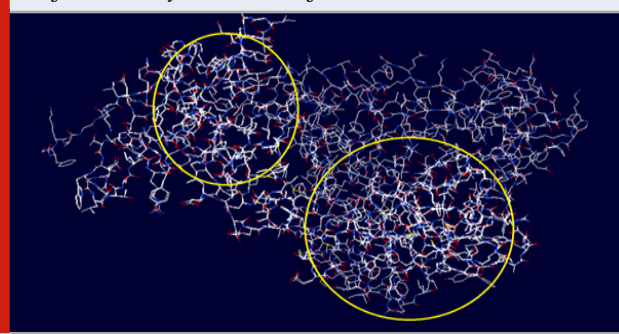


Table 3: Showing details of nine plants used for MSA of Rubisco enzyme

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

Figure 5: Comparison between different species of *Cassia* for maturase-K enzyme

1. Cladistics analysis between different species of *Cassia* for Maturase-K enzyme-

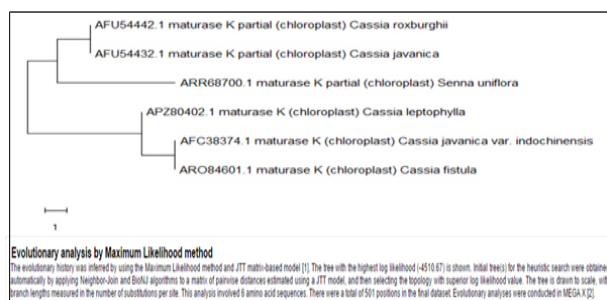
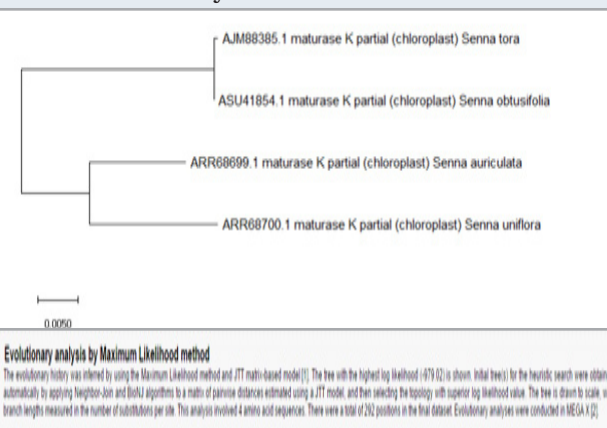


Figure 6: Showing Phylogenetic tree of four weed species for Maturase-K enzyme



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 semi-arid 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).

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

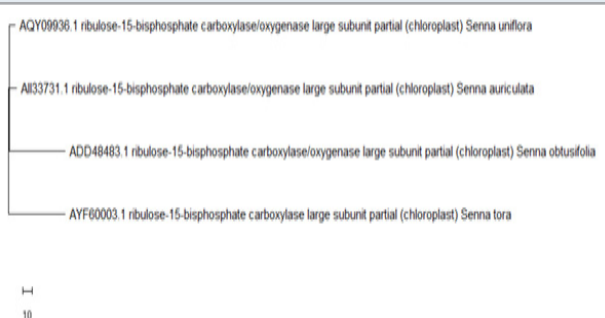
Name of the Plant	Accession Number	Number of Base Pairs (Amino acids)	Included or Excluded	MSA percentage of Sequence Similarity
<i>Cassia uniflora</i>	ARR68700.1	280	Included	All these species show about 90 % sequence similarity
<i>Cassia roxburghii</i>	AFU54442.1	278	Included	
<i>Cassia javanica</i>	AFU54432.1	278	Included	
<i>Cassia leptophylla</i>	APZ80402.1	499	Included	
<i>Cassia javanica var. indochinensis</i>	AFC38374.1	501	Included	
<i>Cassia fistula</i>	ARO84601.1	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
<i>Cassia uniflora</i>	ARR68700.1	280	Included	All these species
<i>Cassia obtusifolia</i>	ASU41854.1	276	Included	show about 95 % sequence similarity
<i>Cassia tora</i>	AJM88385.1	248	Included	
<i>Cassia auriculata</i>	ARR68699.1	261	Included	

