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A morphometric analysis of infraspecific taxa within the *Ixeris chinensis* complex (Asteraceae, Lactuceae)

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Abstract. Morphometric methods were used with 40 morphological characters from each of 110 individuals collected from 11 populations of the *Ixeris chinensis* complex to test hypotheses regarding infraspecific taxa. Individuals of the nearest relative *I. tamagawaensis* were included as an outgroup. To utilize structual associations of the original data and the cumulative values of character variation, a modified data set was generated by matching factor scores with the large original data set. As a result, the original data was reduced to about 10% of its original size. The modified data also emphasized the cumulative values of character variations. Structural associations among characters measured, however, were not significant for most factors extracted even though some obvious trends appeared. Relationships between cumlative values of variation and taxa in the complex are discussed based on the results of the canonical discriminant function analysis, ANOVA, multiple comparison test, and cluster analysis, using the modified data. This study supports Kitamura's (1956) classification of infraspecific taxa in the *I. chinensis* complex. Given that there is no overlap of cumulative values of variation between the species complex and *I. tamagawaensis*, there is probably a 75% character overlap within the complex.

Keywords: *Ixeris chinensis* complex; Infraspecific taxa; Morphometric analysis.

Introduction

The term "species complex" has frequently been applied to flowering plants, but its origin is obscure. It has often been used to describe species aggregations made up of infraspecific taxa such as microspecies, agamospecies, and semispecies (e.g. Fosberg, 1942; Sylvester-Bradley, 1952; Davis and Heywood, 1963; Northington, 1976; Grant, 1981). Several criteria have been used to establish groups of infraspecific taxa, including their morphological discreteness, ecological differences, genetic divergence, and natural reproductive isolation (e.g. Davis and Heywood, 1963; Gilmartin, 1974; Grant 1981; Stuessy, 1990). Morphological discreteness plays a major role in the early stage recognition of infraspecific taxa. A practical difficulty here is that almost all morphological characters and/or character states used for evaluating infraspecific taxa are only slightly differentiated from one another and usually show considerable overlap. Therefore the identification of infraspecific taxa and their hierarchical arrangement within a complex of species usually requires a combination of several morphological characters, especially if other forms of data are not available.

The *Ixeris chinensis* complex (Asteraceae, Lactuceae) is distributed from Siberia to Japan, including Korea, Taiwan, and China (Pak et al., 1997). This complex has a basic chromosome number of eight (Pak and Kawano, 1990), but also contains diploids (2n = 16), triploids (2n = 24), and tetraploids (2n = 32) (Ishikawa, 1921; Babcock et al., 1937; Chuang et al., 1962; Hsu, 1967, 1970; Peng and Hsu, 1978; Pak and Kawano, 1990) and exhibits sympatry and/or allopatry among the ploidy (e.g. Pak et al., 1995, 1997). The diploid plants observed are sexual while triploids and tetraploids are asexual. Many complicated variations in external morphology have been reported in hybrids between sexual and usually asexual plants, which can revert to sexual reproduction under some conditions (e.g. Harlan and de Wet, 1963; Yahara, 1983, 1990). Within this complex a complicated morphological overlap, without any discontinuities, has led to taxonomic difficulty (Kitamura, 1956; Pak and Kawano, 1992; Kim et al., 1999). Kitamura (1956) classified this complex into the three subspecies *Ixeris chinensis* (Thunb.) Nakai subsp. *chinensis*, subsp. *strigosa* (H. Lév. et Vaniot) Kitamura, and subsp. *versicolor* (Fischer) Kitamura. Tzvelev (1964) classified it as three different species in a different genus, *Ixeridium chinensis* (Thunb.) Tzvelev, *I. strigosum* (H. Lév. et Vaniot) Tzvelev and *I. gramineum* (Fisch.) Tzvelev. Pak and

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Kawano (1992) classified it as two subspecies of one species and one different species in the same genus; *Ixeris chinensis* subsp. *chinensis* and subsp. *versicolor* and *I. strigosa* (H. Lév. et Vaniot) Pak et Kawawo. The taxonomic resolution of this complex, therefore, remains uncertain.

