V. TAXONOMIC EVALUATION

The classical concept of taxonomic evaluation of species in recent years has undergone a change. The species which is for most purposes widely accepted as the basic unit of taxonomy has been subjected to violent controversies as regards its definition. Linneaus (1753) propounded the concept of binomial nomenclature for species and believed species are divinely created being discrete and true breeding groups of individuals (or populations). Many evolutionary taxonomists believe that species are formed as a result of evolutionary processes. According to Davis and Heywood (1963) among several classification of species definitions two main classes of species concept are:

(a) Taxonomic (embracing the orthodox, typological, morphological, morphogeographical etc.).
(b) Biological (including biosystematics, genetical, cytogenetical, nondimensional etc.).

In the days of classical taxonomy morphological criteria based on similarities or at times geographical distribution and ecological adaptations of individuals or populations were taken into consideration in specific-delimitation. This species concept of taxonomy is now overwhelmed with modern concept of omega taxonomy or biosystematics. Grant (1960) says "Modern concept of species is no longer based upon morphological concept,
but rather a genetic one in which gene exchange occurs at various degrees—free to highly restricted between individuals grouped in one or more interbreeding populations forming a reproductively isolated unit—the species."

Reproductive isolation or barriers of populations that are intrinsic or extrinsic and have genetic basis in nature rather than under experimentation is generally recognized leading towards speciation (Turill 1938, 1964, Dobzhansky 1951, Stebbins 1950, Love and Love 1956, 1957) hold the same view but add that morphological characters should be clearly observed to separate genetically distinct populations and these morphological differences need not be always great. Heaslop Harrison (1960) and Davis and Heywood (1963) are of the view that in cases where there is conflict between morphological and genetical criteria biological concept of species should not be rigidly applied to taxonomy and primary weightage should be given to morphological criteria.

In the present investigation different species of G. cinerea are of diploid, triploid and tetraploid series. Only one species G. livingstonii has 2n=56 chromosomes and coll.no.156 of G. xanthochymus is an aneuploid with 2n=80 chromosomes. The name of the species under each category is given below:


Tetraploid species: with 2n=96 chromosomes. G. benthami, G. mancostana and G. xanthochymus (coll.nos. 5, 22 and 144).

G. livingstonei with 2n=56 and coll.no.156 of G. xanthochymus with 2n=80 chromosomes.

It has also been shown that these species are interrelated on the basis of cyto-and chemo studies and that the trend of evolution is from species with lower chromosome number to the higher. This is also associated with luxuriant growth habits of species with higher number than those with low chromosome number. It involves (i) tall or gigantic habit (ii) thicker girth of trunk (iii) larger size of leaf (iv) bigger size of fruits (v) larger seeds etc.

The present investigation does not encourage splitting the genus or species into sections or generic taxa as some earlier taxonomists have envisaged on the basis of heterogeneity in the organization of male flower. This is because of two reasons.
1. The species of genus *Garcinia* are dioecious and cytological and chemical investigations of the taxa belonging to two different sexes of the same species have not shown appreciable variation. So any fabrications or divisions of the species or genus based on the variation of male flower is tentative.

2. The division of genus into number of generic taxa cannot be supported in the light of present work. For example *Garcinia cambogia* Desr. was earlier put under generic taxa *Mangostana* Gaertn. and named as *Mangostana cambogia* Gaertn. Similarly, *Garcinia mangostana* Linn. was named as *Mangostana garcinia* Gaertn. It may be pointed out here that *Garcinia cambogia* Desr. and *Garcinia mangostana* Linn. are distinct on the basis of cytological and chemical investigations.

*Garcinia cambogia* is a triploid with $2n=72$ chromosomes, whereas *Garcinia mangostana* is a tetraploid with $2n=96$ chromosomes. As such the possibility of two species being kept under generic taxa *Mangostana* Gaertn. is entirely ruled out. Chemical analysis of two species also shows *G. mangostana* is closely related to *G. benthami* (tetraploid) and other triploid species of *Garcinia* than *G. cambogia* (see Figs. 158,159). Moreover, it has distinct spots for substances that are typical or specific to it and more in number than in any other species. On these grounds both the species cannot be held under one section.
Further in assigning particular species under a section or generic taxon there has been a duplication of nomenclature e.g. Stalacmitis oowa G.Don. Syst. 1: 1621. 1831 and Oxycarpus gangetica Buch. Ham. Wern. Soc. 5: 344. 1824 being the name given for one species Garcinia oowa Roxb. These subdivisions have not only created a confusion for the delimitation of species but have bewildered the taxonomic status of the genus. Present findings show that various species of Garcinia to form a series of diploid, triploid, tetraploid and aneuploid taxa and on the basis of cytological and chemical grounds each species under a particular category of ploidy is distinct. Any attempt of subdividing the genus or species into a number of sections or generic taxa on the floral morphology is imaginary. The distinct nature of each species can be enunciated as follows by taking into consideration the morphological, cytological and chemical data.

