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Studies on the DNA Base Composition of Varying Higher Plants

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The structure of complementary nucleotides of the two chains of the DNA double helix, plays a fundamental role in the cell. The complementary relations between nucleotide pairs are important not only in the duplication of DNA, but in the transcription and translation of genetic information. The order of nucleotides within each polynucleotide chain differs among strains, species and genera, and it is the difference in nucleotide content and sequence that accounts for strain and species difference in information. It is now well established that all characteristics, both morphologic and metabolic, are under the direct or indirect control of the hereditary information residing in nucleic acids more specifically in nucleotide sequence of DNA molecules that make up the genes or hereditary determinants must have two supreme missions, e. g., genetic instruction and replication. These specificities of DNA molecules are attributed to their unique structure and sequence of four nucleotides possesing major purine and pyrimidine bases such as adenine(A), guanine(G), cytosine (C) and thymine(T). The genetic code which is ascribed to nucleotide sequence of DNA, is translated into amino acid sequence or protein synthesis. Since that specific proteins not only form many of the structural cellular components but, more importantly. control as enzymes most of the biosynthetic and metabolic events in living cells, the nucleotide sequence of DNA is proved to be the basic information site presiding the specific biochemical events and structures of living organisms. It is generally agreed that the content of DNA per cell is constant in the different tissues of same organisms (1), as well as the proportions of its purine and pyrimidine bases (2). And these base compositions do not vary regardless of physiological state of cells (3). It can be expected, however, the divergence of the base compositions among different organisms. In fact, the base composition of bacterial DNAs is extremely variable (2)(4)(5)(6), there are bacterial DNAs with base compositions from 28 to 78% G+C (7). Much more works have been done with the DNA of microorganisms than with that from other sources. For this group of organisms, in any taxonomy based upon phylogenetic considerations, molecular studies of the genetic meterial are of primary importance (7). Studies of bacterial DNA, particularly assays of base ratios, have proved extremely valuable for taxonomic purposes. It is also agreed that a wide variability exists among the DNAs of protozoa and invertebrates (8)(9)(10)(11)(12). In most cases, however,

the DNA base compositions of organisms classified together in a group are fairly similar. Analytical data available in references showed that DNA of the diatoms was of the high A-T type (13)(14), whereas that of algae of the high G-C type (13)(14)(15)(6). We examined the DNA base compositions of a wide range of animals and reported diversity of the DNA base proportions of invertebrates and existence of close relationship of base composition with other criteria of classification (16)(17). The DNA of all vertebrates has generally the similar base composition (12)(14). We previously reported the DNA base composition of several species of moss (*Bryophyta*) which was shown to be G-C type (18). The investigation of DNA base composition of higher plants, however, are scanty and fragmentary and it indicated that the variations in the DNA nucleotide composition in higher plants keep within narrow range as in higher animals (15). We already reported analytical data of the DNA base composition of Monocotyledons as higher plant and discussed its divergence and possible taxonomic value (19). We analyzed the DNA base composition of a wide variety of higher plants, as one of the series of our study concerning the DNA nucleotide composition of a very wide range of living matters and report the results in this paper.

