

Population Genetics of Klamath Basin Suckers

Phase III Report: Development and Analysis of Microsatellite Markers

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Summary

Herein we describe the development of microsatellite markers for five Catostomid species (*Catostomus snyderi*, *Catostomus rimiculus*, *Chasmistes brevirostris*, *Deltistes luxatus*, and *Catostomus occidentalis*) and their application to Klamath Basin suckers. A total of 89 primer pairs were developed from enriched (CA)_n and (GATA)_n libraries created from the *D. luxatus* genome. The successful amplification of 82 polymorphic loci across three Catostomid genera indicates that the microsatellite markers described in this study will be broadly applicable.

Using 15 tetranucleotide loci, we analyzed 315 samples to detect the genetic population structure of Klamath Basin suckers. The collection includes individuals from the Lost River, Upper Klamath Lake, Sprague River, Upper Williamson River, Lower Klamath River, and the Rogue River. The data were analyzed using two different mutation models to maximize the overall resolution for detecting population structure. Additionally, the pairwise relationships of all individuals were calculated. In all comparisons, smallscale suckers were the most divergent group. Largescale suckers from the Upper Williamson River and Lost River suckers from the Lost River were also easily distinguished. Within the Lost River and in the Upper Klamath Lake and Sprague River complex, Shortnose suckers were indistinguishable from largescale suckers. Lost River suckers from the Upper Klamath Lake and Sprague River were not distinguished from Shortnose suckers. We discuss several explanations for the lack of resolution among species in the Upper Klamath Lake and Sprague River system. Based on these analyses, we recommend more sampling and analysis for Phase IV, including: an examination of larval Shortnose and Lost River sucker samples collected from Upper Klamath Lake and sampling of independent runs from the Sprague River to test for genetic variation among cohorts, and an examination of additional samples collected throughout the basin to increase the statistical power of our analysis.

Introduction

The Catostomid family of freshwater fishes comprises over 60 species that are widely distributed throughout North America (Miller 1959). Catostomids, or suckers, are believed to have an allotetraploid genetic heritage and retain the expression of some duplicate gene systems

(Uyeno and Smith 1972; Ferris and Whitt 1980). Several Catostomid species are currently listed as threatened or endangered under the U.S. Endangered Species Act and have become the focus of recovery efforts in many western states. Notably, four sucker species are native to the Klamath River Basin, Oregon: the Klamath largescale (*Catostomus snyderi*) and smallscale suckers (*Catostomus rimiculus*) and federally endangered Shortnose (*Chasmistes brevirostris*) and Lost River suckers (*Deltistes luxatus*). Currently, no information exists on the population structure or levels of gene flow occurring among populations in the Klamath Basin. In this paper we describe the development and analysis of microsatellite markers for Klamath Basin suckers and demonstrate their suitability for use in the Sacramento sucker (*Catostomus occidentalis*).

Part I – Development of microsatellite markers.

Methods and Materials

Genomic DNA was extracted from dried fin samples of *D. luxatus* using the TNES-urea procedure (Belfiore and May 2000). Two sub-genomic libraries were constructed by Genetic Identification Services (Chatsworth, CA) by partially digesting genomic DNA with *BsrBR* 1, *EcoR* V, *Hae* III, *Pvu* II, *Sca* I, and *Stu* I. An oligonucleotide linker containing a *HinD* III site was ligated to fragments in the range of 300-700 bp. These fragments were enriched by magnetic bead capture (Jones *et al.* 2000) to create two separate libraries for the repeat motifs (CA)_n and (GATA)_n. The captured fragments were ligated into the *HinD* III site of pUC 19 and the products electroporated into *E. coli* DH5 α . Transformed DH5 α cells were plated on LB ampicillin plates. Approximately 500 recombinant clones (sampled with a toothpick) were amplified directly in 15 μ l reactions containing: (20mM Tris-HCl , pH 8.4, 50mM KCl), 5 mM MgCl₂, 1.5 mM dNTPs, 0.5 μ M pUC19 forward and reverse sequencing primers, and 0.5 units Taq DNA polymerase (GIBCO). Reaction mixtures were amplified in an M.J. Research PTC-

100 96V thermocycler using the following procedure: 94⁰ C for 3 min, 25 cycles of (94⁰ C for 30 s, 57⁰ C for 30 s, 72⁰ C for 30 s), and 72⁰ C for 5 min. Approximately 1 μ l of PCR product was run on a 3% TAE-agarose gel stained with 0.01x TMVistra Green nucleic acid stain to identify inserts of 300 to 800 bp. Colonies containing the desired inserts were grown overnight in LB and plasmids were purified using the QIAprep Spin Miniprep Kit (Qiagen). A total of 220 clones from both libraries were sequenced using the ABI Big Dye TM Terminator cycle sequencing protocol and visualized on an ABI 377 DNA sequencer (Applied Biosystems).

