7.1 INTRODUCTION

You have already read about ‘Tools of a taxonomist’. In this unit, you will study about recent trends in plant taxonomy. The unit deals with how different branches of biology help in synthesising the classification. Each and every classification collected by taxonomists never becomes obsolete and dispensable. It is retained progressively refined and continually added to its by successive waves of new information which accumulate rapidly in the wake of important biological discoveries. In addition, new tools and techniques for studying various organisms provide interesting observations which are successively exploited by taxonomists. Thus, taxonomists are synthesisers of this information and the process of taxonomy and systematic botany is an unending synthesis.

Today, the modern taxonomist realises that the ultimate taxonomy of higher plants must be based on an understanding of the morphology, anatomy, embryology, cytology and breeding behaviour, besides chemistry and other features. This requires a multi-disciplinary approach and the taxonomist also uses computers to help him analyse data from different aspects of plant biology.

Thus, taxonomy includes both the latest developments and also the present state of the conventional approaches. The next unit deals about modern trends in animal taxonomy.

Objectives

After studying this unit you will be able to:
- describe various approaches in the study of plant taxonomy,
- differentiate between classical or alpha taxonomy and modern or omega taxonomy,
- explain the importance of morphology, anatomy and embryology in relation to taxonomy,
- appreciate the use of chromosomal information in cytotaxonomy and biosystematics,
- list the significance of plant chemistry in taxonomy,
- define numerical taxonomy with suitable examples.

Before we begin our study of modern trends in plant taxonomy, it is necessary to know about alpha and omega taxonomy.
7.2 ALPHA TAXONOMY AND OMEGA TAXONOMY

7.2.1 Alpha Taxonomy
This relates to the basic or preliminary classification based almost entirely on external morphology. This can be considered as the empirical approach in taxonomy where the classification is synthesised from the observed facts. Alpha taxonomy has also been called Classical or Orthodox or Formal taxonomy. This has been practised since ancient times and different aspects of this approach are in use even today. The name ‘Alpha taxonomy’ was given by Turrill (1935), while two phases of development in taxonomy come under this approach according to other taxonomists such as Valentine and Love (1958), Davis and Heywood (1963). These phases are:

1. The exploratory phase involving collection and subsequent classification;
2. The systematic or consolidation phase involving extensive herbarium collections and field studies for preparing floras, monographs and detailed systems of classification.

7.2.2 Omega Taxonomy
After synthesising a basic classification, the taxonomist can attempt to improve upon it. Therefore, the observed facts are interpreted in Omega taxonomy to provide an interpretive classification. Evolutionary and phylogenetic approaches are applied to understand taxonomic and evolutionary relationships of plants at all levels. The name Omega taxonomy was also provided by Turrill (1935). However, this has also been called Beta taxonomy or Neotaxonomy or Modern taxonomy. According to Valentine and Love (1958), this represents the biosystematic or experimental phase in the development of taxonomy involving detailed cytological and genetical studies. Davis and Heywood (1963) suggest that Omega taxonomy represents the biosystematic phase as well as the encyclopedic or holotaxonomic phase in which the taxonomist analyses and synthesises all kinds of information.

7.3 MORPHOLOGY IN RELATION TO TAXONOMY
Morphology is the basic tool of taxonomy, because identification is primarily based on the characters of the plant. The morphological characters are easily observable in both living plants and in herbarium specimens. They have provided the basic information for a majority of the classification systems in plant taxonomy. In recent years, electron microscopy has provided a valuable tool to the modern taxonomist to study different morphological characters at high magnification and this information is used for purposes of identification, classification and for establishing relationships.

Heywood and Dakshini used the scanning electron microscope (SEM) to study the surface patterns of the fruit (called mericarp) in 40 species from 12 genera of the family Umbelliferae. They found that many microcharacters on the fruit wall observed with the help of the SEM are of great value in clarifying the relationships of the different genera. They also observed a great diversity in the structure of the fruit in these species and this provides new information of significant practical value for taxonomic purposes.

Most taxonomists have traditionally separated the genus Glinus Linn. from the genus Mollugo Linn. on the basis of seed characters, but sometimes there were difficulties in proper identification of the two genera. With the help of the SEM, the seed surface patterns have been examined in detail to establish the importance of seed surface microcharacters in the identification of the genera. Also, within the genus Mollugo, seed-coal micromorphology has helped in identifying different species.

These and other similar studies show that even in the present era of specialised and sophisticated botany, morphological characters continue to provide valuable taxonomic information.

7.4 ANATOMY IN RELATION TO TAXONOMY
The use of anatomical characters in taxonomy began with the development of the microscope which provided the biologist a new tool to observe the internal structure...
of organs and tissues. It was realised that anatomical characters are just as valuable as morphological ones. All parts of a plant provide numerous features which have been used for taxonomic purposes. Some anatomical features are very diagnostic and are commonly used in routine identification. We also know that this subject is of great importance to scientists who are called upon to identify small samples/specimens of plant material for particular purposes such as pharmacognosists in the determination of the source of a drug, or by a forensic expert who may be able to provide clues to a crime investigation, besides others. These and other similar observations have firmly established the role of anatomy in plant identification and classification.

The leaf is perhaps the most varied organ of the angiosperms and provides many anatomical characters of potential taxonomic significance. In your Plant Physiology Course (Block 3, Unit 13) you have read about \( \text{C}_4 \) and \( \text{C}_3 \) pathways in photosynthesis. Investigation of the anatomy of leaves from plants following these pathways has brought out several significant features associated with the two types. The most distinct character observed in the leaves, is the presence of prominent chlorenchymatous sheath surrounding the vascular bundles in the leaves of plants showing the \( \text{C}_4 \) pathway and their absence in the leaves of plants showing the \( \text{C}_3 \) pathway. Thus, the leaf anatomy also provides information about the photosynthetic efficiency of a plant.

As a student of botany, from an early age, we learn that the basic pattern of venation differs in the two major divisions of the angiosperms. Within each division there are numerous leaf venation patterns and this feature has been used by taxonomist for understanding taxonomic and phylogenetic relationships in various plant groups.

Dr Lalitha Sehgal surveyed the leaf venation patterns in 150 species of the genus Euphorbia. She was able to recognise 12 major patterns and used this information along with other characters to identify and classify these species. She also correlated the leaf venation pattern with the habitat of the species and showed that xerophytic members of the genus had 'accumulated groups of tracheidal elements', while the herbaceous species having prostrate and ascending habit possessed a sheath around the veins. Several other features of the venation pattern were also found to be of taxonomic significance (Table 7.1).