Materials and Methods

The fresh tender leaves were carefully chosen for materials and fresh hair roots were also used for samples. Materials were first soaked in water for 20 minutes, and washed to get rid of contaminants. These soaking and washing were repeated with distilled water. The well drained materials were cut in proper size and cooled. The homogenization or grinding of materials was conducted in the cold in Waring blendor or in mortar with sea sand after adding 0.02 M Tris (0.4M sucrose-0.01 M NaCl-0.005 M EDTA) buffer solution pH 8.0 (*20*). The homogenates were filtered through several layers of cheeze cloth and the filtrates were spun at 700 g for 10 minutes. After washing with 0.02 M Tris-0.25 M sucrose solution pH 8.0, the nuclear pellets were then suspended in proper amount of saline-EDTA (0.15 M NaCl-0.1 M ethylenediamine-tetraacetate disod.) solution pH 7.4 adding sodium lauryl sulfate(SLS) solution to 1% final concentration. This entirety was again ground in the mortar in the cold with pyrex glass powder, followed by heating to 50°C for 20 minutes under constant stirring. These homogenates were added by $NaClO_4$ crystals to the final concentration of 1 M and agitated for 30 minutes, then centrifuged at 9.000 g for 10 minutes. After several applications of Sevag's procedure (21), the supernatant was gently mixed with two volumes of cold ethanol to precipitate crude DNA and placed in refrigerator for several hours. After sedimentation, the residue was washed several times with 70% ethanol and dried by successive washing with ethanol and ether in usual manner. This powder was then added by 1 N NaOH and incubated at 37°C for 18 hours. The solution, after cooling, was acidified by acetic acid to pH 4 and then added two volumes of cold ethanol, followed by allowing to precipitate DNA in the cold. The sediment was dissolved in 1 M NaCl solution and deproteinized by Sevag's method. This DNA solution was again adjusted to pH 4, and added by two volumes of cold ethanol to precipitate DNA and the DNA sediment was washed again by 70% ethanol and dried in usual manner.

Analysis of purine and pyrimidine bases

The purine and pyrimidine bases were sepa-

rated by paper chromatography according to Wyatt's method (22). DNA samples were hydrolyzed in small sealed pyrex tube with formic acid (98-100%) at 175°C for 40 minutes. Hydrolyzates were evaporated to dryness *in vacuo* and residues were dissolved in 1.0 N HCl and solutions were subjected to paper chromatography using Whatman No. 1 filter paper and HCl-isopropanol-H_2O (17+68→100) as developing solvent, then the separated spots of purine and pyrimidine bases on dried paper chromatograms were detected employing UV lamp (2537 Å) and cut off to be eluted with 0.1 N HCl solution. Each eluate was subjected to determination of optical absorbancy at each maximum absorption as well as at 290 mμ as internal reference. The amounts of each base were calculated as moles using each molar extinction coefficient (23).

Results

Analytical data of the DNA bases of various higher plants (62 species) were presented in Table I and the G-C% distribution of DNA of varying species in each group was summarized in Figure I.

I. Cryptogams

The DNA base compositions of leaves of gingko (*Ginkgoceae*) and larch (*Abietaceae*) are 31 and 37 G-C mole% respectively, which are the same values of corresponding pollens that we previously reported (18).

II. Phanerogams

Salicaceae (2 species): The DNA of *Salix* and *Populus* has the same 36 G-C %.

Papaveraceae (2 species): The DNA of *Papaver* and *Chelidonium* contains the same G-C % of 34.

Betulaceae (1 species): *A. tinctoria Sarg.*.....35 G-C%.

Rosaceae (3 species): Apple, wild rose and *Kerria japonica* of this group have the same 37 G-C% of DNA.

Brassicaceae (5 species): The DNA G-C content of these species is 36-38%.

Fabaceae (15 species): These plants have a relatively broad spectrum of G-C % of DNA, but most of them lie in 32-36 G-C% except their much higher value (40-43%) in two specices of clover (*Trifolium*).

Apiaceae (4 species): These species have relatively lower DNA G-C% of 30-32, as compared to that of other higher plants.

Solanaceae (9 species): The seven species of *Solanaceae*, such as egg plant, tomato, ground cherry, red pepper, etc., contain the same 33 G-C % of DNA, whereas the DNA of 2 other species (*Tabacum* and *Lycium*) has distinctly high G-C % of 41. If it proves to be true, the conventional taxonomic criteria can be challenged.

Labiatae (1 species): *L. amplexicaule*.....32 G-C%.

Cucurbitaceae (7 species): The seven species of this group have a narrow range of G-C content (33-35%), as that of *Asteraceae*.

Asteraceae (11 species): The DNA of 11 species of this class has 33-36 G-C%. As indicated avove, the DNA of many higher plants has no great divergence of G-C content (30-43%) and the DNA base composition of a majority of higher plants we examined, keeps a narrow range of G-C spectrum (32-38%). But the DNA base composition is similar in species under the same class or group and in closely related species even in higher plants. It is, however, noteworthy to finding that the species of same group could be markedly distinct from viewpoint of DNA G-C content, and *Solanaceae* might thus be separated into two categories by G-C content of DNA.