PCR primers were developed for 36 dinucleotide and 76 tetranucleotide loci using *PrimerSelect* software (Lasergene 5.1, DNASTAR Inc.). For all samples screened, a total of 5 ng genomic DNA was amplified in 15 μ l reactions containing: (20mM Tris-HCl , pH 8.4, 50mM KCl), 1.5 mM MgCl₂, 0.5 mM dNTPs, 0.5 μ M primers, and 0.5 units Taq DNA polymerase (GIBCO). Reaction mixtures were amplified using the following procedure: 94⁰ C for 2 min, 30 cycles of (94⁰ C for 30 s, 52⁰ C for 30 s, 72⁰ C for 1 min), and 72⁰ C for 5 min. Amplification products were mixed 1:1 with 98% formamide loading dye, denatured for 3 min at 95°C and cooled on ice before running on 5% denaturing acrylamide gels at 60 W for 30 min. Products were fluorescently detected using the agarose and TMVistra Green overlay procedure of Rodzen *et al.* (1998) and scanned with a Molecular Dynamics 595 fluorimager.

Results

Hereafter, individual primer identifiers, consisting of the species scientific name from which it was cloned (“Dlu”) and the laboratory identification number will be used to identify each locus. Primers are referred to in the text by using a regular font (e.g., Dlu 461) whereas references to loci use italics (e.g., *Dlu 461*).

A total of 31 dinucleotide and 58 tetranucleotide primer pairs amplified unambiguous PCR products in *D. luxatus*, *C. brevirostris*, *C. snyderi*, *C. rimiculus*, and *C. occidentalis* using identical reagent and thermal cycling conditions. With the exception of Dlu 4339, all loci exhibited patterns consistent with disomic inheritance. Of the 89 primers tested across five species, seven were monomorphic. Amplification product details for *D. luxatus* are reported in Table 1 and cross-amplification results are reported in Table 2. As indicated by a high amplification success across three Catostomid genera, the microsatellite markers described herein will be useful in future studies involving suckers.

Part II – Population analysis with microsatellite markers.

Methods and Materials

All samples (N=315) were screened for genetic variability using oligonucleotide primers for 15 microsatellite loci cloned from the Lost River sucker, *Deltistes luxatus* (Tranah et al. in press). Amplification was done in 200 µl 8-tube strips with 1 unit Taq DNA polymerase (GIBCO), 0.4 µM each primer, 3-10 ng template, 100 or 175 µM dNTPs, and 1.5-2.5 mM MgCl₂ in 50 µl of buffer. Reaction mixtures were amplified in an M.J. Research PTC-100 96V thermocycler with a “hot bonnet” lid using the following procedure: the mixture was preheated at 94⁰ C for 3 min, amplified for 35 cycles (denaturing at 94⁰ C for 1 min, annealing at 52⁰ C for 30 sec, polymerization at 72⁰ C for 30 sec), and a final polymerization at 72⁰ C for 5 min. Amplified products were run on a 5% denaturing acrylamide gel and visualized with a Molecular Dynamics 595 fluorimager. The amplification products were fluorescently detected using single-primer labeling with fluorescein. Alleles were sized using FragmeNT Analysis (Molecular Dynamics; Sunnyvale, CA).

Codominant genotypes were classified and recorded for each microsatellite locus. Allele frequencies for each locus and F_{IS} (Weir and Cockerham 1984) were calculated using FSTAT 2.9.1 (available from <http://www.unil.ch/izea/softwares/fstat.html>) updated from Goudet (1995). All populations were tested for conformance to Hardy-Weinberg expectations with Genes in Populations 2.2 (Program designed by B. May and C. C. Krueger; written in C by W. Eng and E. Paul, available from <http://animalscience.ucdavis.edu/extension/Gene.htm>).

The degree of population subdivision was determined from multilocus estimates of F_{ST} (Weir & Cockerham 1984) and R_{ST} (Slatkin 1995) for all population pairs using FSTAT 2.9.1 (Goudet 1995) and RST CALC (Goodman 1997), respectively. By assuming no random mating within samples, a more conservative measure of differentiation among populations was made. Pairwise significance tests for F_{ST} using likelihood ratio G (Goudet et al, 1996) were performed by permutation and resampling of multi-locus genotypes among pairs of samples. Performing 6600 randomizations allowed for a table-wide significance at the 5% nominal level after standard Bonferroni corrections. Pairwise significance tests were also carried out for R_{ST} using permutation with RST CALC, allowing for a table-wide significance at the 5% nominal level.