In an attempt to resolve difficulties caused by morphological overlap, multivariate methods have increasingly been applied, especially in species complexes of flowering plants (e.g. Sokal and Sneath, 1963; Gilmartin, 1967; Jensen and Eshbaugh, 1976; McNeil, 1984; Jensen et al., 1993). Several multivariate analyses are applicable to this problem, and the adoption of different statistical procedures in dealing with such problems is common. The classificatory schemes proposed for the *Ixeris chinensis* complex based on morphological characters can be tested using multivariate statistical analysis of the huge amount of raw data that can be collected from such a morphologically variable group. As a first step in such a process, a factor analysis capable of regenerating reduced data might be effective in order to yield a clear output in later treatments.

This study aims to establish a theoretical model for the categories of infraspecific taxa and to provide taxonomic resolution of the *Ixeris chinensis* complex based on morphometric analyses. We will not only discuss categories at the level of both species and infraspecies, but we will also test the taxonomic schemes previously proposed for this complex.

Materials and Methods

Specimens of the *Ixeris chinensis* complex were selected from among 81 populations, chosen on the basis of ploidy and geographic distribution (Pak et al., 1997, Figure 1). Twenty individuals from two populations of *I. Tamagawaensis* (Makino) Kitamura were collected near Tamagawa, Ozaku, Oome-shi, Tokyo, Japan and were added to the analysis because this species is regarded as the nearest relative of *I. chinensis* (Kitamura, 1956; Pak and Kawano, 1990, 1992, Figure 1). The complex has generally been recognized as comprising three taxa although their taxonomic category and nomenclature differs among researchers (Kim et al., 1999). To begin with, Kitamura's (1956) two subspecies of *I. chinensis* were recognized, with subspecies *chinensis* only being diploid and subspecies *strigosa* being both triploid and tetraploid. Individuals of the triploid and tetraploid populations of *I. chinensis* subsp. *strigosa* were identified and separated for morphological analysis. Kitamura's (1956) *Ixeris chinensis* subsp. *versicolar,* distinguished within the complex by having a different corolla color and branched roots, is restricted to North Korea, Manchuria, and Russia, and was omitted here due to lack of sufficient material for comparison. Three representative populations of each ploidy out of the 81 populations documented (Pak et al., 1997) were selected, and ten specimens from each population were investigated. The specimens were obtained from field collections and from the following herbaria: KYO, SKK, SNAU, TI, TNS, KNU, Chonnam National University, and Kangwon National University (Figure 1).

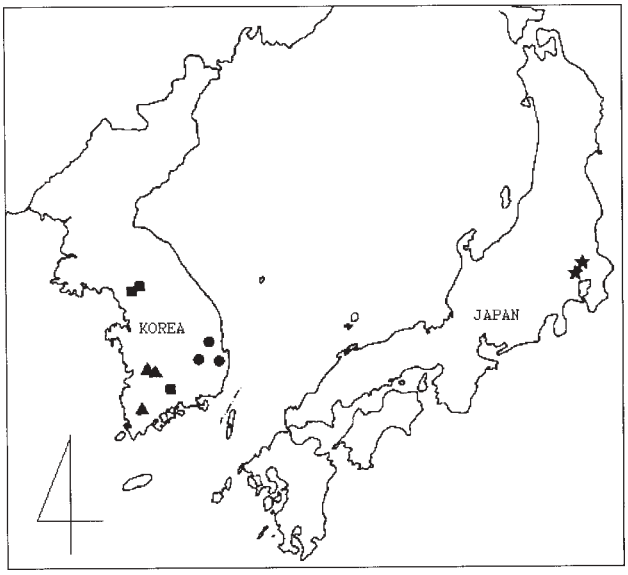

Figure 1. Map showing collecting localities of the *Ixeris chinensis* complex and its nearest relative *I. tamagawaensis.* ●=*I. chinensis* subsp. *chinensis* (Mt. Keumo, Janghang-ri and Mokye-ri in Kyungbuk); ▲=*I. chinensis* subsp. *strigosa* (triploid) (Moraejae and Malgoljae in Chonbuk, Damyang-up in Chonnam); ■=*I. chinensis* subsp. *strigosa* (tetraploid) (Is. Nami and Taebong-ri in Kyunggi, Sanchong-up in Kyungnam), ★=*I. tamagawaensis* (near Tamagawa in Tokyo).

