SUMMARY
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1. Studies were conducted on seventy one genotypes of Citrus, classified under 3l species, to understand the variability among them; the nature and magnitude of variation; and the genetic diversity and genotypic affinity relationships among them. Leaf peroxidase isoenzyme electrophoretic studies were also conducted to substantiate these studies.

2. The genotypes exhibited a wide range of variation for several characters, revealing that nearly every genotype had some striking characteristic.

3. The genotypes were described for 175 characters, comprising vegetative, floral, fruit and chemical parameters. The studies revealed that the genotypes varied for several vegetative, fruit and chemical characters while striking many similarities for most of the floral characters. This trend indicated that the high inter-specific fertility in Citrus may be due to the low variability among the genotypes for floral characters.

4. Numerical analysis of 52 important characters representing the vegetative, floral, fruit and chemical characters was helpful in quantifying the descriptive information and analysing the differences among the genotypes statistically. The analysis revealed that the genotypes
varied significantly for all the characters studied, thus confirming the indications obtained through descriptions.

5. The descriptive data and numerical analysis revealed that the genotypes generally varied for several gross morphological and chemical characters at inter-specific level and presented same similarities at intra-specific level.

6. A comparative study of the genotypes through polygraphic method, for thirty two selected characters revealed that each genotype presented its distinct polygraphs corresponding to their distinct characteristics.

7. The studies on genetic analysis, viz., genotypic and phenotypic coefficients of variation, heritability in a broad sense, genetic advance as percentage of mean and correlation among the characters, have conclusively proved that the characters studied were genetic in nature, reliable as selection indices, amenable to improvement and can be used to study the genetic divergence and genotypic affinity relationships in Citrus.

8. The affinity relationships among the different genotypes and the divergence in Citrus established through the morphological descriptions, numerical analysis and polygraphic studies were quantified through Mahalanobis' $D^2$ analysis, revealing the genetic distances among them in quantitative terms. Very narrow relationships, between
Rangpur limes, to very wide relationships, for example between pummelo and Naruto sour orange, revealed the broad nature of genetic divergence in *Citrus*. Based on the minimum generalised distances, the seventy one genotypes were grouped into four distinct clusters.

9. Studies on leaf peroxidase isoenzyme banding pattern have conclusively proved that the *Citrus* types studied were genetically different and distinct genotypes. Every genotype exhibited its distinct banding pattern. A total of 20 bands were resolved among the seventy one genotypes with varying Rf. values. These 20 bands were assigned to five loci, depending on their relative mobility rates. These studies revealed the utility of leaf peroxidase banding pattern in resolving the genetic differences between the seemingly similar types of *Citrus*, particularly at intra-specific level.

10. The studies revealed that inspite of the enormous diversity found in *Citrus*, some genotypes, viz., mandarin oranges, sweet oranges, acid limes and Rangpur limes exhibited close affinity relationships among themselves. The information on genotypic affinity could be effectively utilized in practical crop improvement programmes and also in taxonomical studies. Scope for hybridization and selection appears to be present among the genotypes under cluster III, for evolving hybrids between acid limes and lemon types.
Hybridization between sweet oranges and pummeloes may also be promising in evolving grape fruit like hybrids. Hybridization between mandarin oranges and the species which have mandarin like fruits, viz., *C. nobilis*, *C. sunki*, *C. depressa*, *C. reshni*, *C. lycopersicaeformis* and *C. oleocarpa* may provide greater variability among the mandarin oranges for effective selections. The genotypes under Cluster II are potential candidates for evolving citrus rootstocks through hybridization and selection.