Summary & Conclusion:

Analyzing the properties of J. curcas plant, it is clear that it has great economical importance and should be harvested in a wide range to overcome the bio energy crisis. The agronomical and physiological study shows that considerable genetic variability exists in this species with respect to growth performance, which offers scope for selection and breeding. It is clear that the Kohima (Nagaland) source (*Jc-14*) is good in growth, particularly in the prevailing conditions at Jorhat. Highest seed yield and high seed weight observed in this source has been attributed to higher photosynthetic rate, stomatal conductance and leaf area. Further, clay and sandy texture of the soil having level topography might have provided better aeration, facilitating good exchange of gases aiding in increased photosynthetic activity. This source (*Jc-14*) can be safely used for large-scale reforestation programme in the region for high seed yield and vegetative growth. Germplasm used in afforestation programs in India and other countries generally utilizes only locally available material. Thus, opportunities for using materials with higher yield potential or with more desirable characteristics might have been missed. This work will facilitate selection of promising accessions for multi-location evaluation and will also hasten the process of utilization of germplasm. It further gives a direction for genetic improvement of this species. The composition of triglyceride oils does not seem to be the main factor that can influence the oil value of the analyzed accessions, whereas FFAs or phorbols seem more important factors for selection of best *Jatropha* accessions. Furthermore, integration of biochemical data with physiological and agronomical data shows that the best accessions obtained by one criteria are the same also with the others. Accession *Jc-14* seems best suited for further studies, evaluation and propagation in Jorhat habitat.

From time to time a number of molecular techniques had been efficiently employed for characterization of genetic diversity of *J. curcas* accessions selected from different geographical locations of the world and results gave the notion of low level of genetic variability among the species despite of higher phenotypic variability and significant levels of oil content among them (Singh *et al.,* 2010), but the reason behind the low level of genetic variability among this species is still unclear. In this study, however, it should be inferred that

DNA methylation is not the likely mechanism responsible for large phenotypic variability observed in *J. curcas* accessions. Whatever the answer, molecular basis for such a diversity should also be identified at the level of differential expression of those genes that are involved in growth and development. Bhattcharya *et al.* (2005) stated that the reason for inability of researchers to clarify the anthropogenic and environmental influences on genetic variability among the *Jatropha* species are because of its wild nature of distribution with highly stress tolerable characteristics due to adaptive genomic characters. They also stated that, since this plant is known to exhibit apomixis, a limited stock has been vegetatively and apomictically propagated. One most important point they mentioned that the *J. curcas* L. is not a crop, instead a well surviving undomesticated plant. Whatever the answer, the molecular basis for such a diversity should also be identified at the level of differential expression of those genes that are involved in growth and development (Saikia et al., 2015). Identifying suh genes may present the key to finally unlock the mystery of J. curcas' phenotypic variation with respect to a very conserved genetic and epigenetic background status.

From the observations of this study as well as of other researchers till date, it has become clear that, constructing a genetic map to assist breeding and mining genes of key biological interests will be the two main objectives for *J. curcas* development.

Identifying such genes may represent the key to finally unlock the mystery of *J. curcas* phenotypic variation with respect to a much conserved genetic and epigenetic background status. Both approaches are now well placed to corroborate the development of *J. curcas* as a valuable industrial crop. Therefore, considering its potential for biodiesel production and other industrial uses, a collaborative global *Jatropha* genetic diversity evaluation effort is immediately needed for better use of this valuable species in breeding programs to make it more valuable in coming future Singh *et al.* (2010).