Table 7.1: Classification of Euphorbia species on the basis of leaf venation patterns.*

<table>
<thead>
<tr>
<th>Category 1</th>
<th>Uni-veined</th>
<th>6 species, e.g. E. lacta</th>
</tr>
</thead>
<tbody>
<tr>
<td>Category 2</td>
<td>Bi-veined 4 species, e.g. E. polygonifolia</td>
<td></td>
</tr>
<tr>
<td>Category 3</td>
<td>Tri-veined a majority of the species</td>
<td></td>
</tr>
<tr>
<td>Subgroup 1.3.2.1 Three-stranded midrib</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Type 1.3.2.1.1 e.g. E. indivisa</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Type 1.3.2.1.2 e.g. E. hirta</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Type 1.3.2.1.3 e.g. E. granulata</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Subgroup 1.3.2.2 Single-stranded midrib</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Type 1.3.2.2.1 e.g. E. gorgonii</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Table 7.1: Classification of Euphorbia species on the basis of leaf venation patterns.*</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

*Data courtesy Dr Lalitha Sehgal
In another interesting study, Biesbér and Mahlberg (1981) examined the laticifer cells and scanning electron micrographs of the starch grains for interpreting the evolution within the genus Euphorbia.

Several other features of the leaf anatomy have been used for taxonomic purposes. Some of these include the nature of the epidermis, stomatal types, the type of mesophyll, presence and type of sclereids and crystals etc. Foliar sclereids vary in their kind and distribution amongst various groups of angiosperms.

Another important anatomical feature used in taxonomy and phylogeny, is the structure of the secondary wood. Wood anatomy has been used at all taxonomic levels. This data along with other characters provides useful evidence for determining the taxonomic position of taxa whenever two or more possibilities are suggested. The classification of a genus or a family in its appropriate higher category can be determined in this manner. Similarly, petiole vascularization pattern and nodal anatomy provide increasingly useful taxonomic evidences.

Behnke and his associates have investigated more than 1500 species from 380 families to understand the ultrastructure of the sieve tube plastids. There are broadly two types of sieve tube plastids: one is called S-type that accumulates starch; while the other type is called P-type that accumulates protein. This anatomical information obtained by using the transmission electron microscope (TEM) has been used for understanding relationships amongst different groups of both dicotyledons and monocotyledons.

![Figure 7.1: TEM micrographs showing A. S-type plastids and B. P-type plastids in sieve tubes.](image)

It is, however, important to remember that anatomical features have provided outstanding data for taxonomy. These characters when used alone may not provide viable system of classification, but when they are combined with knowledge from other disciplines, they have solved many taxonomic problems. Taxonomists should not separate anatomical data from morphological characters and they should incorporate this information in their formal taxonomic descriptions.

**SAQ 1**

a) In the following statements, put a tick (✓) mark on correct ones and a cross (✗) on the wrong ones in the given boxes.

i) Modern taxonomists can use knowledge from different fields of investigation. [✓]

ii) Alpha taxonomy follows an interpretive approach. [✗]

iii) Omega taxonomy is also called formal taxonomy. [✗]

iv) Morphological characters are not used in omega taxonomy. [✗]
v) Plant anatomy provides characters for both alpha and omega taxonomy.

vi) Morphology of foliar sclerids in different varieties of the tea plant can be correlated with the presence or absence of certain chemical substances in the leaf.

b) Classical taxonomy and modern taxonomy follow distinct methods in solving taxonomic problems. Name the significant difference in the approach of these methods.

...................................................................................................................................................................

...................................................................................................................................................................

c) Plants showing the C₃ and C₄ photosynthetic pathways can be identified by their leaf anatomy. Which is the most significant anatomical feature?

...................................................................................................................................................................

...................................................................................................................................................................

d) In what ways does information from sieve-tube plastids help taxonomists?

...................................................................................................................................................................

...................................................................................................................................................................

7.5 EMBRYOLOGY IN RELATION TO TAXONOMY

Embryological information has been used for taxonomic purposes at various levels of classification. You know of a very basic division of the plant kingdom into 2 units; the Thallophytes and the Embryophyta where plants are recognised on the basis of the behaviour of the zygote in addition to other characters (Table 7.2).

Table 7.2: Embryological characters used in taxonomy.

| 1. Anther |
| 2. Quadripartition of the microspore mother cell |
| 3. Pollen grain |
| 4. Development and structure of the ovule |
| 5. Origin and extent of the sporogenous tissue in the ovule |
| 6. Megasporogenesis and development of the embryo sac |
| 7. Form and organisation of the mature embryo sac |
| 8. Fertilisation |
| 9. Endosperm |
| 10. Embryo |
| 11. Seed-coat |
| 12. Special features |

In the same way you are also aware that the characters of the embryo along with several other features provide the basis for the division of the angiosperms into 2 major groups, the monocotyledons and the dicotyledons.

In the following paragraphs we shall elaborate on the value of embryological data as a modern trend in taxonomy of plants. By studying this section, you shall be able to know the various kinds of embryological characters used by taxonomists, understand the importance of embryological characters in taxonomy, and apply this knowledge from embryology for solving taxonomic problems.
Embryology strictly refers to the study of the development of the embryo and the structure of the mature embryo. However, Professor P. Maheshwar and many other famous botanists included, all events which led to the process of fertilisation besides the study of the embryo, under the term embryology. This enlarged concept has proved very useful for providing a large number of characters which can be used for taxonomic purposes, and during the last 50 years or so, a vast amount of knowledge has been accumulated which has been used for taxonomic purposes. These features from sporogenesis, gametogenesis, fertilisation and embryogenesis in flowering plants have been recognised as less prone to adaptive stress and therefore relatively stable. They are, therefore, of great significance in plant taxonomy, especially when external morphology has suggested two or more possibilities concerning taxonomic relationships.

There are several aspects which favour the use of embryological characters in taxonomy. The most significant and important feature is the high degree of correlation amongst embryological characters. There are, for example, as many as 10 embryological characters which always present themselves together in all plants classified under the order Ericales (Table 7.3). This highly significant correlation of characters is very important for identification of this order, and no other group of angiosperms shows all these characters together.