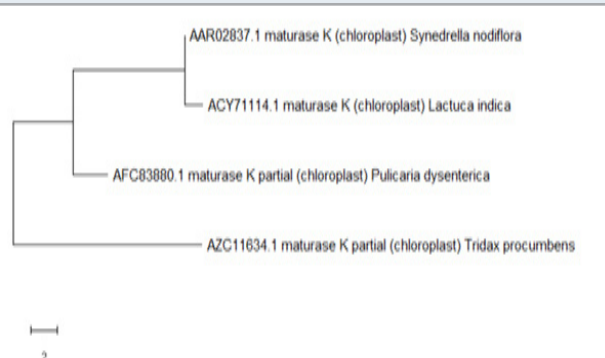
we examined the cladistics patterns of different species of *Cassia* for both the enzymes (Figures 6, 7 and Tables 5, 6), it was observed that *C. auriculata* is lineally related to *C. uniflora*, indicating similar or parallel functional traits which are essential for invasion. Martyniuk et al. (2009) 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 co-evolution 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 7: Showing phylogenetic tree of weedspecies for Rubisco enzyme



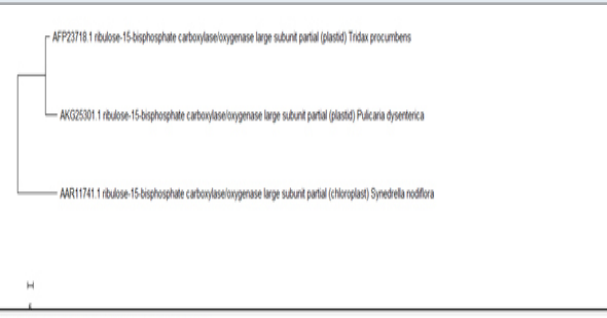
Evolutionary analysis by Maximum Likelihood method
 The evolutionary history was inferred by using the Maximum Likelihood method and JTT matrix-based model [1]. The tree with the highest log likelihood (-2933.43) is shown. Initial trees for the heuristic search were obtained automatically by applying Neighbour-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. This analysis involved 4 amino acid sequences. There were a total of 290 positions in the final dataset. Evolutionary analyses were conducted in MEGA 1 [2].

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



Evolutionary analysis by Maximum Likelihood method
 The evolutionary history was inferred by using the Maximum Likelihood method and JTT matrix-based model [1]. The tree with the highest log likelihood (-4473.62) is shown. Initial trees for the heuristic search were obtained automatically by applying Neighbour-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. This analysis involved 4 amino acid sequences. There were a total of 290 positions in the final dataset. Evolutionary analyses were conducted in MEGA 1 [2].

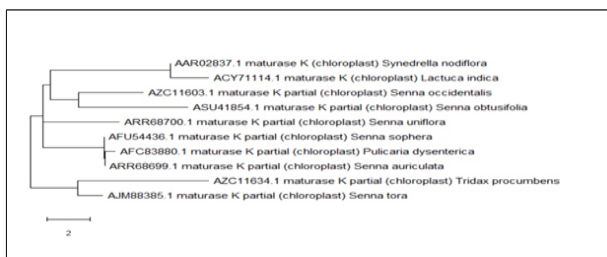
Figure 9: Showing Phylogenetic tree of herb species of members of Asteraceae for Rubisco enzyme



Evolutionary analysis by Maximum Likelihood method
 The evolutionary history was inferred by using the Maximum Likelihood method and JTT matrix-based model [1]. The tree with the highest log likelihood (-3976.67) is shown. Initial trees for the heuristic search were obtained automatically by applying Neighbour-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. This analysis involved 4 amino acid sequences. There were a total of 468 positions in the final dataset. Evolutionary analyses were conducted in MEGA 1 [2].