Forty characters were scored for the morphometric analysis (Table 1). They were measured using a digimatic caliper and hand lens. Of these characters, radical leaf blade length (RLL) was measured from three leaves in order of size among those attached at the base; internode length (INL) was measured at the second node up from the base; length and width of inner-phyllary (IIL and IIW) were measured on three randomly selected leaves; length and width of the outer-phyllary (OIL and OIW) were measured on three replicates; and length and width of the achene (ACL and ACW) were measured on one mature specimen.

Factor analysis was used to interpret structural associations among the 40 morphological characters, as well as to reduce the large amount of data measured. Factors >1 in eigenvalue were selected and scored. An analysis of variance of the modified data, generated by matching the factor score (Σfactor score coefficients of character measurement to factor 1 × standard scores of taxa to characters) of the original data, was performed to determine whether significant differences among members of the *I. chinensis* complex and its nearest relative *I. tamagawaensis* exist or not. Multiple comparison by four different methods, Duncan, Tukey-HSD, Tukey-B and Scheffe test, was conducted on the modified data for the first two factors. Canonical discriminant functions were also conducted to ordinate relationships between variables

Table 1. Morphological characters of the *Ixeris chinensis* complex and its nearest relative *I. tamagawaensis* evaluated in the numerical analyses.

PLH = plant height
FRLL = first radical leaf blade length
FRLWF = first radical leaf blade width in tooth free region
FRLWT = first radical leaf blade width in toothed region
SRLL = second radical leaf blade length
SRLWF = second radical leaf blade width in tooth free region
SRLWT = second radical leaf blade width in toothed region
TRLL = third radical leaf blade length
TRLWF = third radical leaf blade, width in tooth free region
TRLWT = third radical leaf blade width in toothed region
NCL = number of cauline leaves
CLL = cauline leaf length
CLWF = cauline leaf blade width in tooth free region
CLWT = cauline leaf blade width in toothed region
NFPI = number of capitula per plant
NIN = number of internodes
INL = internode length
NOI = number of outer-phyllaries
FOIL = first outer-phyllary length
FOIW = first outer-phyllary width
SOIL = second outer-phyllary length
SOIW = second outer-phyllary width
TOIL = third outer-phyllary length
TOIW = third outer-phyllary width
NII = number of inner-phyllaries
FIIL = first inner-phyllary length
FIIW = first inner-phyllary width
SIIL = second inner-phyllary length
SIIW = second inner-phyllary width
TIIL = third inner-phyllary length
TIIW = third inner-phyllary width
IVL = phyllary length
IVW = phyllary width
NFPC = number of florets per capitulum
FLL = floret length
FLW = floret width
ACL = achene length
ACW = achene width
PAL = pappus length
NPPF = number of pappus setae setae per floret

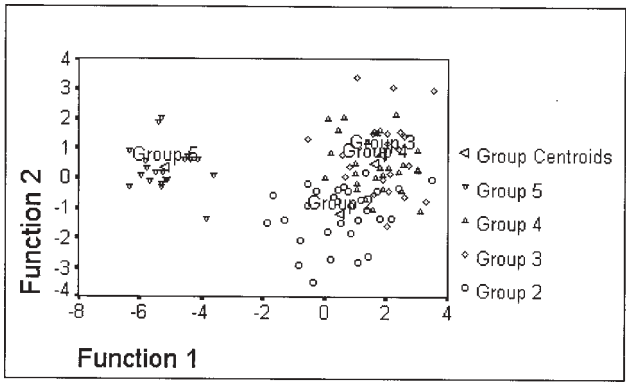

Figure 2. Canonical discriminant functions using the four factor scores of the *Ixeris chinensis* complex and its nearest relative *I. tamagawaensis* (Group 2: *I, chinensis* subsp. *chinensis*; Group 3: *I. chinensis* subsp. *strigosa* (triploid); Group 4: *I. chinenisis* subsp. *strigosa* (tetraploid); Group 5: *I. tamagawaensis*).

and cumulative values of variation produced by factor scores. A cluster analysis using average linkage was performed on the modified data to evaluate similarity among variables and to identify taxa. All significance levels were determined at $p \leq 0.05$. The numerical analysis was performed using SPSS for MS WINDOWS, Version 6.1.