Table 7.3: Embryological characters of the order Ericales

<table>
<thead>
<tr>
<th>No.</th>
<th>Character</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.</td>
<td>Undifferentiated endothecium</td>
</tr>
<tr>
<td>2.</td>
<td>Glandular tapetum with multinucleate cells</td>
</tr>
<tr>
<td>3.</td>
<td>Pollen in permanent tetrads</td>
</tr>
<tr>
<td>4.</td>
<td>Unistegic, teninnucellate ovules</td>
</tr>
<tr>
<td>5.</td>
<td>Endothelium present</td>
</tr>
<tr>
<td>6.</td>
<td>Monosporic 8-nucleate megagametophyte</td>
</tr>
<tr>
<td>7.</td>
<td>Elongated zygote</td>
</tr>
<tr>
<td>8.</td>
<td>Cellular endosperm with the first 4 cells in a linear row</td>
</tr>
<tr>
<td>9.</td>
<td>Straight embryo</td>
</tr>
<tr>
<td>10.</td>
<td>Single layered seed-coat</td>
</tr>
</tbody>
</table>

Similarly, reproductive organs show less variability in different climatic conditions providing stable embryological characters for the purposes of identification. They also do not show ecotypic variation and remain unchanged at different ploidy levels in a polyploid series. These aspects and the fact that most biologists are of the opinion that embryological characters are conservative, increase the value of embryology as an important trend in modern taxonomy.

The value of embryology in solving taxonomic problems can be appreciated by studying some specific cases. Amongst the classical examples cited by embryologists is the taxonomic position of the genus Paeonia. In a majority of the classical systems of angiosperm classification, this genus is considered as a member of the family Ranunculaceae. However, several botanists have been recognising several characters of Paeonia which distinguish it from other members of the family Ranunculaceae. These include vascular and floral anatomy, basic chromosome number as well as the size and morphology of the chromosomes. The most significant difference between the genus Paeonia and other members of the family Ranunculaceae concerns several embryological characters and this study was carried out independently by Russian botanists Yakovlev and Yoffe as well as by the Indian botanist Prem Murgai. The most significant observation relates to the embryogeny in Paeonia. Unlike other angiosperms, this genus exhibits a unique type of embryogeny. According to the Russian botanists, the zygote nucleus undergoes repeated nuclear divisions forming a coenocytic structure. Later, the nuclei lodge themselves in a peripheral layer of the cytoplasm, and this is followed by wall formation so that the peripheral region becomes cellular. Some of the peripheral cells then function as embryo initials but only one of these develops into an adult embryo. Murgai on the other hand observed a division of the zygote into a 2-celled proembryo and the basal cell of this proembryo develops into the coenocytic structure leading to the development of the adult embryo as described by the Russian botanists. The other embryological characters which
differentiate *Paeonia* from the rest of the Ranunculaceae are tabulated below. This justifies the separation of the genus *Paeonia* from family Ranunculaceae and its classification in the family Paeoniaceae (Table 7.4).

<table>
<thead>
<tr>
<th>Feature</th>
<th><em>Paeonia</em></th>
<th>Ranunculaceae</th>
</tr>
</thead>
<tbody>
<tr>
<td>Stamen</td>
<td>Spirally arranged, centrifugal</td>
<td>Spirally arranged, centripetal</td>
</tr>
<tr>
<td>Anther</td>
<td>Multilayered endothecium, mostly 2-layered tapetum</td>
<td>One-layered endothecium and one-layered tapetum</td>
</tr>
<tr>
<td>Pollen</td>
<td>Reticulately pitted exine, large and elongate generative cell</td>
<td>Granular, papillate or smooth exine, small lenticular generative cell</td>
</tr>
<tr>
<td>Female archesporeum</td>
<td>Multicelled, many megaspore mother cells function</td>
<td>Uni- or multicelled, one cell function</td>
</tr>
<tr>
<td>Antipodal cells</td>
<td>Persistent, not polyploid</td>
<td>Persistent (ephermal in <em>Adonis</em>), nuclei one or more than one, polyploid</td>
</tr>
<tr>
<td>Embryogeny</td>
<td>Unique</td>
<td>Onagrad or, rarely, Solanad type</td>
</tr>
<tr>
<td>Seed</td>
<td>Arillate</td>
<td>Non-arillate</td>
</tr>
<tr>
<td>Fruit</td>
<td>Follicle</td>
<td>Achene</td>
</tr>
</tbody>
</table>

We are familiar with the 'water chestnut' commonly called 'Singhara' and botanically known as *Trapa bispinosa*. The classification of this plant has seen many changes. Bentham and Hooker classified the genus *Trapa* in the family Onagraceae, but other taxonomists including Engler and Hutchinson moved the genus *Trapa* to the family Trapaceae listing several morphological characters as evidence for this separation. Dr Manasi Ram undertook a detailed embryological study of *Trapa bispinosa* and listed several characters by which *Trapa* differs from Onagraceae thus supporting the classification of *Trapa* in a separate family Trapaceae (Table 7.5).

<table>
<thead>
<tr>
<th>Feature</th>
<th><em>Trapa</em></th>
<th>Onagraceae</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pollen grain</td>
<td>Pyramidal with 3 much folded meridional crests</td>
<td>Bluntly triangular, and basin-shaped</td>
</tr>
<tr>
<td>Ovary</td>
<td>Semi-inferior, bicollar with a single pendulous anatropous ovule in each chamber</td>
<td>Inferior, mostly trilocular with many ovules per chamber on an axile placenta</td>
</tr>
<tr>
<td>Embryo sac</td>
<td>Polygonum type</td>
<td>Oenothera type</td>
</tr>
<tr>
<td>Endosperm</td>
<td>Absent</td>
<td>Present and Nuclear</td>
</tr>
<tr>
<td>Embryo</td>
<td>Solanad type</td>
<td>Onagrad type</td>
</tr>
<tr>
<td>Suspensor</td>
<td>Well developed suspensor haustorium</td>
<td>Short and inconspicuous</td>
</tr>
<tr>
<td>Cotyledons</td>
<td>One cotyledon extremely reduced</td>
<td>Cotyledons: equal</td>
</tr>
<tr>
<td>Fruit</td>
<td>Large, one-seeded drupe with prominent spines</td>
<td>Loculicidal capsule</td>
</tr>
</tbody>
</table>

Besides the examples discussed above, there are many other interesting observations on the genera *Exocarpus*, *Pentaphragma*, *Butomus*, *Daphniphyllum*, and the families Podostemaceae, Onagraceae, and Loranthaceae where embryological characters have been used for understand taxonomic relationships.

**SAQ 2**

.a) Using embryological information, differentiate between:

i) Thallophytes and Embryophytes
ii) Monocotyledons and Dicotyledons

b) List six embryological characters used for taxonomic purposes:
   i) .................................................................
   ii) .................................................................
   iii) .................................................................
   iv) .................................................................
   v) .................................................................
   vi) .................................................................

c) Mention 3 features which render embryological characters significant in solving taxonomic problems.
   i) .................................................................
   ii) .................................................................
   iii) .................................................................

d) List 3 genera and 3 families of flowering plants in which embryological characters have helped in understanding taxonomic relationships.

