Conclusions
The *in vivo* assay carried out in the present study was able to differentiate between resistant and susceptible cultivars against fusarium wilt caused by *Fusarium oxysporum f. sp. ricini*. It was concluded from the present investigation that $10^5$ spores ml$^{-1}$ of *For* was required to develop symptoms in castor bean cultivars.

The results obtained from biochemical analyses support the contention that these analyses can prove as an efficient tool for identification of resistant cultivars at early stages of plant development and thereby decreasing the time required for breeding of the cultivars.

In the present study, both leaf disc and callus mediated *in vitro* bioassays proved to be reliable to discriminate castor varieties against Fusarium infections. The results of *in vitro* assays showed correlation with *in vivo* assay carried out in field. It is therefore concluded that *in vitro* bioassay could be employed to identify resistant and susceptible varieties of Castor.

Based on the amplification pattern of R gene, a $\geq1000$ bp PCR amplification product was obtained from both resistant and susceptible cultivars of castor bean. The sequence was obtained from resistant plant that was found to be homologous to reported NBS-LRR regions of other Euphorbiaceae members. This result leads to conclusion that that alteration in gene sequence may occur regardless of similar band pattern obtained in susceptible and resistant cultivars or probably the gene is present in both
the resistant and susceptible checks but functional domain is present only in resistant cultivars.

- A new set of primers was obtained from the conserved region of sequence obtained from ≈1 kbps band. This was able to differentiate the resistant cultivars GCH-7, GCH-4 and GCH-4F2 by amplifying a single band of ≈500 bp.

- Use of Microsatellite markers (SSR markers) proved to be an efficient molecular technique to study polymorphism in castor. Band pattern obtained during SSR analysis conclude that High degree of polymorphism occurs within the same family. Cluster analysis and dendrogram construction revealed that SSR based technique was able to discriminate between resistant and susceptible cultivars against fusarium wilt at molecular level. Further analyses of these markers may help in the identification of a marker linked to wilt resistance.

- Fungal pathogen *Fusarium oxysporum* f. sp. *ricini* is found to secrete a protein that probably aids the pathogen in overcoming plant defense mechanism. Protein required for virulence i.e Avr protein was found to be expressed in only in susceptible castor plants infected with Fusarium wilt and amino acid sequence obtained by MS/MS analysis confirmed that protein is secreted by *Fusarium oxysporum* during host invasion.

- In the present study, an avirulence protein of *F. oxysporum* f. sp. *ricini* secreted during invasion of castor plant is reported for the first time. In
addition, a novel method of flask experiment to induce virulence proteins is being reported which can reduce the time consumed during *in vivo* experiments of xylem sap collection.

- A 1864 bp was amplified from *Fusarium oxysporum* f. sp. *ricini* using specific primers for Avr gene, but partially sequencing and low homology prove to be main drawbacks for identification of Avr gene. Sequence obtained from RNA of *Fusarium oxysporum* f. sp. *ricini* using same set of primers may help in elucidating the functional gene sequence required for virulence.