Both $(\delta\mu)^2$ (Goldstein et al. 1995) and Nei's (1978) genetic distances were calculated for all population pairs using RST CALC and Genes in Populations 2.2, respectively. Multivariate factor analyses were performed for $(\delta\mu)^2$ and Nei's genetic distances with Statistica for Windows version 5.1 (Statsoft Inc.). Factors were extracted using a maximum likelihood method (Harman 1976).

The Queller and Goodnight (1989) index of relatedness (R_{xy}) was calculated for pairs of individuals using Relatedness 4.2 software. Principal Components analyses were performed for relatedness values with Statistica for Windows version 5.1 (Statsoft Inc.).

Results

Allele frequencies for each locus, sample sizes per population and F_{IS} measures are summarized in Table 3. Individual phenotypes at the 15 polymorphic loci were either single banded or symmetrically double-banded suggesting that they were disomic. A range of 15 to 48 alleles were observed per locus.

The data were analyzed using two different mutation models to maximize the overall resolution when detecting population structure. Both R_{ST} and $(\delta\mu)^2$ are analogues to Wright's F_{ST} (Wright 1951) and Nei's genetic distance, respectively, adapted to microsatellite loci by assuming a stepwise mutation model. Generally, genetic distance measures, such as $(\delta\mu)^2$ and Nei, are geometric representations of the differences in allele frequencies between groups. These measures are often used to visualize the relationships of groups either through branching tree networks or with multivariate clustering approaches. Both Rst and Fst are gene flow models that partition genetic within and between groups and are used for detecting population subdivision.

When considering R_{ST} and F_{ST} (Tables 4 and 5, respectively) for statistical differentiation, there were several consistent results using both gene flow models. In all pairwise tests, Rogue River and Klamath River smallscale suckers, Lost River suckers from the Lost River and Largescale suckers from the Upper Williamson River were the most divergent groups. Within the Lost River and in the Upper Klamath Lake and Sprague River complex, Shortnose suckers were indistinguishable from largescale suckers using either statistical model. In the Upper Klamath Lake and Sprague River, Lost River suckers from were not distinguished from Shortnose suckers (especially for F_{ST}) but were different from largescale suckers. Also, Upper Klamath Lake Shortnose and Lost River suckers were not different from Sprague River Shortnose and Lost River suckers. When genetic distance measures are considered, $(\delta\mu)^2$ and

Nei (Tables 4 and 5, respectively), the results parallel those based on gene flow. A factor analysis of $(\delta\mu)^2$ genetic distance (Figure 1) shows smallscale and Lost River suckers to be the most divergent species, regardless of sampling location. Also, Shortnose and largescale suckers are indistinguishable in this analysis. The factor analysis of Nei's genetic distance (Figure 2) presents a different, although not entirely conflicting, relationship. This analysis presents largescale suckers from the Upper Williamson River as the most divergent group. In general, the samples are grouped geographically rather than taxonomically. Although Shortnose and largescale suckers from the Lost River group closely, they do not overlap with their conspecifics from any other location. Lost River suckers from Upper Klamath Lake group with Shortnose suckers from Upper Klamath Lake and the Sprague River. Lost River suckers from the Sprague River, though, group more closely with their conspecifics from the Lost River. Smallscale suckers from the Rogue River are not clustered with any other group, while smallscale and Shortnose suckers from the Lower Klamath River group closely. Largescale suckers from the Sprague River also form an independent group.

Using pair wise relatedness (R_{xy}) values, individuals were examined by geographic location. In the Lost River Basin (Figure 3), largescale and Shortnose suckers overlapped considerably while Lost River suckers formed an independent group, having nearly no overlap with the other species. In Upper Klamath Lake (Figure 4) and the Sprague River (Figure 5), Lost River, Shortnose and largescale suckers overlapped completely. Within the Upper Klamath Basin (Figure 6), all Shortnose, Lost River and largescale suckers from Upper Klamath Lake and the Sprague River completely overlapped, while largescale suckers from the Upper Williamson River formed a distinct cluster.

Discussion

Microsatellites are assumed to follow the stepwise mutation model where length polymorphisms are due to slippage mechanisms (Levinson and Gutman 1987). The size of a new allele depends on the size of the allele from which it mutated (DiRienzo et al. 1991). Both $(\delta\mu)^2$ and R_{ST} were derived specifically for microsatellite loci and assume mutation in stepwise fashion, whereas F_{ST} and Nei's genetic distance are formulated for the infinite alleles model (Ohta and Kimura 1973), which has no size constraints and states that every mutation erases information about the previous allelic state. Some microsatellite loci exhibit biases toward the addition or loss of repeats and can involve single or multiple repeat expansions (Gaggiotti et al. 1999 and references therein). Previous simulation studies (Ruzzante 1998; Gaggiotti et al. 1999) demonstrated that for certain conditions (large sample sizes and many loci examined), the stepwise model performs better than the infinite alleles model. Therefore, no single model can accurately describe the mutational properties of all microsatellite loci, so we included both models in our analysis.