Table 1. DNA base compositions of higher plants

Name	A	T	G	C	MC	$\frac{A+T}{G+C+MC}$	$\frac{G+C+MC}{A+T}$	(G+C) mole%
	molecules %							
Ginkgoaceae								
Ginkgo biloba L.	34.2	34.5	15.6	13.0	2.6	2.19	0.46	31
Abietaceae								
Larix kaempferi Sargent	31.5	31.8	18.4	15.0	3.2	1.73	0.58	37
Salicaceae								
Salix gracilistyla Miq.	32.2	32.0	17.8	14.8	3.0	1.80	0.55	36
Populus alba L.	32.0	31.8	18.0	15.4	2.6	1.77	0.56	36
Betulaceae								
Alnus tinctoria Sargent	32.5	32.1	17.6	15.3	2.3	1.83	0.54	35
Papaveraceae								
Papaver Somniferum L.	32.9	32.9	17.1	13.3	3.7	1.92	0.52	34
Chelidonium sinensis DC.	32.5	32.8	17.1	13.7	3.4	1.91	0.52	34
Brassicaceae								
Brassica campestris L. var. Pekinensis Makino	32.0	31.6	18.1	15.1	2.9	1.75	0.57	36
Brassica cernua Hemsi	31.7	31.3	18.4	15.4	2.9	1.71	0.58	37
B. oleracea L. var. Capitata L.	32.3	31.5	17.9	14.1	3.9	1.77	0.56	36
Raphanus acanthiformis Moor. var. raphanistroides Makino	31.6	31.7	18.5	15.3	2.6	1.73	0.58	37
Capsella Bursa-pastoris Medicus var. triangularis Grun	31.1	31.1	19.1	16.2	2.3	1.65	0.61	38
Rosaceae								
Malus pumila Mill	31.8	31.5	18.3	16.1	2.1	1.73	0.57	37
Rosa polyantha S. & Z.	31.5	31.5	18.4	15.4	3.0	1.71	0.58	37
Kerria japonica DC	31.7	31.4	18.4	15.1	3.3	1.71	0.58	37
Fabaceae								
Phaseolus angularis Wight	34.0	32.8	16.5	13.8	2.7	2.02	0.49	33
P. nipponensis	33.4	33.4	16.5	14.5	1.9	2.02	0.49	33
P. aureus Roxb	33.8	33.9	16.1	12.1	3.8	2.10	0.47	32
Glycine max Merr.	32.8	32.6	17.1	14.3	3.0	1.90	0.53	35
G. ussuriensis R. & M.	33.5	33.2	16.6	13.2	3.4	2.01	0.50	33
Arachis hypogaea L.	33.6	33.6	16.2	13.1	3.2	2.06	0.48	33
Pisum arvense L.	32.7	31.3	18.2	13.7	3.9	1.78	0.56	36
Cassia nomame S. & Nakai	32.5	33.0	17.0	14.0	3.3	1.90	0.52	34
Sophora angustifolia S. & Z.	33.5	33.9	16.2	14.8	1.3	2.08	0.48	32
Trifolium repens L.	30.4	29.7	19.9	15.4	4.3	1.51	0.66	40
Trifolium pratense L.	28.2	28.5	21.6	17.5	4.0	1.31	0.76	43
Robinia Pseudo-Acacia L.	31.3	30.8	18.9	16.0	2.8	1.64	0.61	38
Wistaria japonica S. & Z.	33.7	33.6	16.2	14.5	1.7	2.06	0.48	33
Styphnolobium japonicum Schott	33.8	33.6	16.3	13.4	2.7	2.07	0.48	33
Alidizzia julibrissin Durazz	32.4	32.5	17.6	14.0	3.4	1.85	0.53	35
Apiaceae								
Oenathe Stolonifera (Rox) DC	34.8	34.9	15.1	11.1	3.8	2.31	0.43	30
Petroselinum sativum Hoffm. var. japonicum Koidzumi	35.1	34.8	14.9	12.5	2.5	2.33	0.43	30
Coriandrum sativum L.	34.0	33.8	16.0	13.0	3.0	2.10	0.47	32