**Diploid species: 2n=48 chromosomes**

*G. morella.* It has distinct karyotype with short and very short chromosomes. Absolute length of chromosomes (31.03 μ) is the smallest of all species. Two biochemical patterns of 13 spots are observed. Both have one usual amino acid L-Ala. The other spots are for secondary substances. Both patterns have spots B0 (0.03), LBR (0.08), LBR (0.12) and G (0.25) in common. The remaining spots vary and are invariably found in other species. Fruit extract shows only one pattern with 7 spots. All the spots can invariably be found in other
species. The spots $G(=0.34)$ from fruit and $G(=0.25)$ from leaf are typical to this species.

Morphologically there is no appreciable differentiation among various taxa studied. Genotypically they are similar. Biochemical variation with respect to certain spots could be attributed as environmental. The species has smallest reddish fruits and seeds as compared to other species investigated. Both exude a yellowish pulp rich in pigment 'morellin'. The stem is very lean as compared to other species and is straight. It also exudes a yellow resin or pulp rich in morellin. All these characters show that this species is distinct. G. indica: It has a heteromorphic karyotypes showing variation in types of chromosomes, number of satellites and absolute lengths. Cytotype-1 shows much similarity to G. morella as both have in their karyotypes short and very short chromosomes. Absolute length shows little variation. In G. morella it is 31.03 $\mu$m and in this cytotype 32.56 $\mu$m. Cytotypes-2 and 3 have medium, short and very short chromosomes and are relatively similar as compared to cytotype-1. Both show similarity in absolute lengths 36.18 $\mu$m, 36.19 $\mu$m, 3 pairs of satellited chromosomes and 1 pair with secondary constrictions. The differences are limited to the presence or absence of 1 pair of symmetrical chromosomes and in position of satellite on the arm. However, both cytotypes-2 and 3 are related to cytotype-1 as they have 1 pair of chromosomes with secondary constrictions.
There is also little variation in the proportion of asymmetrical and symmetrical chromosomes present among them which is again limited to one pair. It is obvious that cytotypes-2 and 3 have evolved from cytotype-1 as they have larger size of chromosomes.

Each cytotype has its typical chemotype and the chemotypes are interrelated in a similar fashion as their cytotypes. No appreciable variations are observed from collections of different ecological niches. Variations, however, are observed at sexual level. Cyto- and chemotype-1 is comprised of male collections and cyto- and chemotypes-2 and 3 are comprised of female collections.

Morphologically, there is slight variation observed at sexual level. Leaves are broader in female trees and male flowers are pedicellate. Fruits in this species are typical, reddish and bigger in size. Reddish pulp exuding from fruit is used for syrups and dried rind forms a substitute for tamarind. The "Kokum butter" exuding from seeds is an edible fat and is usually exported. Due to heteromorphic karyotype and their typical chemotype this species forms a genetic complex. On the basis of these cytological, chemical and morphological features this species stands distinct.

G. oow: The karyotype of this species is characteristic as it has long chromosomes. Very short chromosomes are not
present in this species. There are 3 pairs of satellited chromosomes. Absolute length of chromosomes 57.39 μ is also higher than other diploid species and falls within the range of triploid species. Biochemical pattern of leaf extract has 9 spots. Presence of unusual spot (=0.06) for free amino acid makes this species related to other triploid species. Biochemical pattern of fruit extract has 14 spots. Unusual amino acids (=0.47, 0.48), the spot LBR(=0.27) from fruit and B(=0.25) from leaf extracts are typical to this species. There is no genotypic or chemical variation observed at sexual level. Morphologically this species is distinct from other diploid species for its arborescent habit and leaf morphology for which it resembles triploid species G. cambogia. Absolute chromosome length of the two species also shows similarity. This species can be mistaken for diploid species G. indica in its habit but for these characters. However, the characteristic fruit shape and size makes this species distinct. Cytological, chemical and morphological features of this species show characteristic affinity both for diploid G. indica and triploid G. cambogia and in this way it forms a link between diploid and triploid species.