Results

For the morphometric analysis of the *Ixeris chinensis* complex, 40 characters of external morphology were measured from each of 110 individuals collected from 11 populations. After a factor analysis, the 10 factors that had eigenvalues that summed to > 1 were extracted (Table 2). Total cumulation of the extracted factors accommodated 78.1% of variation in the original data. These factors were characterized with respect to morphological characters that had high absolute values for factor loading. Factor loadings indicate the overall importance of each character, while eigenvalues for each factor indicate the portion of total variance accounted for by that factor. In distinguishing high factor loading, loading with values ≥ 0.5 of the absolute value were arbitrarily adopted as the biological standard.

The fifth to tenth factors contained only one or no characters with a factor loading > 0.5 in absolute value. Furthermore, these factors had eigenvalues < 2, and accounted for only 16.4% of the original data (Table 2). The first four factors, however, contained several morphological characters with factor loadings > 0.5 in absolute value. Each of these factors also had high eigen values (> 3), and they accounted for about 60% of the original data (Table 2). Accordingly, the focus is mostly on aspects of the first four factors.

Factor 1 had high loadings for 14 characters; first, second and third radical leaf blade length in the tooth region (FRLWT, SRLWT, TRLWT), numbers of cauline leaves, internodes and outer-phyllaries (NCL, INL, NII), cauline leaf blade width in the tooth region (CLWT), first, second and third inner-phyllaries length (FIIL, SIIL, TIIL), involucre and achene length (IVL, ACL), and length and width of floret (FLL, FLW). The structural relationships among these characters were complex and scattered, but the factor was strongly influenced by several related groups of characters such as the length of radical leaves in the tooth region, the length of inner-phyllaries, and the length and width of florets (Table 2). Factor 2 had high loadings for 10 characters; plant height (PLH), first, second and third radical leaf blade length (FRLL, SRLL, TRLL), number of capitula per plant (NFPI), first, second and third outer-phyllaries length (FOIL, SOIL, TOIL), second outer-phyllary width (SOIW), and number of pappus setae per floret (NPPF). This factor was also difficult to circumscribe because of complex structural relationships among characters. However, two groups of characters, the lengths of radical leaves and outer-phyllaries, were characteristic of this factor (Table 2). Factor 3 had high loadings for two characters, the first and third outer-phyllaries

Table 2. Factors, eigenvalues and cumulative percentages obtained by factor analysis with 40 morphological characters from the *Ixeris chinensis* complex and its nearest relative *I. tamagawaensis*.