Based on the results using two mutational models for analyzing the data, the most consistently distinct groups in the dataset are the Rogue River and Klamath River smallscale suckers, Lost River suckers from the Lost River and Largescale suckers from the Upper Williamson River. It is interesting that, wherever largescale and Shortnose suckers are sympatric (Lost River and Sprague River), they are genetically indistinguishable. This can be observed in the plots based on both genetic distance models ($(\delta\mu)^2$ and Nei), and is further supported by each plot of individual relatedness values and with both R_{ST} and F_{ST} testing. Perhaps the lack of resolution could be explained by a lack of statistical power due to low sample size or that the loci used herein were not sufficient for distinguishing between largescale and Shortnose suckers. Our

analysis, though, demonstrates that largescale suckers from the Upper Williamson River are distinct and suggests that this set of markers is sufficient for distinguishing between these species. If this is the case, then, there is likely another explanation to account for the genetic similarity of sympatric largescale and Shortnose suckers. Although difficult to confirm, this genetic pattern could be the result of introgression between largescale and Shortnose suckers.

The Lost River suckers are particularly interesting due to the differing patterns of genetic differentiation exhibited between the Lost River and the Upper Klamath populations. In the Lost River, Lost River suckers are a clearly distinct group statistically, and when genetic distance and individual relatedness values are considered. This is in contrast to what is found in Upper Klamath Lake and the Sprague River system. Our analyses did not distinguish between Lost River and shortnose suckers, which is supported statistically (F_{ST}), with Nei's distance and with pairwise relatedness values. In addition, when considering pair wise relatedness values, Lost River and largescale suckers had considerable overlap. There are several possibilities that could account for the different trends between Lost River and Upper Klamath Basin suckers. It is possible that, due to low sample sizes for each of the representative species in Upper Klamath Lake and the Sprague River, we lack statistical power to resolve species differences. Sample sizes in the Lost River, are: Lost River suckers (N=19); shortnose suckers (N=65); and largescale suckers (N=39). In the Sprague River, sample sizes are: Lost River suckers (N=6); shortnose suckers (N=8); and largescale suckers (N=31), and in Upper Klamath Lake sample sizes are: Lost River (N=18); shortnose (N=25), and Largescale (N=2). By analyzing more samples collected from the upper basin, we would have greater statistical power to resolve species differences or to consider alternate hypotheses (if the results do not change). Since Klamath basin suckers are long lived and iteroparous, it is likely that our samples represent consistent spawning across multiple age classes. If this is the case, the variability introduced by the

overlapping of generations could obscure or even erase underlying geographic and taxonomic patterns. To determine the extent of interannual genetic variation, an examination of larval shortnose and Lost River sucker samples representing multiple cohorts should be analyzed. This would allow us to detect significant shifts in allele frequencies across known cohorts (within species) and eliminate the potential variance introduced from an examination of mixed of age classes. Knowledge of interannual genetic variation would assist in the interpretation of the present analysis, which did not distinguish between Lost River and shortnose suckers. A further examination of independent spawning runs within a season would allow us to account for the within year genetic variability likely to be encountered in the proposed larval cohort analysis. If there are genetic differences based on run timing, this would add variance to the analysis that would require explaining. It is also possible that hybridization between Lost River and Shortnose suckers (and, perhaps, largescale suckers) may be more prevalent in Upper Klamath Basin than in the Lost River. In order to determine if this is indeed the case, it is necessary to account for the many sources of variation in order to consider all potential hypotheses.

Research Direction for Phase IV (2001)

- 1) Examine additional basin wide samples to be collected in 2001 with microsatellite loci.**
- 2) Examine larval shortnose and Lost River sucker samples collected in 1995, 1998, 1999 for cohort fluctuations in microsatellite allele frequencies.**
- 3) Examine independent spawning runs to be collected from the Sprague River in 2001 with microsatellite loci.**

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Table 1. Characterization of 82 microsatellite loci in the Lost River sucker (*Deltistes luxatus*) based on three individuals from the Klamath River Basin: GenBank accession numbers, repeat motif, observed and expected heterozygosity (H_O and H_E from Genes in Populations V 2.2), number of alleles, allele size range, clone size, and primer sequences.