G. livingstonii: 2n=56 chromosomes

This species is a hybrid of parents with n=24 and n=32 chromosomes with similar or related genomes. Karyotype of this species has medium, short and very short chromosomes and is related to cytotypes—2 and 3 of G. indica from diploids.
Three biochemical patterns of 17 spots are observed. All of them have unusual amino acid (=0.12) which is typical or species-specific. All the three patterns are related since they have common spots. Variation in biochemical pattern could be environmental as no variation is observed at sexual level.

The collections from different areas do not show much morphological variations. Its stunted growth as compared to other species and distinct venation in leaves makes it conspicuously distinct in comparison to other species and could be easily mistaken for a member of some other group.

The karyomorphology, presence of unusual amino acid (=0.12) and typical morphological habit makes it enjoy the status of a distinct species.

**Triploid species: 2n=72 chromosomes**

*G. parviflora:* This species has a primitive karyotype as compared to other triploid species with more number of symmetrical chromosomes. Also there are 7 pairs of satellited chromosomes. Biochemical pattern has 10 spots and shows close relationship to other triploid species *G. cornea,* *G. xanthochymus,* *G. spicata,* *G. cambogia* and tetraploid species *G. benthemi.* It also shows relationships with diploid species *G. cowa,* *G. indica* and *G. morella.* In this way it forms a link between diploid, triploid and tetraploid species. The spot
YG(=0.20) is typical. Because of its primitive karyotype other triploid and tetraploid species may have evolved from this species by structural changes in chromosomes. In its morphological habit this species shows similarity to diploid *G. cornea* and in seed shape and other characters with *G. oowa*, *G. benthami* and *G. xanthochymus*. Fruits are small, reddish, oblong depressed and can be distinct from *G. morella*, which also has small fruits, but for its round nature. Apart from the interrelationships of this species with diploid, triploid and tetraploid taxa it enjoys a status of distinct species taking into consideration its primitive karyotype, number of satellited chromosomes and morphology of fruit.

*G. cambogia*: Two varieties of this species have been investigated. Both Var. *cambogia* and Var. *papilla* have similar karyotypes. There are 4 pairs of satellited chromosomes and 1 pair of chromosome with secondary constrictions in the karyotype. Satellite size is larger 0.47-0.62 μ and so are secondary constrictions 0.78 μ. Biochemical patterns are observed with 10 spots. No variation is observed at sex level. Var. *cambogia* is observed with both the patterns. The collections showing these patterns are from different areas but they are genotypically same. It is obvious that the variations are environmental. Var. *papilla* has pattern similar to pattern 2 of Var. *cambogia* and is collected from a different area. Fruit extracts with 7 spots have similar patterns. Present investigation shows both genotypically and chemically that these varieties are similar.
Morphologically slight variation is observed. In var. *cambogia* berry is ovate-oblong, 4-8 grooved with terminal mamilla. Since on cyto-and chemo studies the two varieties show similarity it is obvious that variation in fruit morphology is environmental and both could be merged and considered as ecotypes of one species *G. cambogia* Dear. The phenolic spots YS=0.08), LY(=0.22) and ER(=0.33) from fruit extract and G(=0.12), LER(=0.20) and V(=0.67) from leaf extract are typical to this species. All these features support independent status of this species. From karyomorphological studies this species might have evolved from primitive triploid species *G. parviflora* or directly from diploid species *G. cowa* with which it shows similarity in morphology and absolute length.

*G. cornea*: The karyotype has 3 pairs of chromosomes with satellites and 2 pairs with secondary constrictions which are smallest in size (0.23-0.31 μ) as compared to other species. Karyotype might have evolved from *G. parviflora* as mentioned above or directly from diploid species *G. cowa* since the absolute length of latter falls within the range of triploids.

Characteristic feature of the karyotype is its close relationship with triploid collections of *G. spicata* and *G. xanthochymus* which differ in floral morphology (perianth of sepals petals 5, stamens in 5 bundles). It also shows relationship with tetraploid species *G. benthami*. Both *G. cornea* and *G. benthami* have flowers of perianth of sepals
petals 4 and stamens monoadalpʰou or in 4 bundles. Karyo-
morphologically half of the chromosomes of total complement
are similar in the triploid species whereas 17 pairs of H
type chromosomes are showing similarity in the tetraploid.
This is also reflected in remarkable similarity of their
biochemical patterns especially for the presence of unusual
amino acids. The spot LB(0.84) is typical. This species
forms a link between G.parviflora and G.xanthochymus on the
basis of cytological and chemical studies. Morphologically
also they show similarity but for the characters of fruit
and flower. All these features show that this species is
distinct and independent.