Character[a]	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5	Factor 6	Factor 7	Factor 8	Factor 9	Factor 10
PLH	0.47166	0.61231[b]	0.32087	-0.07271	0.00188	-0.31542	-0.09764	0.09391	0.12791	0.03675
FRLL	0.49631	0.57612[b]	0.48683	-0.02136	-0.10009	-0.12856	-0.08032	-0.03968	-0.22629	0.05732
FRLWF	0.06491	0.11049	0.07478	0.65560[b]	-0.28878	0.05489	0.07090	0.45424	0.10895	-0.01875
FRLWT	0.70044[b]	-0.12974	0.09602	0.08381	0.49635	-0.10491	-0.22397	0.05198	-0.09121	-0.00361
SRLL	0.42804	0.62339[b]	0.48664	-0.07041	-0.17335	-0.07436	-0.13748	-0.03251	-0.18354	0.08382
SRLWF	0.03415	0.21172	0.27652	0.68194[b]	-0.23523	0.10741	0.08731	0.21782	-0.06384	-0.15566
SRLWT	0.73143[b]	-0.16295	0.06753	0.16826	0.32792	0.08055	-0.22475	0.23300	0.07936	0.04892
TRLL	0.37770	0.63486[b]	0.43793	-0.10337	-0.14606	-0.01277	-0.14613	0.04034	-0.19756	0.12155
TRLWF	0.07242	0.15687	0.24693	0.68833[b]	-0.21734	0.18047	0.12887	0.27678	0.08182	-0.12936
TRLWT	0.67485[b]	-0.12580	0.08664	0.12158	0.50697[b]	-0.10565	-0.18738	0.07502	-0.09222	0.00036
NCL	-0.61687[b]	0.47107	0.17976	0.05906	0.12354	-0.04776	0.06912	-0.17728	0.34179	-0.09081
CLL	0.37409	0.43242	0.41358	0.17345	0.00364	-0.12241	0.14378	-0.50920[b]	0.04853	-0.10186
CLWF	0.11444	0.33327	0.19558	0.63121[b]	0.20243	0.02551	0.10976	-0.05385	0.12666	-0.10186
CLWT	0.59862[b]	-0.11551	0.34751	0.29936	0.32281	-0.02187	0.07037	-0.24854	0.04128	-0.20096
NFPI	-0.21889	-0.53508[b]	0.38094	0.22934	0.20364	0.17567	0.10741	-0.09802	-0.21722	0.10174
NIN	-0.50919[b]	0.46866	0.25153	0.02663	0.10020	-0.01830	0.10922	-0.26639	0.33720	0.14293
INL	0.28923	0.35174	0.02320	-0.25473	-0.07409	-0.44815	-0.21155	0.31432	0.31232	0.24738
NOI	-0.64240[b]	0.45564	0.07136	0.02704	0.03356	0.15632	-0.08737	0.10774	-0.05033	0.05086
FOIL	-0.06210	0.71338[b]	-0.49383	-0.07529	-0.15538	0.14985	-0.14425	-0.02433	-0.18354	-0.15911
FOIW	0.25804	0.34397	-0.59110[b]	0.18473	0.21418	-0.14604	0.02262	0.05330	0.16561	0.08786
SOIL	-0.02830	0.75456[b]	-0.49226	-0.05484	-0.06925	0.08117	-0.18637	-0.01855	-0.16079	-0.16526
SOIW	0.18154	0.52636[b]	-0.44223	-0.01340	0.32026	-0.05264	0.07603	0.10637	0.13579	-0.12069
TOIL	-0.14205	0.74776[b]	-0.49800	-0.05142	-0.04543	0.13013	-0.11215	-0.04716	-0.10557	-0.17059
TOIW	0.20787	0.45705	-0.59146[b]	-0.12926	0.05686	0.00407	-0.06430	0.06490	0.12820	-0.21775
NII	0.12968	0.04487	0.30927	-0.12925	0.03328	0.40584	-0.49649	-0.01160	0.22277	0.14435
FIIL	0.87070[b]	0.07627	-0.04122	-0.28798	-0.18372	0.13242	0.15679	-0.05553	0.10394	-0.03034
FIIW	0.16572	0.12852	-0.23337	0.41643	-0.08637	0.13980	0.31581	-0.14635	0.11663	0.54822[b]
SIIL	0.85989[b]	0.05927	-0.00775	-0.29265	-0.20529	0.15319	0.17250	-0.06980	0.11989	-0.03168
SIIW	0.18595	0.27573	-0.34933	0.07297	0.24679	0.06090	0.45694	0.07527	-0.35317	0.28206
TIIL	0.84319[b]	0.03773	-0.00946	-0.28608	-0.21702	0.15776	0.18568	-0.02989	0.13391	-0.05456
TIIW	0.19067	0.38466	-0.49125	0.22916	0.12805	-0.23021	0.18321	-0.03989	0.03816	0.14844
IVL	0.72644[b]	0.06298	0.06965	-0.34746	-0.02144	0.25087	0.01894	0.08852	-0.10611	-0.15559
IVW	0.30870	0.03907	-0.19927	0.51483[b]	0.11438	0.49390	-0.26545	-0.09476	0.07250	0.04928
NFPC	0.18015	-0.07497	-0.05192	-0.25975	0.15881	0.65395[b]	-0.00635	-0.08817	0.09505	0.18719
FLL	0.73575[b]	-0.22923	-0.21302	-0.04821	-0.30967	-0.05346	0.10376	-0.05735	0.14610	-0.03056
FLW	0.60534[b]	-0.28137	-0.14908	0.13875	-0.03812	0.06273	0.08193	0.08821	0.07892	-0.23209
ACL	-0.13537	0.17963	0.42411	-0.48127	0.30410	0.17987	0.43524	0.32128	0.04372	-0.12321
ACW	-0.39300	0.28957	0.34078	-0.51581[b]	0.27423	0.14545	0.33689	0.27918	0.03184	-0.08603
PAL	0.75819[b]	0.20086	-0.05858	-0.07834	-0.11083	-0.07568	0.20634	-0.04502	-0.00643	0.09127
NPPF	-0.38534	0.60582[b]	0.12061	-0.24646	-0.05554	0.16003	-0.10812	0.07386	0.25513	0.23950
Eigenvalue	8.93241	6.17121	4.08240	3.68078	1.82244	1.68541	1.54108	1.23595	1.07062	1.01916
Cumulative percent	22.3	37.8	48.0	57.2	61.7	65.9	69.8	72.9	75.6	78.1

[a]Characters correspond to those in Table 1.