Locus names	GenBank accession no.	Repeat motif	H_O	H_E	No. of alleles	Allele size range (bp)	Clone size (bp)	Primer sequence (5' - 3')
Dlu 21	AF314663	(CA) ₁₂ (TC) ₁₂	0.67	0.67	4	220-300	253	TGTTTGTGCTCATCACCA TGACTTCTAAACTAAATCACTGTC
Dlu 22	AF314664	(CA) ₁₂	0.33	0.28	2	130-160	152	CGTGTGCGGC GTGTCTTC TATCCATAACGGTTGCCTTCCCT
Dlu 25	AF314665	(CA) ₃₀	1.00	0.50	2	130-175	189	CAATCCTGAGGC GGGTGTG TTAAATAGTTGTGAAAGGTGAA
Dlu 26	AF314666	(AG) ₂₄	0.67	0.44	2	160-175	193	ATATACTTATTAAATTCAACAC TTCTGACAGTCATTAATCTTAGAC
Dlu 27	AF314667	(CA) ₁₃	1.00	0.61	3	180-210	204	AGCCAATGAATAAACACAAGAGG TCATCCAAGAGCAGGTAAGC
Dlu 28	AF314668	(CA) ₃₂	0.33	0.50	3	180-200	203	CCGCCATGAGGAAGGGAGAT GACATAATGAGTGATAGCCAGGTG
Dlu 203	AF314669	(CA) ₁₆	0.67	0.67	4	180-200	186	GTGGTGGAGGGGGCACTGTAG AAACGTTCCAATAACTGTCTTTA
Dlu 206	AF314670	(CA) ₂₂ (CT) ₆	1.00	0.78	5	160-240	189	GGATTCACACCAAAGGTCTCCTG TCTCTGGCTGTGCCAATCTC
Dlu 207	AF314671	(CA) ₁₈	0.67	0.72	4	180-210	193	TACAGGAAGAGACTGACTGACTAA TCAAAGCTATCTGAAATCGCTAAT
Dlu 209	AF314672	(CA) ₁₈	1.00	0.78	5	150-180	168	CCCCCAGTCTCTGACAAT CTCTAACATGCGACTTTACAAG
Dlu 210	AF314673	(CA) ₂₇	0.67	0.61	3	150-220	185	TGTGTCCAGAAAGAGCAGAGAT TTTAATTAGCCCCTGAAACAT

Dlu 213	AF314674	(CA) ₁₅	0.67	0.44	2	150-180	171	ATCACCTCTTCAGGCTACTTTG ATCCCAGAAGCGATCCCTCTCAT
Dlu 216	AF314675	(CA) ₁₅	1.00	0.83	6	140-220	157	GTAAACCCGCCACAACGTGCT CGCCACCGACACCTCCTATTTAC
Dlu 229	AF314676	(CA) ₄₂	1.00	0.78	6	130-200	188	TACCAGCCAGGTGTGCAAGCTATG CACACTGGAATGTTCACATGG
Dlu 230	AF314677	(CA) ₄₀	1.00	0.72	4	120-180	168	CTATATTTCGCCAAGTGTGAT AATTCCCATTCCCCATTG
Dlu 232	AF314678	(CA) ₂₂	0.33	0.28	2	60-130	117	GCCCCGGAGATTCCAGTTGAAGA AGCAGCCGCCACTGATAGACA
Dlu 233	AF314679	(CT) ₁₄ (CA) ₃₇	1.00	0.78	5	150-200	180	GTAAAAGAACCTGCAGCCTTATGC CATCAGGGGTTTGAGTGTG
Dlu 235	AF314680	(CA) ₂₃	1.00	0.61	3	140-160	148	GTGACGCCACCGCCACTTAGT AGTCCTCCACTGCTGTCTGTG
Dlu 243	AF314681	(CA) ₁₄	0.67	0.44	2	160-180	181	CCGTTTGTGTTGGGCACCTT AGCAGCACAGAGCGAGAT
Dlu 245	AF314682	(CA) ₁₂	0.67	0.50	3	180-200	194	ATTCAAGAGCAGCACAGGTATTGG TGAAGTTGTTATCGCTCTGTGA
Dlu 246	AF314683	(CA) ₁₁	1.00	0.78	5	170-220	197	ACTTCCTCTCACTCTCAACTG AAATCTCTGGGAACTTACAAAT
Dlu 257	AF314685	(CA) ₁₉	0.33	0.61	3	160-190	181	TACACCTGGCCGAAAATATGAAT GCTGTTCTGAGGGAAAGGACAAATC
Dlu 259	AF314686	(CA) ₃₄	1.00	0.78	5	140-220	184	ACCGCAACTCTAACATACACAAG TGAGCTCAGTACAAAAACCATTAC
Dlu 266	AF314687	(CA) ₅₂	1.00	0.78	5	170-200	181	GCCAACAGCCCCCTCTAGTGCT TTGCTGGATCAAGAGGGAGGTGAG
Dlu 271	AF314688	(CA) ₂₁	1.00	0.83	5	140-170	160	TCCCCCCAAGCCATCAGTCTCC