Genera | Families
--------|---------
i) .................................................................
j) .................................................................

7.6 CYTOTAXONOMY AND BIOSYSTEMATICS

Towards the end of the 19th century and in the early years of the 20th century, botanists were faced with a problem of analysing variations occurring naturally in plants. This led to a shift in the emphasis from descriptive classical methods in plant taxonomy to a new approach called experimental taxonomy whereby attempts were made to understand the cause of these variations. This new approach, also called biosystematics, depended largely on establishing the cytological basis of variation. This use of cytological data in taxonomy is now referred to as cytotaxonomy.

For the purposes of discussion, this trend in plant taxonomy may be considered under three broad headings:

i) chromosome number,
   ii) chromosome morphology, and
   iii) chromosome behaviour at meiosis.

7.6.1 Chromosome Number

We are generally aware that the number of chromosomes in each cell of all individuals of a single species is constant. It is also established that the more closely related species are likely to have similar chromosome numbers while the more distantly related ones shall have different numbers. Due to this relative conservativeness, chromosome number becomes an important and frequently used taxonomic character. In addition, there is a very wide range of chromosome numbers in the angiosperms from as low as 2n = 4 (in Haplopappus gracilis) (Asteraceae) to as high as 2n = 530 (in Poa littlerosa) (Poaceae). A large number of angiosperms have been analysed for their chromosome numbers, providing useful taxonomic information.

\[ 2n \] is equal to the diploid or somatic chromosome number, while \( n \) is the haploid or the generic number.
Many interesting ideas have developed from knowledge of chromosome numbers. For example, in the genus *Festuca*, different species have different chromosome numbers forming a mathematical series. The chromosome numbers are $2n = 14, 28, 42, 56, 70$, etc. From this information, a generalisation can be made, that different species may have some common basis. If we assume that these chromosome numbers are based on a common denominator called $x$ (and $x = 7$), then we can consider the different species to have multiples of this number. This denominator or base number ($x = 7$) can be considered as the basic set of genetic information carried by a plant, and due to the multiplication of this basic genetic set, the evolution of different species has occurred. Such a series is said to be polyploid in which the basic number ($x$) is equivalent to the haploid number of chromosomes in a diploid species ($i.e., x = n = 7$). The other species would then be tetraploid, hexaploid, octaploid, decaploid, etc. respectively.

### 7.6.2 Chromosome Structure

Cytologists have studied chromosome morphology and have pointed out that the most interesting feature about the chromosome structure is the position of the centromere. The centromere or constriction in the length of the chromosome provides information about the relationship of the 2 arms of the chromosome. Thus, depending on the position of the centromere, chromosomes are described as metacentric, acrocentric, and telocentric (Fig. 7.2).

![Fig. 7.2: Chromosome structure — a) acrocentric, b) metacentric, c) telocentric.](image)

The appearance of the basic chromosome set in a dividing cell is known as the karyotype of the cell. This can be analysed to provide information not only of the chromosome number, but also about chromosome size, chromosome volume, and type of chromosomes in the cell. This information is used by taxonomists for identifying plants and understanding relationships. The karyotype can be represented diagrammatically as an ideogram or karyogram, and these diagrams can be compared for taxonomic purposes. Another interesting observation is that the absolute size of the chromosomes of a karyotype is fairly constant since it is controlled by the genotype. Taxonomists have found that monocots generally have larger chromosomes than dicots, and that smaller chromosomes are found in hardwood plants in comparison to their herbaceous relatives.

### 7.6.3 Chromosome Behaviour

When we study meiosis, we not only observe the regularity of pairing which is important for the fertility of the plants, we are also able to make a chromosome to chromosome comparison. This provides valuable information about the role of chromosomes in heredity. Taxonomists use this information to understand relationships amongst different species of plants. We can also determine the nature of the genome to find out if it is homogenous or heterogenous. Genome analysis in plant taxonomy has been particularly useful in understanding polyploidy and for establishing the parentage of polyploids. A very significant study in this regard is the
case of the common hexaploid bread-wheat, *Triticum aestivum*. The genome of this economically important plant has been designated as AABBDD with $2n = 42$ chromosomes. Detailed genome analyses have established that 3 diploid species have contributed to the evolution of this hexaploid wheat. The A genome is from the diploid *Triticum monococcum* ($2n = 14$), the B genome is from a wild grass *Aegilops speltoides* ($2n = 14$), and the D genome has been contributed by *Aegilops squarrosa* ($2n = 18$).

Finally, we must remember that as with any other character, the value of cytotoxic data depends upon the group or category under investigation. A combination of cytological information with data from other disciplines will provide a more useful tool to the taxonomist.

SAQ 3

a) Define

i) Basic chromosome number

ii) Haploid chromosome number

iii) Diploid chromosome number

b) By consulting books in your study centre, find out the diploid chromosome number in the following plants:

   i) Rice (*Oryza sativa*)

   ii) Potato (*Solanum tuberosum*)

   iii) Tea (*Thea sinensis*)

   iv) Coffee (*Coffea arabica*)

   v) Mango (*Mangifera indica*)

   vi) Onion (*Allium cepa*)

c) Where is the centromere located in a

i) acrocentric chromosome

ii) metacentric chromosome


7.7 CHEMOTAXONOMY

Chemotaxonomy is a science which uses chemical information as a character for taxonomic purposes. Before we analyse the basis of this modern trend in plant taxonomy, let us for a moment think about the different kinds of plants in our daily lives. When we drink tea or coffee, we appreciate the flavour or aroma and differentiate the two by this character. Similarly, when we eat fruits such as the mango, the banana or the apple, we find that they taste differently. This difference is due to the chemical constituents of these foods and this forms the basis of chemotaxonomy where the chemical features or chemical constituents serve as the evidence for taxonomy. The potential importance of chemical evidence in plant taxonomy has been suggested by both botanists and chemists and this has become an important recent trend especially because newer techniques for quick analysis of plant material have been developed. Chemotaxonomists suggest that chemical characters have a particularly high taxonomic value because they are i) stable, ii) unambiguous, and iii) not easily (if at all) changeable. Further, chemical characters will show chemical relationships amongst plants in the same way as morphological characters show morphological relationships.