Name	A	T	G	C	MC*	$\frac{A+T}{G+C+MC}$	$\frac{G+C+MC}{A+T}$	(G+C) mole%
	molecules %							
Apium graveolens L.	33.9	34.1	16.3	12.2	3.2	2.14	0.47	32
Solanaceae								
Solanum melongena L.	33.7	33.3	16.5	12.9	3.4	2.04	0.49	33
S. nigrum L.	33.8	33.5	16.3	13.7	2.7	2.05	0.48	33
S. tuberosum L.	33.1	33.6	17.1	13.5	3.0	2.00	0.50	33
Lycopersicon esculentum Mill	33.5	33.6	16.1	13.6	3.0	2.05	0.49	33
Capsicum annuum L.	33.0	33.7	16.6	14.4	2.2	2.00	0.50	33
Physalis Francheti Mast. var. Bunyardii Makino	33.2	33.8	16.3	14.0	2.5	2.03	0.49	33
Datura alba Nees	34.1	33.8	15.9	14.2	1.7	2.12	0.47	33
Nicotiana Tabacum L.	29.5	29.4	20.5	15.6	4.8	1.43	0.70	41
Lycium chinense Mill	29.5	29.2	20.2	17.4	2.9	1.43	0.70	41
Cucurbitaceae								
Cucurbita moschata Poir. form. Toonas Hara	32.6	33.0	17.2	15.8	1.3	1.91	0.52	34
Cucumis sativus L.	32.5	32.1	17.6	14.8	2.8	1.83	0.54	35
C. Melo L.	33.5	33.2	16.9	15.1	2.2	1.92	0.52	34
Lagenaria siceraria Standl	33.0	33.5	16.8	15.0	1.6	1.98	0.50	34
Luffa cylindrica Roem	33.5	33.4	16.5	14.5	1.9	2.02	0.49	33
Citrullus Battich Forsk	33.6	33.6	16.3	14.0	2.3	2.05	0.49	33
Momordica charantia L.	32.0	32.9	17.5	15.6	1.7	1.85	0.54	35
Asteraceae								
Chrysanthemum coronarium L.	33.2	32.9	16.8	14.3	2.6	1.96	0.51	34
C. morifolium Ram	32.4	31.7	17.8	13.9	4.0	1.79	0.56	36
C. lavandulae solium Makino	33.0	33.0	16.9	13.5	3.3	1.94	0.51	34
C. boreale Makino	32.8	32.4	17.3	14.1	3.1	1.88	0.53	35
Lactuca Scariola L.	32.9	33.7	16.4	15.6	1.2	2.00	0.50	33
Lactuca Bungeana Nakai	32.8	32.7	17.1	15.0	2.2	1.90	0.52	34
Artemisia asiatica Nakai	33.0	33.5	16.9	13.0	3.3	2.00	0.50	33
A. selengensis Turcz	32.9	32.3	17.6	13.9	3.1	1.87	0.53	35
Taraxacum platycarpum Dahlst	32.8	32.7	17.3	14.9	3.4	2.00	0.50	33
Helianthus annus L.	33.1	33.0	17.4	14.2	2.6	1.90	0.51	34
Aster tartaricus L.	32.9	32.9	17.1	13.5	3.6	1.90	0.52	34

* MC……Methyl-cytosine.

Discussion

We previously made extensive analysis of DNAs of a wide range of microorganisms and observed the base compositions of bacterial DNA being extremely variable, and established the valuable taxonomic significance of DNA nucleotide compositions in microorganisms (2). This fact was confirmed later by other investigators (4)(5)(7)(24). We also examined the DNA base compositions of a very wide range of animals, and reported the diversity and significant taxonomic value of the DNA base proportions in invertebrates (25)(26)(17). It is generally believed that the DNA of almost all vertebrates has essentially very close base composition. We previously reported the analytical data of DNA base composition of many species of Monocotyledon and discussed its divergence and possible taxonomic significance(19).