Dlu 272	AF314689	(CA) ₄₇	0.33	0.72	4	100-160	160	ATTGTTATGCTCATTGTGTTAC AATCAGAACATGAGCTTAATTGTCAA TTAACATCGGCTTGTATATTC
Dlu 276	AF314690	(CA) ₃₇	0.67	0.78	5	140-165	162	AACTTTAGATTTCAGCAGA ATAGAGATAAAAGGAGAGGAGATG
Dlu 282	AF314692	(CA) ₁₅	1.00	0.61	3	140-170	151	CACACTCCACAGGTAGGTTT GTTTCACTGGTGTTCTTAG
Dlu 284	AF314693	(CA) ₁₇	0.67	0.44	2	160-180	160	ACCCAGCGGCTCGGAACTAAG TTCCAAGGATCTGAATTACAGG
Dlu 45	AF314694	(GATA) ₂₉	1.00	0.61	3	300-500	458	TGGGCCTTAGTGCAGAGGA TGGTTAGGCAGAATTCTCCAG
Dlu 403	AF314695	(GACA) ₉ (GATA) ₂₃	0.33	0.50	2	290-350	325	AGATGGACAGATGGACAAATAGAC CTATCGTCCTATCGTCTTCTCC
Dlu 405	AF314696	(GATA) ₂₁	0.33	0.28	2	200-220	207	CAGCCCTCCGCGTGAAAACAAT ACCGTAAGGGGGCAGCAGAAGG
Dlu 408	AF314697	(GATA) ₁₀	0.67	0.44	2	200-250	243	TGCAAATGTTGCCCAAGAGATGT ACCCCCCTCGCCTGAGTTAACCC
Dlu 409	AF314698	(GATA) ₂₀	1.00	0.78	5	160-250	206	TGCGATCCTAGAAGGAGTAAACAA ATTCCATTGCTGTCAACTTCAA
Dlu 416	AF314699	(GATA) ₂₆	1.00	0.78	6	150-260	214	TATTAATCACATAACTGACAAAG TTCTGAAATGATGAAAAAGTC
Dlu 420	AF314700	(GATA) ₂₆	1.00	0.78	5	120-280	186	TGATCGTGCCTTCATAGTCAATG CAGACAACCAGGGATCGTAACAGT
Dlu 433	AF314701	(CAGA) ₁₂ (GATA) ₁₈	1.00	0.78	5	220-350	287	AACAGCGATAAAATGGGGCTAATA CCTGACATAGTGGATGAATAAACCC
Dlu 434	AF314702	(GATA) ₁₉	1.00	0.72	4	230-250	252	ACGAGATGCCATTGATGTGAGTGC ATGGGTGGATGGATGAATGGAATG

Dlu 439	AF314703	(ACAG) ₇ (GATA) ₂₅	1.00	0.83	6	200-360	240	GAGACAGTCCACACTTCACATTGT TTCCATAATACACTCTTGGCATAG
Dlu 451	AF314704	(GATA) ₁₃	0.67	0.78	5	230-280	246	GGCGGACGGACGGATGG GTCCC GGCGGAACCACAG
Dlu 454	AF314705	(GATA) ₂₈	1.00	0.67	3	200-300	247	CAGAACAA TTT CCTAAGCAAGTG GCTCACAA ATCAATTATGTCAGC
Dlu 455	AF314706	(GATA) ₂₃	1.00	0.78	5	170-240	216	AAATTAAA ATCCTGAATTCAATAT TATATGCAGGTAAAAATTAACAAAC
Dlu 456	AF314707	(GACA) ₁₀ (GATA) ₁₉	1.00	0.72	4	225-285	251	TTGCAACTGCTGAGAAAATACACA CACACGAGGAGACAGAAACACAG
Dlu 461	AF314708	(GACA) ₂₆ (GATA) ₁₃	1.00	0.78	5	120-200	242	ATAGCTTTGTGCAAATAAGTCTG TAAAAGGTGAGTCAAGCAGAAGTG
Dlu 463	AF314709	(GA) ₂₅ (GATA) ₁₇	0.67	0.78	5	170-300	217	TACAAGCACTCCAGTAATCAATCA GGGGGTCAAACACAGTATTAGTAG
Dlu 466	AF314710	(GATA) ₁₄	1.00	0.72	4	220-280	253	CTGCGCATGCATTTTCATTCTG TTTGTTTACGCTGCA CGCTTGAGC
Dlu 467	AF314711	(GATA) ₁₇	1.00	0.78	5	270-344	334	ACGTGGGTACCTTGCTCGGAGTAT ACGCGCTAATAGACAGTGGACCAA
Dlu 476	AF314712	(GATA) ₃₅	1.00	0.83	6	160-380	263	ATGGTTGGCTACTTTAACATCAA TACACCTCCAATCTGTTCTAA
Dlu 482	AF314713	(GATA) ₂₁	1.00	0.72	4	170-250	209	GAAGAGGGCAGTAGGGTCAGATG GGCGTGTCA GGGGAGGAA
Dlu 488	AF314714	(GATA) ₂₂ (GATG) ₇	1.00	0.83	5	130-220	232	ACCCATCAATAACAGAGGTGAGG ATCAAATACTCCGGATACCACAC
Dlu 498	AF314716	(GATG) ₁₀ (GATA) ₄₅	1.00	0.78	6	130-520	254	TTTGAGGACCGGA ACTA ACTGTAG TTCATGCAGCCTTAATGCTTAA
Dlu 4105	AF314717	(GATA) ₃₃	1.00	0.83	6	65-165	214	AAGCAAGTGTAA TGCTAAA