Although chemotaxonomy is considered to be a relatively recent development in modern taxonomy, its origin can be traced to very early classical taxonomy. You will recall that the spice plants were identified on the basis of their aromatic properties, or the medicinal plants by their curative value. These aromatic properties or the curative value was largely based on the chemical constituents of the plants and taxonomists have classified them since ancient times using these chemical features along with morphological characters. However, it is only in recent years that chemotaxonomy as an important field of study has been established.

A review of the large amount of literature published in this field reveals that chemical data may be obtained from any part of the plant. Secondly, depending on the purpose of the investigation, the chemical information may be used for description or identification of plants, or for establishing relationships. This evidence assumes greater significance when it is used to sort out differences in taxonomic relationships when 2 or more possibilities are suggested on the basis of morphological characters.

Although theoretically, all chemical constituents of a plant are potentially valuable to a taxonomist, in practice some kinds of molecules are more useful than others. Thus we can use directly visible chemical constituents such as crystals, raphides, or starch grains occurring in different plants as chemical characters.

Alternatively, we can chemically analyse plant material for different chemical constituents and use this information for taxonomic purposes. Most chemotaxonomists recognise three broad categories of chemical compounds, primary metabolites, secondary metabolites, and sementides, as important taxonomically.

7.7.1 DIRECTLY VISIBLE CHEMICAL CHARACTERS

Very few chemical substances in plants can be observed directly, but the few substances such as starch grains which are present in most green plants as food
reserves have been used for chemotaxonomic purposes. The type of starch grains present in different plants are very specific and this information can be used without any ambiguity. Reichert (1913) examined the starch grains in 350 species of plants and established their differentiation and specificity of occurrence in relation to genera and species, thus providing chemotaxonomic information. Tateoka (1962) reviewed the starch grain form in the grass family (Gramineae) and used this as additional information to classify the family into tribes. For example, in the Tribe Hordeae, the typical members such as Hordeum have compound starch grains, while other genera like Lolium, Nardus, and Papapholis have simple starch grains.

<table>
<thead>
<tr>
<th>STARCH GRAINS</th>
<th>RICE</th>
<th>WHEAT</th>
<th>MAIZE</th>
<th>BAJRA</th>
</tr>
</thead>
<tbody>
<tr>
<td>RAGI</td>
<td>OATS</td>
<td>JOWAR</td>
<td>BARLEY</td>
<td></td>
</tr>
<tr>
<td>GRAM</td>
<td>CANNA</td>
<td>BANANA</td>
<td>TAPIOCA</td>
<td></td>
</tr>
<tr>
<td>POTATO</td>
<td></td>
<td></td>
<td>TRAPA</td>
<td></td>
</tr>
</tbody>
</table>

Fig. 7.3: Types of starch grains (After Kocher 1981).

Raphides are the crystals of calcium oxalate which are present in large cells in different plant tissues and can be observed directly. They are long needle shaped crystals, pointed at both ends and usually occur in bundles, thus being easily identified. They have been observed in as many as 35 families of angiosperms. Several families of the Order Centrospermae and the Family Cactaceae show the presence of raphides. This feature along with other chemical characters and the similarity in embryological characters strengthens the suggestion that the Family Cactaceae shows some relationship with the Order Centrospermae.

7.7.2 Primary Metabolites
As the name indicates, primary metabolites are molecules involved in vital metabolic pathways. They are of universal occurrence and not very significant in chemotaxonomy. However, these molecules become useful as chemotaxonomic features when the quantity of such molecules varies considerably between taxa. For example, the sugar containing carbohydrate 'sedoheptulose' is stored in large quantities as a reserve food in the genus Sedum. Thus members of this genus can be easily identified by the presence of this primary metabolite. Interestingly, sedoheptulose diphosphate is a part of the photosynthetic carbon cycle and in a majority of the plants sedoheptulose does not accumulate at all. In the same way, the 22 amino acids are of universal occurrence. They serve as the building blocks of proteins. They can provide useful macromolecular data for chemotaxonomy. The amino acid sequence of different proteins can be investigated and the degree of similarity is presumably proportional to the degree of genetic relationship. However, only a few out of about 3 lakh species of angiosperms have been analysed for amino acid sequences. For example, the amino acid data on wheat and barley confirms the relationship of these genera as suggested by classical taxonomists.

7.7.3 Secondary Metabolites
Secondary metabolites or secondary plant products are those macromolecules that lack nitrogen and are of restricted occurrence and therefore of greater taxonomic
importance than primary metabolites. This group includes different kinds of compounds such as phenolics, alkaloids, terpenoids, etc. They are usually not involved in vital functions and are largely storage products or pigments.

Amongst the secondary metabolites, flavonoids, which are the commonest phenolic compounds of leaves, have been very useful for chemotaxonomic purposes. Both monoterpenes and diterpenes have been extensively surveyed for these compounds which show structural variability and chemical stability besides widespread distribution. They can be rapidly and easily identified and provide important chemical characters for taxonomic purposes. For example, 80 species of plants from the family Ulmaceae were investigated for their flavonoid chemistry by Giannasi (1978). A majority of the species contain flavonols, but a few species have glyco-flavonols and these two types of flavonoid compounds are never present together in any species. Interestingly, enough, in most classical systems of classification, the family Ulmaceae is divided into two subfamilies called Ulmoideae and Celtideae which are also distinguishable by the flavonoid chemistry. Therefore, morphological criteria combined with flavonoid dichotomy can be used to divide the family Ulmaceae (sensu lato) into two distinct families: family Ulmaceae (sensu stricto) characterised by the presence of flavonols, and family Celtaceae characterised by the presence of glucosylflavonols.

Several other studies have used flavonoid chemistry for taxonomic purposes in families such as Arilidaceae, Cornaceae, Labiatae (Lamiaceae), Leguminosae (Fabaceae), Orchidaceae, Rutaceae, Lemnaceae and others.

A second group of secondary metabolites commonly examined by chemotaxonomists are the terpenes. Chemically speaking, these compounds can be classified on the basis of their molecular structure into monoterpenes, diterpenes, triterpenes, sesquiterpenes, etc., and each group can be used for taxonomic purposes. For example, in the genus Salvia, 19 species could be distinctly identified and classified on the basis of their monoterpenes. The terpene composition was as useful as the morphological characteristics in the analysis of introgression and hybridisation within the genus. Similarly, triterpenes and sesquiterpenes have been particularly important and useful in the classification of the families Cucurbitaceae and Compositae (Asteraceae) respectively.

Other secondary metabolites used in chemotaxonomy include the iridoid compounds, the alkaloids, and the ellagitannins.