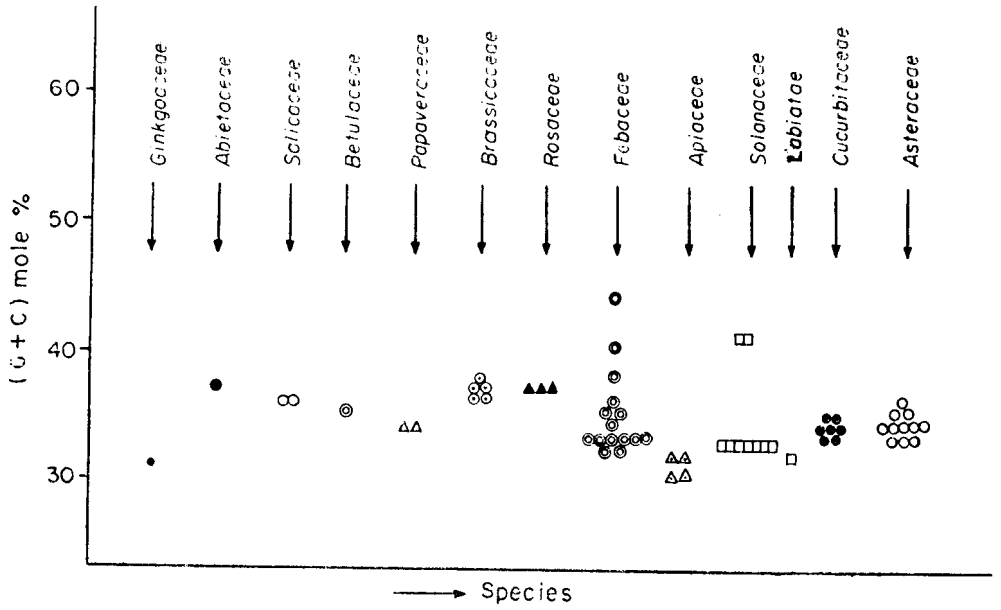

Figure 1. The distribution of G-C mole % of DNA in various species of higher plants.

Among the algae thus far studied, the diatoms manifest the mean 37-40 G-C% in the DNA, whereas 54-64 in green algae and 59 in one brown alga (13)(14)(15). Our analytical data (18) also proved that the DNA of 5 species of moss (*Bryophyta*) was of the G-C type (53-58 G-C%), as other algae.

As mentioned above, there exists no great divergence of G-C content (30-43%) in the DNAs of various higher plants as reported in our previous paper(19) and the DNA base composition of almost all higher plants we examined, lies in a narrow range of G-C spectrum (32-38%). The DNA base composition is almost similar in species under the same group, as shown especially in *Salicaceae* (2 sp.), *Papaveraceae* (2 sp.), *Brassicaceae* (6 sp.), *Rosaceae*(3 sp,). *Apiaceae* (4 sp.), *Cucurbitaceae* (7 sp.), and *Asteraceae* (11 sp.),

The available data for higher plants also indicate that the variation in the DNA nucleotide composition in higher plants keep within the same range as in higher animals (27).

Among the higher plants we examined, 4 species have the lowest DNA G-C content (30-32%) which is equivalent to that of *Alliaceae* (29-33 G-C%) of Monocotyldon, we previously reported (19).

The DNAs of 9 species of *Solanaceae* are distinctly divided into two groups containing G-C % of 33 and 41 each, as shown in Fig. I, and its difference amounts to about 7%. Both of *Nicotiana* and *Lycium*, having the same G-C content (41%), may not be included in *Solanaceae* in terms of DNA base composition, but it can be finally decided only by their base sequence homology. The DNA base composition is only a preliminary guide to relationship and base sequence homology(7)(12). The DNAs of 15 species of *Fabaceae* manifest a relatively broad spectrum of G-C content (32-43%), but most of them (12 sp.) contain 32-36 G-C%, except two species of clover (*Trifolium*) with its much higher value (40-43%). This divergence between the clovers and other members, however, cannot be fully explained relative to its significance without examining the base sequence homology of DNA.