Dlu 4123	AF314719	(GATA) ₂₀	1.00	0.78	5	130-200	177	GGCTTTAAATTTATTCTGTT ACGAGATGCCATTGATGTGAGT AGACGGCGGCAGACAGATA
Dlu 4126	AF314720	(GATA) ₂₈	1.00	0.83	6	130-170	172	CACAGTCCTAACAGTCGAACTAAA AATATTTTGCTATGTAGGCTAAA
Dlu 4128	AF314721	(GATA) ₂₄	0.00	0.00	1	180	210	TCGAAATCTATCTTCTATCTAC GCTGGAAAGACAAGTAGAGTT
Dlu 4131	AF314722	(GATA) ₂₃	1.00	0.78	6	150-220	188	AACCCTATATTATAACCTCTAAT CACCACAATGACATACAAGTA
Dlu 4139	AF314723	(GATA) ₂₄	0.67	0.67	4	170-230	199	TAATTAAAAGCTATTGTTGAACTT GACATTGAATCTATTAAAACATAC
Dlu 4146	AF314724	(GATA) ₂₁	0.67	0.78	5	160-520	169	TTTATGTGATTATATGGGTGTAT TTAATTGAAGCTCCTGACCTGTAT
Dlu 4153	AF314726	(GATA) ₃₂	0.67	0.50	3	60-120	205	GGTCATGACACTAGAAGGTGTTAA CAGTGAGCCAATTGATAGACAGAC
Dlu 4166	AF314728	(GATA) ₂₅	1.00	0.72	4	275-400	323	CTCTCGCTGAACCTCACCAATC AAAAGCAGGACTGAGAATGAGAG
Dlu 4171	AF314729	(GATA) ₂₃	1.00	0.83	6	75-160	191	TGGCATCTGCTTCCAGTTTAT GGGCCAAATCGCACTCTT
Dlu 4183	AF314730	(GATA) ₂₇	1.00	0.83	5	65-220	209	CTGAAAGCACCTCCTCCATTAG GTTCTCTCTCCTGTTCGCTTAT
Dlu 4184	AF314731	(GATA) ₁₅	1.00	0.83	6	75-165	166	CCATGCATGCACCAATGTAGAAAT CAGCAGTCCCCATATGATTACACA
Dlu 4201	AF314732	(GATA) ₂₁	1.00	0.83	6	85-170	189	CCAACCTCTGAACAACTGTAAAT GTGGTAAAGAGGTCTGCCTGTAT
Dlu 4211	AF314733	(GATA) ₁₃ (GACA) ₁₇	0.67	0.78	5	60-200	198	TGTCTGAACGCCACAACCTG CACCCATACAGATGAGGGGGAGAG