[b]Factor loadings considered to be important to each factor.

width (FOIW, TOIW). These characters, therefore, were correlated with the width of outer-phyllaries, even though confidence in this relationship is lower because the second outer-phyllary was not included (Table 2). Factor 4 had high loadings for five characters; first, second and third radical leaf blade width in the tooth free region (FRLWF, SRLWF, TRLWF), cauline leaf width in the tooth free region (CLWF), and involucre width (IVW). These characters came from three different parts of the plant, and were apparently related to leaf width development. The character most strongly influencing this factor was the width of radical leaves in the tooth free region (Table 2).

To examine the relationship between variables and cumulative values of variation generated, a canonical discriminant function was ordinated with modified (compressed) data (Figure 2). All data for *Ixeris tamagawaensis* were clustered in a single group and clearly isolated by function 1 from the values of other variables. However, some data for *I. chinensis* subsp. *chinensis* and *I. chinensis* subsp. *strigosa* were not isolated from each other but overlapped to some extent in both function 1 and 2. For functions 1 and 2, triploid and tetraploid populations of *I. chinensis* subsp. *strigosa* overlapped almost completely (Figure 2).

In order to estimate whether there are significant differences within variables, an analysis of variance was performed on the modified data (Table 3). The taxa differed significantly in the first three factors, those with the highest eigenvalues and covering about 50% of the initial data. However, they did not differ significantly in factors 4, 6, 7, 9 and 10, which appears to reduce the implications that can be drawn from the original data (Table 3).

The analysis of variance demonstrates that the variables are quite different in their significance levels. To determine these levels, various multiple comparison tests were conducted on the modified data for factors 1 and 2 (Table 4). *Ixeris tamagawaensis*, which was included as an outgroup, differs significantly from all other taxa in the *I. chinensis* complex. Furthermore, within the complex *I. chinensis* subsp. *chinensis* was significantly different from both triploid and tetraploid populations of *I. chinensis* subsp. *strigosa*. However, triploid and tetraploid populations of *I. chinensis* subsp. *strigosa* were not significantly different from one another (Table 4).

Table 3. ANOVA test for diploid, triploid and tetraploid populations in the *Ixeris chinensis* complex and its nearest relative *I. tamagawaensis* with the factor scores obtained by factor analysis.

Variable	Sig. of F
Factor 1	0.000
Factor 2	0.000
Factor 3	0.001
Factor 4	0.725
Factor 5	0.038
Factor 6	0.337
Factor 7	0.125
Factor 8	0.025
Factor 9	0.140
Factor 10	0.155

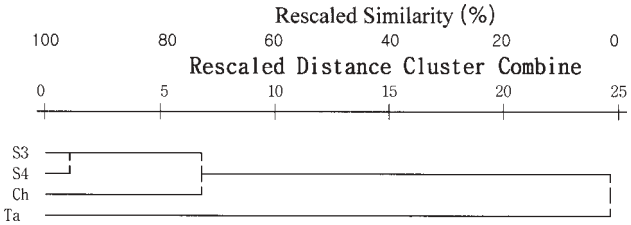

Figure 3. Average linkage dendrogram for the members of the *Ixeris chinensis* complex and its nearest relative *I. tamagawaensis* (Ch: *I. chinensis* subsp. *chinensis*; S3: *I. chinensis* subsp. *strigosa* of triploids; S4: *I. chinensis* subsp. *strigosa* of tetraploids; Ta: *I. tamagawaensis*).

To investigate similarity among the variables considered, a cluster analysis was performed on the modified data (Figure 3). Triploid and tetraploid populations of *I. chinensis* subsp. *strigosa* clustered first at a rescaled distance of < 2. *Ixeris chinensis* subsp. *chinensis* formed the second cluster with *I. chinensis* subsp. *strigosa* at a rescaled distance of < 7. Lastly, the outgroup, *I. tamagawaensis*, clustered at a rescaled distance of about 25 (Figure 3).