It is of interest and indispensable to assess base sequence homology of DNA of these two groups using hybridization approach (31)(32)(33)(34).

Base sequence homologies are detectable in many mammals, but no sequence homology can be found between the vertebrate and bacterial DNAs. Generally, the extent of base sequence homology is in good agreement with accepted phylogenetic relationships. But no attempt was made to examine the extent of base sequence homology among higher plants.

There also reported that certain nucleotide segments of the DNA of higher organisms were repeated hundreds of thousands of times and such repeated sequences occurring widely and probably universally in the DNAs of higher organisms (34). In general, more than one-third of the DNA of higher organisms is made up of sequence which recur anywhere from a thousand to a million times per cell. Thus, the genetic material is not a collection of different and unrelated genes. A large part is made up of families of sequence in which the similarity must be attributed to common origin. We do not know at present time whether or not the occurrence of many repetitive nucleotide sequences of higher organisms is ascribed to the fact that within highly evolved groups of organisms, such as the vertebrates and higher plants, little or no spread in the mean base composition of DNA exists.

Our data also showed relatively higher content of 5-methyl-cytosine in DNA of higher plants than that of fishes and this is in good agreement with the data of Belozersky (27).

Nonchromosomal DNA such as that of chloroplasts and mitochondria (20)(35), was not taken into consideration in the present study. These nonchromosomal DNAs will be reported elsewhere (36).

Summary

The DNAs were extracted and purified from varying higher plants, and the plants we examined are as follows.

Ⅰ. Cryptogams	
Ginkgoaceae	1 species
Abietaceae	1 species
Ⅱ. Phanerogams	
Salicaceae	2 species
Betulaceae	1 species
Papaveraceae	2 species
Brassicaceae	5 species
Rosaceae	3 species
Fabaceae	15 species
Apiaceae	4 species
Solanaceae	9 species
Labiatae	1 species
Cucurbitaceae	7 species
Asteraceae	11 species

The DNA bases were analyzed chemically and the following results were obtained.

Ⅰ. **Cryptogams**

The DNA base compositions of leaves of gingko (*Ginkgoaceae*) and larch (*Abietaceae*) are 31 and 37 G-C % respectively, showing the same values of the corresponding pollens.

Ⅱ. **Phanerogams**

Salicaceae; The DNA of *Salix* and *Populus* has the same 36 G-C%.

Papaveraceae; The DNA of *Papaver* and *Chelidonium* contains the same 34 G-C%,

Betulaceae: A. tinctoria…… 35 G-C%.

Rosaceae: The DNA of three species has the same 37 G-C%.

Brassicaceae: The DNA G-C contents of these species are 26-38%.

Fabaceae: Most of these species possess 32-36 G-C% of DNA except higher one of 40-43% in two species of clover (*Trifolium*)

Apiaceae: The DNA of these species has lower G-C% of 30-32, as compared to that of

other higher plants.

Solanaceae: The DNA of seven species of this group has the same 33 G-C%, while that of 2 other species (*Tabacum and Lycium*) has much higher G-C % of 41.

Labiatae: L. amplexicaule…… 32 G-C %

Cucurbitaceae: The DNA of these species has a narrow range of G-C content such as 33-35%.

Asteraceae: The DNA of 11 species of this group has 33-36 G-C%.

The DNA of all higher plants examined, contains 5-methyl-cytosine as minor base. Thus, the DNA of varying higher plants has no great divergence of G-C content (30-43%) and the DNA base composition of a majority of higher plants we examined, keeps a narrow range of G-C spectrum (32-38%). But the DNA base composition is similar in species under the same class or group and in closely related species even in higher plants. And it is noteworthy to mentioning that some species of same group are markedly different from its other members in DNA G-C content, in certain classes, such as *Solanaceae and Fabaceae.*

The classical taxonomic criteria was discussed in special reference to such a divergence of DNA base composition in the species under the same class or group. It should be noted that a similarity of DNA base compositions among different species does not mean its sequence homology.