On the basis of its close relationship with other
triploid or tetraploid species especially with respect to
G.xanthochymus and G.spicata (which differ in floral morphology)
it could be assumed these two species might have evolved later.

G.spicata: The karyotype has 5 pairs with satellites on
short arm, 1 pair with satellite on long arm and 2 pairs with
secondary constrictions on long arm. Like all the other
triploid species this species has also medium, short and very
short chromosomes. G.spicata is thus related to them. It
also shows strong relationship karyomorphologically with
G.xanthochymus (especially with triploid collections) with
respect to more than half of the complement in their
karyotypes. Biochemical pattern shows 9 spots. The pattern for free amino acids is similar to *G. xanthochymus* especially for the presence of unusual free amino acids. Other spots are observed invariably in other triploid species. The phenolic spot B (=0.12) is typical.

Taking into consideration morphology of the flower *G. spicata* is closely related to *G. xanthochymus* and was earlier described as the species of genus *Xanthochymus* Roxb. or subgenus *Xanthochymus* T. Anders. This species was then named as *X. ovalifolia* Roxb. Present investigation shows while this species is closely related to *G. xanthochymus* because both have flowers with perianth of sepals and petals 5 and stamens in 5 bundles, it also shows strong relationship to other triploid species (*G. cornea, G. parviflora*) on the basis of cyto- and chemotaxonomical aspects. They have flowers with perianth of sepals and petals of 4 and stamens monadalpous or in 4 bundles. These studies show that this species is interrelated with other triploid species although there is variation in their floral morphology. On these grounds *G. spicata* cannot be segregated from the genus *Garfinia* as proposed by earlier taxonomists and should be treated as one of the species of *Garfinia* Linn. itself.

Tetraploid species: 2n=96 chromosomes

*G. benthamii*: This species has a characteristic karyotype with all the four types of chromosomes. There are 5 pairs
of chromosomes with satellites. The karyotype forms a link with triploids *G. cornea*, *G. cambogia*, *G. spicata* and tetraploid *G. xanthochymus* (coll. nos. 22, 144). *G. xanthochymus* and *G. benthami* have in common 4 pairs of satellited short chromosomes \( (s_2, s'_2) \) and 17 pairs of short chromosomes with submedian primary constrictions \( (H_{34}) \). The absolute length does not show much variation \( (89.24-89.49 \mu) \). Also this species is related to *G. parviflora* as they have in common two pairs of satellited short chromosomes \( (s_2, s'_2) \). Karyomorphological studies suggest that *G. benthami* might have evolved from *G. parviflora* which has primitive karyotype or any other triploid species and *G. xanthochymus* might have also evolved from *G. benthami*.

The biochemical pattern supports the above view. *G. benthami* shows relationship with *G. xanthochymus* (tetraploid coll. nos. 22, 144) with respect to spots of unusual amino acid \( (=0.08) \), L-Ala, BG\( (=0.03) \), Y\( (=0.12) \), YG\( (=0.40) \) and BG\( (=0.45) \). The biochemical pattern of this species is also related to *G. parviflora*, *G. cornea* and *G. spicata* in respect of certain common spots e.g., BG\( (=0.03) \), LBR\( (=0.16) \), L-Ser, L-Ala and unusual \( (=0.08) \). The presence of unusual amino acid and some phenolic substances are of great taxonomic significance as regards their interrelationships. LBR\( (=0.28) \) is species-specific.