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

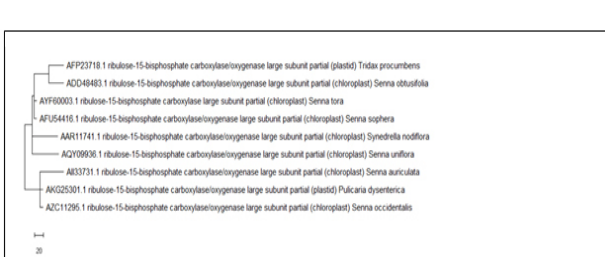
6. Cladistics analysis for weed related species of both *Cassia uniflora* and *Synedrella nodiflora* for Maturase-K enzyme –



Evolutionary analysis by Maximum Likelihood method
 The evolutionary history was inferred by using the Maximum Likelihood method and JTT matrix-based model [1]. The tree with the highest log likelihood (-4760.87) is shown. Initial trees for the heuristic search were obtained automatically by applying Neighbour-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. This analysis involved 10 amino acid sequences. There were a total of 536 positions in the final dataset. Evolutionary analyses were conducted in MEGA 1 [2].

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 –



Evolutionary analysis by Maximum Likelihood method
 The evolutionary history was inferred by using the Maximum Likelihood method and JTT matrix-based model [1]. The tree with the highest log likelihood (-4700.68) is shown. Initial trees for the heuristic search were obtained automatically by applying Neighbour-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. This analysis involved 4 amino acid sequences. There were a total of 468 positions in the final dataset. Evolutionary analyses were conducted in MEGA 1 [2].

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
<i>Cassia uniflora</i>	AQY09936.1	249	Included	All these species show about 90 % sequence similarity
<i>Cassia obtusifolia</i>	ADD48483.1	234	Included	
<i>Cassia tora</i>	AYF60003.1	238	Included	
<i>Cassia auriculata</i>	AII33731.1	290	Excluded	

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
<i>Synedrella nodiflora</i>	AAR02837.1	506	Included	All these species show about 60 % sequence similarity
<i>Tridax procumbens</i>	AZC11634.1	254	Included	
<i>Lactuca indica</i>	ACY71114.1	506	Included	
<i>Pulicaria dysenterica</i>	AFC83880.1	324	Included	

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
<i>Synedrella nodiflora</i>	AAR11741.1	468	Included	All these species show about 90 % sequence similarity
<i>Tridax procumbens</i>	AFP23718.1	461	Included	
<i>Lactuca indica</i>	-	-	Excluded	
<i>Pulicaria dysenterica</i>	AKG25301.1	439	Included	

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
<i>Cassia uniflora</i>	ARR68700.1	280	Included	All these species together show about 80 % sequence similarity
<i>Cassia obtusifolia</i>	ASU41854.1	276	Included	
<i>Cassia tora</i>	AJM88385.1	248	Included	
<i>Cassia auriculata</i>	ARR68699.1	261	Included	
<i>Cassia occidentalis</i>	AZC11603.1	269	Included	
<i>Cassia sophera</i>	AFU54436.1	278	Included	
<i>Synedrella nodiflora</i>	AAR02837.1	506	Included	
<i>Tridax procumbens</i>	AZC11634.1	254	Included	
<i>Lactuca indica</i>	ACY71114.1	506	Included	
<i>Pulicaria dysenterica</i>	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
<i>Cassia uniflora</i>	AQY09936.1	249	Included	All these species together show about 90 % sequence similarity
<i>Cassia obtusifolia</i>	ADD48483.1	234	Included	
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<i>Cassia occidentalis</i>	AZC11295.1	416	Included	
<i>Cassia sophera</i>	AFU54416.1	202	Included	
<i>Synedrella nodiflora</i>	AAR11741.1	468	Included	
<i>Tridax procumbens</i>	AFP23718.1	461	Included	
<i>Lactuca indica</i>	-	-	Excluded	
<i>Pulicaria dysenterica</i>	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 (Ordóñez, 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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