<국문초록>

各種高等植物의 DNA 鹽基組成에 關한 硏究

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各種 高等植物 13科 62種에서 主로 新鮮한 幼葉을 擇하고 또는 때로 幼毛根을 使用하여 DNA를 抽出, 分離精製한後 主로 化學的 方法으로 paper chromatography 法을 利用하여 DNA의 purine, pyrimidine 鹽基를 分析하였다.

얻은 結果를 要約하면 다음과 같다.

Ⅰ. 隱花植物

銀杏(*Gingko*)과 落葉松(*Lorix*)잎의 DNA 鹽基組成을 보면 各各 31과 37의 guanine+cytosine mole %(以下 G-C%로 略記함)로 前報에서 發表한 銀杏 및 落葉松의 花粉의 DNA 鹽基組成과 同一하다.

Ⅱ. 顯花植物

버드나무科(*Salicaceae*) (2種):

갯버들(*Salix*)과 銀白楊나무는 DNA의 G-C%가 同一하여 36이다.

양귀비꽃科(*Papaveraceae*) (2種):

이 科에 屬하는 양귀비(*Papaver Somniferum*)와 애기똥풀(*Chelidonium*)은 DNA의 鹽基組成이 同一하여 G-C %가 34이다.

자작나무科(*Betulaceae*) (1種):

산오리나무(*A. tinctoria*)에서는 DNA의 G-C 含量은 35%이다.

장미科(*Rosaceae*) (3種):

이 科에 屬하는 3種의 植物에 있어 DNA 組成은 同一한 37 G-C %이다.

배추科(*Brassicaceae*) (5種):

이 科에 屬하는 植物은 DNA의 G-C %는 36~38이다

콩科(*Fabaceae*) (15種):

이 科에 屬하는 大部分의 植物들은 DNA의 G-C%는 32~36이나, 2種의 clover의 그것은 높아 40~43%이나 된다.

미나리科(*Apiaceae*) (4種):

이 科의 植物은 DNA의 G-C %는 30~32로서 딴 高等植物에 比하여 얕다.

가지科(*Solanaceae*) (9種):

分析한 가지科 植物 中 7種에 있어서는 DNA의 G-C %는 同一하여 모두 33이지만 2種의 딴 植物 即 담배와 枸杞子나무에서는 이 보다 훨씬 높은 41 G-C %를 차지하고 있다.

唇形科(*Labiatae*) (1種):

광대나물(L. *Amplexicaule*)의 DNA는 32 G-C %을 含有하고 있다.

박科(*Cucurbitaceae*) (7種):

7種의 植物에 있어 DNA의 G-C 量은 33~35%이다.

국화科(*Asteraceae*) (11種):

이 種에 屬하는 植物들은 DNA의 G-C 量은 33~36%이다.

以上 調査한 모든 高等植物에 있어 minor 鹽基인 5-methyl-cytosine이 發見되였으며 그 含量은 魚類의 그것보다 높다.

上記한 바와 같이 高等植物의 DNA 鹽基 組成을 보면 大部分이 G-C %가 32~38%로써 微生物이나 algae 等의 下等生物에서와 같은 큰 差異를 볼 수 없는 것이 特徵이다.

또한 同一한 科나 分類學上 類似한 種에 屬하는 高等植物에서는 DNA의 G-C %은 거이 비슷하다.

그러나 어떤 科(*Solanaceae, Fabaceae*)에 있어서는 同一科에 屬하는 植物들을 DNA의 G-C%로 보아 두 group로 區別할 수 있다. 이와 같은 DNA 鹽基組成의 差異가 지니고 있는 意義를 在來式 分類學的 問題와 關聯하여 考察하였다. 그러나 DNA 鹽基組成이 同一한 것이 鹽基配列의 homology를 意味하는 것은 아니다.

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