Discussion

The *Ixeris chinensis* complex is exceedingly polymorphic, and this is reflected in its diverse taxonomic treatment (e.g. Kitamura, 1956; Tzvelev, 1964; Pak and Kawano, 1992). The complex, however, has generally been recognized as having three taxa even though their taxonomic level and nomenclature has differed considerably among researchers (Kim et al., 1999). Kitamura (1956) described the root morphology, plant height, number of cauline leaves, and involucre and achene length as diagnostic characters of this complex. He circumscribed *Ixeris chinensis* subsp. *chinensis* by a plant height of 20-35 cm, 2-4 cauline leaves, involucres 6-8 mm long, achenes 4-6 mm long, yellow corolla, and roots that branch often. *Ixeris chinensis* subsp. *strigosa* is 25-50 cm in height and has 1-2 cauline leaves, involucres 9-10 mm long, achenes 5.5-7 mm long, whitish ligules with slightly purple surfaces, and roots that are often unbranched. *Ixeris chinensis* subsp. *versicolor* is the smallest taxon in the complex at 10-20 cm in height, and has 1-2 cauline leaves, involucres 8-9 mm long, achenes 4.5-5.5 mm long, variously colored corollas, and roots that branch often. These characters described by Kitamura (1956) reveal some degree of overlap among the three taxa of the complex except for corolla color. Tzvelev (1964) revised Kitamura's classification, producing three *Ixeridium* species, *I. chinensis*, *I. strigosum* and *I. gramineum*. Pak and Kawano (1992) concluded that *Ixeris strigosa* clearly differs from *I. chinensis* in having erect stems, a few cauline leaves, and whitish ligules with slightly purple outer surfaces. They revised this complex

Table 4. Multiple comparison by the Duncan method with the first two factor scores resulting from a factor analysis for the *Ixeris chinensis* complex and its nearest relative *I. tamagawaensis*.

	Duncan test	Tukey-HSD test	Tukey-B test	Scheffe test
Mean (f1)	ta ch s4 s3	ta ch s4 s3	ta ch s4 s3	ta ch s4 s3
-1.5405	ta	ta	ta	ta
-0.2069	ch	ch	ch	ch
0.6622	s4	s4	s4	s4
0.8798	s3	s3	s3	s3
Mean (f2)	ch s4 s3 ta	ch s4 s3 ta	ch s4 s3 ta	ch s4 s3 ta
-0.9212	ch	ch	ch	ch
0.0107	s4	s4	s4	s4
0.3687	s3	s3	s3	s3
0.9797	ta	ta	ta	ta

: significantly different at 0.05; ch: *I. chinensis* subsp. *chinensis*; f1: factor 1; f2: factor 2; s3: *I. chinensis* subsp. *strigosa* of triploids; s4: *I. chinensis* subsp. *strigosa* of tetraploids; ta: *I. tamagawaensis*.

into two species, *Ixeris chinensis* and *I. strigosa*, and further split the former into two subspecies, subsp. *chinensis* and subsp. *versicolor*. They also suggested that detailed studies were required to understand the total range of morphological variation in order to provide a more refined taxonomic scheme (Pak et al., 1995, 1997).

In general, if speciation is complete above the population level, new taxa should be compartmentalized not only by discontinuity in morphological characters but also by specific molecular characters. However, if speciation is in process, most morphological characters may overlap rather than exhibit discontinuity, and molecular characters may not be unique. In that case, taxonomic perspective usually relies on a subjective assessment. The term species complex was used to describe species aggregations sharing the specific morphological and molecular features (e. g. Davis and Heywood, 1963; Grant, 1981; Stuessy, 1990; Judd et al., 1999) in taxa that are undergoing speciation. Although their taxonomic affinity may be difficult to determine, some form of taxonomic resolution is desirable.