7.7.4 Semantides

The information carrying molecules in plants are called semantides, and they have been recognised to be 3 kinds; deoxyribonucleic acid or DNA (primary semantide), ribonucleic acid or RNA (secondary semantide) and proteins (tertiary semantide) following the sequential transfer of the genetic code. Of these, the proteins are the most favoured molecules for chemotaxonomic purposes. Plant proteins can be studied by different methods; by electrophoresis or by serological methods, and both processes have been used for obtaining information about the protein chemistry of different plants.

In the common bread wheat, Triticum aestivum, the storage proteins were analysed by electrophoresis. For comparative purposes, the storage proteins of the tetraploid wheat, Triticum dicoccum and the diploid grass Aegilops Squarrosa were analysed electrophoretically. This study confirmed the conclusion that the hexaploid wheat did contain a sum of the proteins possessed by the diploid species which have contributed to the evolution of the hexaploid wheat. This study supports the observations based on morphology and cytological evidence.

Serological analysis of proteins is based on the immunological reaction shown by mammals when a foreign protein is introduced into the system. In other words, this is based on the antibody-antigen reaction. The antibodies being specific to an antigen bringing about coagulation. This information can then be analysed to understand the relationships of the different plants on the basis of the serological evaluation of the plant proteins. Serology has proved a useful taxonomic tool at different levels of classification. J.G. Hawkes (1960) and his co-workers studied several tuber-producing species of Solanum to understand the evolution of the cultivated potato Solanum tuberosum and determine the species of Solanum which could be established as the ancestors of the common cultivated potato. Similarly, in the family Ranunculaceae, serological studies supported cytological data for the classification of the family into...
Tribes and genera. Fairbrothers (1959) and his co-workers have studied several plant groups serologically particularly the members of grass family. A general conclusion from such studies is that the different amount of serological activity in members of different plant families may be interpreted as a reflection of the evolutionary differences in the primary structure of the proteins due to which serological differences can be recognised between members of different families.

SAQ 4

a) List 3 reasons for using chemical characters for taxonomic purposes:

i) .................................................................................................................................

ii) .................................................................................................................................

iii) .................................................................................................................................

b) Name 3 kinds of chemical constituents which are useful to the taxonomists.

i) .................................................................................................................................

ii) .................................................................................................................................

iii) .................................................................................................................................

c) Name 2 ways by which proteins can be analysed for taxonomic purposes and name one genus analysed by each method. Briefly indicate the principles on which these two methods are based.

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7.8 NUMERICAL TAXONOMY

Taxonomy today is, in many details, different from what it was a generation ago. The use of computers by taxonomists has established an interesting modern trend called Numerical Taxonomy or Taximetrics. Mathematical and statistical evaluation of taxonomic information and computation of this data has provided taxonomists with new approaches to understand classification. In this section, you shall learn about the fundamentals of numerical taxonomy, know the principles and important terms used in this science, and understand the procedures adopted by numerical taxonomists in arriving at a classification.

You had studied in Block I, units 1 and 2, that organisms are classified on the basis of evidence obtained from their characters. You have also studied that different kinds of classifications can be designed by using a few or many characters. M. Adanson (1763) proposed that a classification should use a vast range of characters covering all aspects of the plants, and in construction of a classification all characters must be given equal importance. This idea forms the basis of modern numerical taxonomy, also called Neo-Adansonian Taxonomy. So far as the character number is concerned there is no limitation but larger the number better is the approach for generalisation of the taxa. You should remember that numerical taxonomy is not a totally new approach, but it is an organised method of evaluating data with computers in an objective and repeatable manner enabling comparison of many characters from many populations of plants.
7.8.1 Principles of Numerical Taxonomy

Numerical taxonomy is based on the following 7 principles.

1) The greater the content of information in the taxa of a classification is and the more characters on which it is based, the better a given classification will be.

2) Every character is of equal weight in creating natural taxa.

3) The overall similarity between any two entities is a function of their individual similarities in each of the many characters for which they are being compared.

4) Distinct taxa can be recognised because correlations of characters differ in the groups of organisms under study.

5) Phylogenetic inferences can be made from the taxonomic structure of a group and from character correlations, given certain assumptions about evolutionary pathways and mechanisms.

6) Taxonomy is viewed and practised as an empirical science. Classifications are based on phenetic similarity.

7) Classifications are based on phenetic similarity.

7.8.2 Procedures Adopted by Numerical Taxonomists

Since numerical taxonomy is an operational science, the procedure is divided into a number of repeatable steps, allowing the results to be checked at every step.

i) Choice of units to be studied: The first step is to decide what kind of units to study. In numerical taxonomy, the basic unit of study is called the "operational taxonomic unit" (OTU). Thus the OTU can be an individual plant if the taxonomist is studying a single population of plants to find out the range of variations in its characters. Similarly, you may treat an entire population of plants as an OTU if you are studying a single species represented by different populations existing in nature, or the OTU may be different species within a genus that is being evaluated. Therefore, in numerical taxonomy, the OTU varies with the material being studied, and this helps the taxonomists in making an objective study.

ii) Character selection: After selecting the OTU's, it is necessary to select characters by which they are to be classified. By experience, you will learn that characters which vary greatly amongst the OTU's are clearly more useful in numerical taxonomy; and we know that as many characters as possible may be used. Preferably a minimum of 50 and generally 80 to 100 or more characters are needed to produce a fairly stable and reliable classification. The selected characters have then to be coded or given some symbol or mark. There are 2 methods of coding taxonomic information.

a) Binary coding or two-state coding — This is the simplest form of coding adopted in numerical taxonomy where the characters are divided into + and −, or as 1 and 0. The positive characters are recorded as + or 1 and the negative characters as − or 0. It is possible to use this method of coding for all characters studied. In case a particular character is not present in an OTU being examined, the symbol or code NC is used, indicating that there is no comparison for that character. However, we find that by using this method of coding, we tend to increase our work because there are large variations in the plant, and very often a single character such as colour of flower can be represented in a wide range of variation. We can have white, pink, red, yellow and other colours in roses. If we are to use this data in a binary coding, then we will have to use each colour as a character and it would be coded as + or −, as the case may be.

b) Multi-state coding — An alternative method would be to use multi-state coding where a single character can be coded in a number of states, each being represented by a numerical symbol or code (e.g., 1, 2, 3, 4, 5, ... depending on the range of variation. Thus, if we again look at the colour of the rose flower, we can give different codes to different colours such as white = 1, pink = 2, red = 3, yellow = 4, and so on. Besides qualitative characters such as colour of flower type of placenta, etc., multi-state coding is also useful of quantitative...
characters such as plant height, leaf length, leaf breadth, and other characters involving measurements. A code is prepared for the range of variation and appropriate symbols are allotted to each unit in the range.

