SUMMARY AND CONCLUSION

The present investigation entitled “Identification of the geographical origin of jackfruit (Artocarpus heterophyllus Lam.) through multielemental fingerprinting using ICPMS” was carried out during 2016-17 and 2017-18 in plant nutrition and ionome laboratory of Department of Horticulture, Sikkim University, Gangtok, Sikkim with the objectives of collecting the fruit and soil from different jackfruit growing regions of India and profiling them for ionome concentrations as well as correlating the ionome profile of jackfruit with geographical origin.

Seventy accessions of jackfruit from seven geographic locations famous for the jackfruit production belonging to five states of India were collected for the study. Collected fruits of the accessions were subjected to physico-chemical analysis viz. estimation of fruit weight, fruit length, number of flakes per fruit, flake, pulp and seed weight, total soluble solids (TSS), titratable acidity, total sugars as well as multi elemental analysis. In addition, soil samples were also subjected to mutielemental analysis. The results obtained had revealed that

- Most of the Physico-chemical characters studied were within the range of earlier studies. But variation could be observed based on the location and germplasm difference. Especially, the accessions from Panruti showed positive results in most of these characters analyzed followed by Varkala.

- Accessions of Panruti specially PANJ 48 and PANJ 47 were found to be the best accessions as far as physico-chemical characters are concerned. Hence, they could be propagated and commercially exploited. In addition they could be used as a
breeding stock for yield and quality characteristics to all other location accessions of North East India and Kerala.

- Out 24 elements, only Al, Mn, Mo, Si and Xe had either significant positive or negative correlation between its content in fruit and soil. Hence, it may be concluded that, fruit income has been contributed by not just soil alone, but due to the interaction of germplasm, prevailing micro climate in the location and soil. Hence, multielemental finger printing will be reliable.

- PCA of soil ionome and physico-chemical characters gave out three distinct groups accessions. Soil ionome had yielded three distinct groups, first with Nadia, North 24 Parganas and South Sikkim, a second group with West Tripura, Khowai and Varkala and a third group with Panruti. Physico-chemical characters had yielded Varkala, Nadia and Khowai into one group, West Tripura, North 24 Parganas and South Sikkim into another group and Panruti into another group.

- When the groups of physico-chemical characters were matched with the soil ionome PCA grouping, only Panruti maintained its distinctiveness.

- Principal Component Analysis of fruit ionome had produced four groups viz. Panruti into one, West Tripura and Khowai into second, North 24 Parganas and Nadia into third and Varkala and South Sikkim into fourth group. This had revealed the relativeness of these location based accessions.

- Based on the LDA of physico-chemical characters, only the accessions of Panruti were distinguished even at 95% confidence level from other locations. Hence,
physico-chemical characters shall form the basis for identification of Panruti jackfruits.

- LDA of soil ionome at 95% confidence level had given three groups *viz.* samples collected from Panruti and Varkala in one group, samples of North 24 Parganas and Nadia into another and samples of South Sikkim, West Tripura and Khowai into third group which augured well with the earlier classification of Indian soils.

- LDA of the fruit ionome of jackfruit, it's geographical linkage based separation of the accessions were visible even at 95% confidence level as all the location accessions could be distinguished from each other. Only accessions collected from West Bengal (North 24 Parganas and Nadia) had overlapping characteristics.

Hence, it could be concluded that the geographical location based jackfruits shall be distinguished by the multielemental fingerprinting, which is cheaper, easier than the other omics technologies like genomics, proteomics or transcriptomics as well as reliable.