The aims of this study were to establish a model for infraspecific taxa within the *Ixeris chinensis* complex based on morphometric approaches and to use this as a test for published taxonomic schemes. As mentioned above, this complex shows considerable overlap in morphological characters (Kitamura, 1956; Pak and Kawano, 1992), and its taxonomic treatment differs among researchers (Pak et al., 1995, 1997). An important point often overlooked by taxonomists is that the cumulative values of character variation occurring among taxa might be taxonomically useful. Although all morphological characters considered overlap considerably, those cumulative values modified from original measurements may be particularly powerful in recognizing difficult taxa when the degree of character variation differs signficantly among taxa (Whang et al., 1998). That point was the focus of this study, which considered both the structual associations of the original data and the cumulative values of variation as morphometric data. The original data set was obtained by the measurement of 40 morphological characters from each of 110 individuals of the *I. chinensis* complex and *I. tamagawaensis*. Firstly, the 10 factors that had eigenvalues that summed to > 1 were extracted with a factor analysis (Table 2). However, structural relationships between characters were indistinct in most factors extracted even though there were some noticeable tendencies. A modified data set was generated by matching factor scores, calculated by the correlation coefficients of each factor, with the large original data set. The initial data set was reduced to about 10% of its original size and was significant both biologically and statistically. The nature of the modified data also emphasized the cumulative values of character variations. The modified data were examined by a series of multivariate methods in order to recognize taxa in the complex.

A canonical discriminant function analysis was conducted to understand the relationships between the four taxa examined (Figure 2). All the cumulative values of *I. tamagawaensis* were well separated from all other taxa by function 1 (Figure 2). It is likely that, in spite of being the nearest relative, this species had clear morphological discontinuities from the other taxa. However, the cumulative characters did not separate the other taxa with functions 1 and 2, as they overlapped considerably with each other (Figure 2), confirming their close relationship. Tzvelev's (1964) proposal of three species in this complex (which he placed in the genus *Ixeridium*) is not supported by this analysis. Also, the separation of the complex into two species, *I. chinensis* and *I. strigosa* by Pak and Kawano (1992), is not supported here because of the considerable morphological overlap recorded. The results of the ANOVA indicated significant differences for factors 1, 2, 3 and 5, which cover about 60% of the original data (Table 3). Furthermore, several multiple comparison tests, carried out to determine which taxa differed significantly (Table 4), showed that *I. tamagawaensis* (included as an outgroup) differs significantly from all other taxa, and *I. chinensis* subsp. *chinensis* differs significantly from both triploid and tetraploid populations of *I. chinensis* subsp. *strigosa* as well as from *I. tamagawaensis* (Table 4). Therefore, the cumulative character segregation of this complex did not distinguish separate taxa through the canonical discriminant function test, but two taxa were evi-

dent in the complex using the multiple comparison test. These findings are compatible with the taxonomic classification of Kitamura (1956), who separated *I. chinensis* subsp. *strigosa* from *I. chinensis* subsp. *chinensis* based on geographic distribution. The cluster analysis, conducted to determine similarities among taxa (Figure 3), shows no cumulative character overlap between the species complex and *I. tamagawaensis*, but indicates a 75% overlap between *I. chinensis* subsp. *chinensis* and *I. chinensis* subsp. *strigosa*. There appears to be about a 95% cumulative character overlap between two groups (triploids and tetraploids) of *I. chinensis* subsp. *strigosa.*

In conclusion, this study provides morphological support for Kitamura's (1956) classification of infraspecific taxa in the *I. chinensis* complex. Given that there is no overlap of cumulative values of variation between the *Ixeris chinensis* species complex and *I. tamagawaensis*, it is probable that there was 75% overlap within the complex.

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山苦菜複合體的形態修理分析

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為了驗證種內分類群的假設，從山苦菜（*Ixeris chinensis*）復合體 11 類 110 個體中，測出 40 個形質，使用了形態修理分析法。作為外群，包括了 *Ixeris tamagawaensis* 最近的近緣群為了利用原資料與形質變異積材值的結構性相關關係，從大小大的原資料因子點數中，做出了新的變形資料。其結果，原資料的大小縮小了 10%，所變形的資料又強調了形質變異的積材值。儘管，一些形質，表現出某些傾向，但形質之間的結構性相關關係，在抽出的大部分因子中出現為不明顯。本論文依據準確的判別分析法，Anova，多種比較，群集分析，議論了山苦菜複合體內分類群與變異積材值之間的相互關係。本研究支持北村（Kitamura）的（1956）關於山苦菜複合體種內分類群的分類。假設，綜合體與外群之間不重疊形質變異的積材值，那麼複合體內，約 75% 的形質會出現重疊。

關鍵詞：山苦菜複合體；種內分類群；形態修理分析法。