The data obtained by scoring the characters in the OTU’s are then presented in a table as a data matrix giving the OTU’s on one side of the table and the codes for different characters against each OTU. Thus, if one has studied 25 OTU’s and has scored 75 characters from each, the data matrix will contain 25 x 75 = 1875 units of information. This kind of large unit of information in the data matrix necessitates the use of computers to help the taxonomists to digest the knowledge quickly. It is also important to remember that computer programmes are based on mathematical equations and computer language and the data matrix is essential for this purpose. In addition, the next step in numerical taxonomy is entirely dependent on the data matrix.

The information is then presented in a 1 x n table or data matrix consisting of OTU’s scored for n characters (table 7.6).

<table>
<thead>
<tr>
<th>Characters (n)</th>
<th>Taxa OTU’s (t)</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>B</td>
</tr>
<tr>
<td>1. +</td>
<td>+</td>
</tr>
<tr>
<td>2. –</td>
<td>+</td>
</tr>
<tr>
<td>3. +</td>
<td>–</td>
</tr>
<tr>
<td>4. +</td>
<td>+</td>
</tr>
<tr>
<td>5. +</td>
<td>+</td>
</tr>
<tr>
<td>7. +</td>
<td>–</td>
</tr>
<tr>
<td>8. NC</td>
<td>–</td>
</tr>
<tr>
<td>9. +</td>
<td>+</td>
</tr>
<tr>
<td>10. +</td>
<td>–</td>
</tr>
<tr>
<td>11. +</td>
<td>NC</td>
</tr>
<tr>
<td>12. –</td>
<td>–</td>
</tr>
</tbody>
</table>

(Adapted from Sneath, 1962, in Microbial Classification, edited by Ainsworth and Sneath.)

iii) Measurement of Similarity: Overall similarity (s) is calculated by comparing each OTU with every other and is usually expressed as a percentage, 100 per cent for identity and 0 per cent for no resemblance. A similarity table or matrix is then constructed by tabulating the S coefficients for each one of the OTU (Fig. 7.4).

iv) Cluster Analysis: After making a similarity table, it is then rearranged so that OTU’s whose members have the highest mutual similarity are brought together. This can be done by several methods and related taxa or groups are recognised. These clusters are called phenons and can be arranged hierarchically in a tree diagram or dendrogram (Fig. 7.5).

The groups or clusters thus recognised may be treated as equivalent to the categories having ranks in classical taxonomy, such as the genus, family, order, etc. A problem faced by many taxonomists is whether there is any equivalence between the ranks in different taxonomic groups of organisms. Is a family of flowering plants, for example, equivalent in any sense to one of algae, or other organisms? To overcome this problem, numerical taxonomists have advocated a new terminology. Here, the term "phenon" is introduced and the particular phenons are designated by numerical prefixes (e.g., 80 similarity) showing the level of resemblance by which they are defined. The delimitation of the phenons is done by drawing horizontal lines across the dendrogram at a chosen similarity value. Such a dendrogram will have reference to a given study only, and cannot be generalised. Thus, phenons will be arbitrary and relative to groups within the limits of only one analysis.
Percentage similarity

Fig. 7.4: a) Schematic diagram showing a matrix of hypothetical similarity coefficient between pairs of group (taxa); the magnitude of the coefficient is shown by the depth of shading.
b) The same coefficient arranged by placing similar taxa next to each other; this gives a triangle of high similarity values. Phenons are groups by desired rank (After Sneath 1962. Microbial classification).

Fig. 7.5: A dendrogram representing the hypothetical hierarchy of group (taxa) obtained from Fig 7.4. The ordinate indicates magnitude of similarity coefficient at which stems join to form higher ranking groups. Horizontal lines delimit groups of equal rank (per cent phenon lines). (After Sneath, 1962). Microbial Classification, edited by Ainsworth and Sneath. University of Cambridge.)
Of the numerous taxonomic studies, the reclassification of the dicotyledons by Young and Watson (1970) serves as a good example. They studied 83 characters from morphology and anatomy in 543 genera and computed this information to classify these angiosperms. The computer-based classification was in many ways similar to other traditional classification, as well as in some ways different. However, the different genera were clearly distinguishable into distinct categories on the basis of the nature of the ovule into crassinucellate (ovules with a massive nucellus) and tenuinucellate (ovules with a small amount of nucellus). In view of these, some taxonomists are of the opinion that numerical taxonomy may never replace traditional methods as standard procedure. It would, however, be successful where other methods have failed or are laborious or otherwise difficult to apply. The most important contribution of numerical taxonomy has been to help taxonomists analyse their methods, data, and conclusions more logically and objectively.

SAQ 5

a) Why is numerical taxonomy also called Neo-Adansonian taxonomy?

b) Briefly describe the procedure adopted by Numerical taxonomists.

c) What is meant by 'operational taxonomic unit' (OTU)?

d) Differentiate between binary coding and multi-state coding.

e) Mention 2 uses of a data matrix in numerical taxonomy.
What is 'cluster analysis' and how is this arrived at in numerical taxonomy?

7.9 SUMMARY

In this unit, we have briefly discussed various aspects of modern trends in plant taxonomy. This has helped you to study that:

- Taxonomy utilises data from all the other branches of biology.
- Taxonomic information never becomes obsolete, but it is progressively refined and successively exploited by taxonomists to synthesise systems of classification.
- Modern taxonomy follows a multi-disciplinary approach.
- Modern or omega taxonomy follows an interpretive approach using evolutionary information to understand taxonomic and phylogenetic relationships. This involves usage of knowledge from the biosystematic or experimental phase and the encyclopedic or holotaxonomic phase of taxonomy.
- Morphological and anatomical characters can be studied with light as well as electron microscopes, and this information is useful for solving taxonomic problems.
- Plant embryology has proved extremely useful as a source of evidence in taxonomy.
- Cytological and biosystematic data uses information from chromosome number, structure, and behaviour, and this helps taxonomists to understand relationships amongst plants.
- Chemotaxonomy provides useful data from chemical characters which show chemical relationships amongst plants in the same way as morphological characters show morphological relationships. Different kinds of chemical compounds can be evaluated in different ways to provide taxonomically useful information.
- Taxonomists can use computers to analyse large amounts of information in numerical taxonomy.