All these features suggest that this species is distinct.
G. *mangostana*: The karyotype has only long, medium, and short chromosomes. There are seven pairs of chromosomes with satellites and 1 pair with secondary constrictions. This species on the basis of floral morphology is closely related to *G. benthami* as compared to other tetraploid *G. xanthochymus* in which flowers vary in their morphology. Karyomorphologically *G. xanthochymus*, *G. benthami* as well as other tetraploid species are interrelated in respect of 17 pairs of H-type chromosomes. However, the degree of relationship of *G. mangostana* with respect to *G. benthami* is higher as they have in common 52 short chromosomes out of a total number of 96 chromosomes in the complement. Biochemical pattern from leaf extract of this species has 14 spots. With respect to amino acids the results are quite significant as there are 5 spots of unusual amino acids (=0.03, 0.10, 0.18, 0.20, 0.42) present. Fruit extract has 10 spots in its pattern and it has some typical spots for phenols. Taxonomic status of *G. mangostana* makes it distinct from other species as it has more number of typical spots or species-specific substances. These are unusual amino acids in leaves (=0.10, 0.18, 0.20, 0.42) and typical phenolic spots in fruits LBR(=0.30), LBR(=0.40) and LBR(=0.50). Morphologically, also this species has a typical fruit (popularly known in English Mangosteen) which is apple shaped. Inner flesh of the fruit is very delicious and juicy when unripe and is usually served
at dessert. Popularity gained by this fruit also justifies it as a species of *Garcinia*.

*G.* _xanthochymus_: Four cytotypes are observed that fall in 3 polyploid series triploid, aneuploid and tetraploid. Out of these 2 cytotypes are observed at tetraploid level. Tetraploid coll.no.5 has all the four types of chromosomes. Tetraploid coll.nos. 22, 144 and aneuploid coll.no.156 have long, medium and short chromosomes. The triploid coll.nos. 37-39, 123 and 164 have medium and short chromosomes. All the cytotypes are interrelated to themselves as also to other triploid and tetraploid species. It shows despite the variation in floral morphology there exists a strong affinity among the species. There also occurs a correlation among satellited chromosomes and arrangement of flower or fruit in tetraploid, aneuploid and triploid cytotypes. Biochemical patterns of leaf extracts form a chemotype typical to each cytotype. There are 19 spots in total found in them. Fruit extracts do not show any significant variation. Presence of spots for unusual amino acid (=0.08) in all chemotypes is quite significant as it could be observed in other triploid and tetraploid species also with which this species shows strong affinity. The spots for secondary substances make obvious the possible evolution of aneuploid from triploid. Like their cytotypes all the chemotypes are interrelated to themselves as well as to other triploid and tetraploid species (*G.* _cornea_, *G.* _perviflora_, *G.* _benthami_ and *G.* _spicata_).
Cytological and chemical studies show that *G. xanthochymus* is closely related to (i) triploid species *G. cornea*, *G. parviflora* with flowers having perianth of sepals and petals 4, stamens monadelphous or in 4 bundles and *G. spicata* with flowers having perianth of sepals and petals 5, stamens in 5 bundles. (ii) tetraploid *G. benthamii* with flowers of sepals and petals 4, stamens in 4 bundles. Since this species forms genetic complex and at the same time has strong affinity towards other triploid and tetraploid species of *Garcinia* despite their variation in floral morphology the species *G. xanthochymus* cannot be held apart from other species of *Garcinia*. Its elevation to a genus level by Dr. Boxburgh (1824) or subgenus level by T. Anderson (1874) and other workers is not supported on the basis of cyto- and chemotaxonomical studies. Present investigation also supports Hooker's (1874) view of treating this as the species of *Garcinia* Linn.

Since the evolution in *Garcinia* is from species of lower chromosome number and size to the higher, accompanied by luxuriant habit, it is possible the flower with perianth of sepals and petals 5 and stamens in 5 bundles have evolved later from normal flower in *Garcinia* Linn. with perianth of sepals and petals 4, stamens monadelphous or in 4 bundles. The former is highly evolved as these species with higher chromosome number and size are advanced on the basis of karyo-morphological and chemical studies. All these features express
**G. xanthochymus** Hook. as highly specialized species of *Garcinia* Linn.

From the present cyto-and chemotaxonomical study of the genus *Garcinia* each species investigated is typical with respect to its size, number, types, satellites and secondary constrictions, the presence of spots for chemical substances etc. There exists a correlation between cytological and biochemical pattern of each species because of which various species are intricately interrelated. Morphological characters simulate to such an extent that sometimes identification at species level is difficult unless complete material is available. This may be because of greater affinity among species in their relationships with each other. The diploid taxa form a link with triploid and the latter with tetraploids. The composite taxonomic treatment of the genus by earlier workers who were responsible for its split into a number of generic taxa or sections, due to variation in floral morphology especially as regards the heterogeneity in organization of male flower, cannot be supported in the light of present work. Each species has to be treated as a representative of the genus since they are shown to be remarkably distinct and highly specialized.