7.10 TERMINAL QUESTIONS

1) "Systematic botany is an unending synthesis". Elaborate.
2) a) Differentiate between "Ranunculaceae sensu lato" and "Ranunculaceae sensu stricto".
   b) Name the genus which led to this change in the circumscription of the family.
   c) List the important characters responsible for this change.
3) The common breadwheat, Triticum aestivum, is a hexaploid. List evidences from cytotaxonomy and chemotaxonomy to support the evolution of this hexaploid wheat from diploid ancestors.
4) Briefly outline the procedures adopted in numerical taxonomy.
5) Write explanatory notes on:
   a) Biosystematics
   b) Secondary metabolites as characters in chemotaxonomy
   c) Cluster analysis in numerical taxonomy
Self-assessment Questions

1) a) i) ✔, ii) ✗, iii) ✗, iv) ✔, v) ✔, vi) ✔

b) Classical taxonomy follows an empirical approach synthesising a basic classification from observed facts. Modern taxonomy follows an interpretive approach improving upon the basic classification.

c) The most significant anatomical feature differentiating leaves of \( \text{C}_3 \) plants from \( \text{C}_4 \) plants is the absence of a *chloroenceymatous* bundle sheath in the former and its presence in the latter.

d) Sieve tube plastids are basically of two types, called S-type (accumulating starch) and P-type (accumulating proteins). These are recognisable by electron micrographic studies and different plant families have been characterised on the basis of this information. It has also been possible to understand relationships amongst monocotyledons and dicotyledons using sieve tube plastid type as evidence.

2) a) i) In Thallophytes, the zygote directly develops into a new plant or it produces spores which develop into new plants. In Embryophytes, the zygote first develops into an embryo from which the new individual plant is then formed.

ii) In monoecytedons the mature embryo has one cotyledon, while in dicotyledons it has two.

b) List any six characters from Table 7.2.

c) i) There is a high degree of correlation amongst embryological characters.

ii) Due to less variability in floral characters, embryological characters, show stability.

iii) Embryological characters are not affected by ecotypic variation and they remain unchanged.

d) Genera Families

i) *Butomus* i) Loranthaceae

ii) *Daphniphyllum* ii) Podostemaceae

iii) *Esocarpus* iii) Ranunculaceae

or any other genus or family in which embryological characters have been used for taxonomic purposes.

3) a) i) Basic chromosome number refers to the basic set of genetic information in the chromosomes of an individual of a species or a polyploid series.

ii) Haploid chromosome number is the gametic chromosome number present in the sex cells or the gametes.

iii) Diploid chromosome number is the somatic chromosome number usually seen in the vegetative cells of an individual.

b) Diploid chromosome number in:

i) Rice \( 2n = 24 \), ii) Potato \( 2n = 48 \), iii) Tea \( 2n = 30 \), iv) Coffee \( 2n = 44 \), v) Mango \( 2n = 40 \), vi) Onion \( 2n = 16 \)

c) i) The **centromere** is located in between the short arm and the long arm of the chromosome.

ii) It is located in the middle of the two equal arms of the chromosome.

iii) It is located at the tip of the arm of the chromosome.

d) The **karyotype** refers to the appearance of the basic chromosome set (genome) under the light **microscope**. It tells us about the number of chromosomes, their different types and their relationship with each other. This information can be compared for cytotaxonomic purposes.

e) **Genome analysis** is the study of chromosome pairing in diploid hybrids. It helps in the investigation of polyploids for determining the ancestral genomes and this information is used for ascertaining taxonomic relationships.
4) a) i) Chemical characters are stable
   ii) They are unambiguous
   iii) Chemical characters are not easily changeable.

   b) i) Directly visible chemical constituents such as starch grains.
   ii) Secondary metabolites such as phenolic compounds, alkaloids, etc.
   iii) Semantides or information carrying molecules such as DNA, RNA, or proteins.

   c) Proteins can be analysed by gel-electrophoresis or by serological methods. The genus *Triticum* has been analysed by gel-electrophoresis, while the genus *Solanum* has been analysed by serological methods.

5) a) Numerical taxonomy is also called Neo-Adansonian taxonomy because it is based on the same basic taxonomic principles formulated by M. Adanson in the 18th century.

   b) Carefully read the Section 7.8.2 and rewrite the procedure in your own words.

   c) 'Operational Taxonomic Unit' or OTU is the basic unit of study in numerical taxonomy. It can vary with the nature of the material being investigated as well as the purpose of the investigation.

   d) Binary coding is two-state coding according to which every character studied can be analysed in 2 states viz, present (+) or absent (−); whereas multi-state coding analyses more than two states in which a particular character exists and each state is given a definite symbol or code.

   e) The data matrix basically presents taxonomic information in a tabular form for all the OTU's examined and all the characters studies. It also provides information for clustering of the OTU's.

   f) Cluster analysis is a process by which the OTU's are sorted out to form groups or clusters on the basis of their overall similarity. Similarity or dissimilarity coefficients are calculated by comparing each OTU with every other OTU and this is represented as a percentage. This information is used for cluster analysis in numerical taxonomy.

Terminal Questions

1) Taxonomists utilise information from many disciplines for synthesising classifications. This process is a continuous one. The material provided in this unit has briefly described the developments in modern taxonomy to elaborate the unending nature of systematic botany. You must carefully study the entire unit and write out an essay of about 1500 words to answer this question.

2) a) *Ranunculaceae 'Sensu lato'* refers to the broad concept in the taxonomy of the family *Ranunculaceae*. While *Ranunculaceae 'Sensu stricto'* refers to a restricted concept after one or more genera have been removed from the family and classified in a separate family, thus changing the circumscription of the family.

   b) The genus *Paeonia* was first classified in the family *Ranunculaceae* (broad circumscription) but later it was separated from this family *Ranunculaceae* giving it a restricted circumscription.
The origin of the hexaploid breadwheat *Triticum aestivum* from diploid ancestors has been established cytogenetically. *Triticum monococcum* and *Aegilops geniculata* both diploid species can hybridise and the hybrid can, by chromosome doubling give rise to a tetraploid wheat, *Triticum dicoccum.* This in turn can hybridise with another diploid species, *Aegilops squarrosa* and by doubling the chromosomes of the hybrid, the hexaploid wheat, *Triticum aestivum* is produced. In chemotaxonomy, protein gel-electrophoresis of the seed proteins from *Triticum dicoccum, Aegilops squarrosa,* and *Triticum aestivum* provide evidence to show that the hexaploid wheat arose by hybridisation.

4) Carefully read Section 7.6 for (a), 7.7.3 for (b) 7.8 for (c).

a) See Section 7.4
b) See Section 7.5.3
c) See Section 7.8.2, particularly the paragraphs on cluster analysis as in answer 5 f.