Dlu 4217	AF314734	(GATA) ₁₃ (GACA) ₇	0.33	0.72	4	200-275	230	TGGGATGGCATGAGGATGAGTAA CACATGCCTGCAAGATTGACTGAT
Dlu 4219	AF314735	(GATA) ₂₃	0.67	0.50	3	200-296	208	CGCCCCACATCCTCTACACTCAA TCAACAAAGGGACATAGATAAGAT
Dlu 4235	AF314736	(GATA) ₁₂	1.00	0.78	5	175-240	171	TGGTATTAACC GTTTACTTCCACA TAAACTCCGCTTTGTTATCAGC
Dlu 4237	AF314737	(GATA) ₃₁	1.00	0.72	4	210-280	229	CATTTCCCTCCCTTATACATTTC TGCAGCATTAAACACAGCATTGAAC
Dlu 4243	AF314738	(GATA) ₂₄	1.00	0.78	5	50-200	160	TGGTTGGATGCTGAAATAAGTAA TGAGCCTCATCATAGATGGATAGA
Dlu 4259	AF314739	(GATA) ₂₄	1.00	0.78	5	70-220	193	GGGTGCAGAACGTATCCAAAAAC AACGCATCATTCAACACACCACATTCA
Dlu 4276	AF314740	(GATA) ₁₅	1.00	0.78	5	145-200	181	CGAAGCTGCACTGACTGC GGAAATGGACACCTTGACA
Dlu 4283	AF314741	(GATA) ₈	0.67	0.72	4	100-150	107	CAGAAAAACGGTATAAAAGATGAA AAATATTAAACAGTTGGATGGATG
Dlu 4287	AF314742	(GTTA) ₈ (GATA) ₂₇	0.67	0.72	4	230-260	255	TTGACATTTTAAAAGGCCAAACC TGCAAGCTTCCATTAGAAAGGAGT
Dlu 4296	AF314743	(GATA) ₂₇	1.00	0.83	6	165-245	210	AAGAACATTAAAACAGTGAGTG TACCC TTATGTTAATGTGTTAGG
Dlu 4300	AF314744	(GATA) ₂₂	1.00	0.83	6	290-375	234	CACACCTGTTAGTGAGCTCCTCTC AAACCAATAAGCAATAGATAGAA
Dlu 4303	AF314745	(GATA) ₁₉	0.00	0.00	1	200	188	AGATAGGCAGACGGACGGACAGAC AACGAGATGCCATTGATGTGAGTG
Dlu 4307	AF314746	(GATA) ₂₈	1.00	0.72	4	200-275	218	AAGAACATTAAAACAGTGAGTG TACCC TTATGTTAATGTGTTAGG
Dlu 4314	AF314747	(GATA) ₂₅	0.67	0.67	4	220-290	253	GAGGGTCTGTGGAGAACAA

Dlu 4315	AF314748	(GATA) ₂₁	0.67	0.61	3	250-300	257	TTTCACTTCAATGACAAAAATA TGGCCAGTCTTCCATCCT ATGCAAAGCTTATCTTGAGGTGTT
Dlu 4338	AF314750	(CT) ₁₈	0.67	0.72	4	150-185	172	CTTCCTGACAATGTTCATCTTAT CACAAATGCCATGGCAACAAG
Dlu 4339	AF314751	(GATA) ₁₈	1.00	0.83	6	210-300	253	TGTTCCCTCGGTCAGCTCTTCATCA GGCAAAGGGGCAGCACATAC

Table 2. Cross-species amplification of 82 microsatellite loci designed for the Lost River sucker (*Deltistes luxatus*). Three individuals each of *Chasmistes brevirostris*, *Catostomus snyderi*, *Catostomus rimiculus*, and *Catostomus occidentalis* were surveyed. A *P* indicates that the amplified locus was polymorphic, *M* indicates that the amplified locus was monomorphic, and *na* indicates no amplification.

Locus	<i>C. brevirostris</i>	<i>C. snyderi</i>	<i>C. rimiculus</i>	<i>C. occidentalis</i>
Dlu 21	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 22	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 25	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 26	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 27	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 28	<i>P</i>	<i>P</i>	<i>P</i>	<i>na</i>
Dlu 203	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 206	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 207	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 209	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 210	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 213	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 216	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 229	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 230	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 232	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 233	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 235	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 243	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 245	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 246	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 257	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 259	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 266	<i>P</i>	<i>P</i>	<i>P</i>	<i>M</i>
Dlu 271	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 272	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 276	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 282	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 284	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 45	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 403	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 405	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 408	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 409	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 416	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 420	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>
Dlu 433	<i>P</i>	<i>P</i>	<i>P</i>	<i>P</i>

Dlu 434	P	P	P	P
Dlu 439	P	P	P	P
Dlu 451	P	P	P	P
Dlu 454	P	P	P	P
Dlu 455	P	P	P	M
Dlu 456	P	P	P	P
Dlu 461	P	P	P	P
Dlu 463	P	P	P	P
Dlu 466	P	P	P	P
Dlu 467	na	na	P	P
Dlu 476	P	P	P	P
Dlu 482	P	P	P	P
Dlu 488	P	P	P	P
Dlu 498	P	P	P	P
Dlu 4105	P	P	P	P
Dlu 4123	P	P	P	P
Dlu 4126	na	na	P	P
Dlu 4128	M	P	P	M
Dlu 4131	P	P	P	P
Dlu 4139	P	P	P	P
Dlu 4146	P	P	P	P
Dlu 4153	P	P	P	P
Dlu 4166	P	P	P	P
Dlu 4171	P	P	P	P
Dlu 4183	P	P	P	P
Dlu 4184	P	P	P	P
Dlu 4201	P	P	P	P
Dlu 4211	P	P	P	P
Dlu 4217	P	P	P	P
Dlu 4219	P	P	P	P
Dlu 4235	P	P	P	P
Dlu 4237	P	P	P	P
Dlu 4243	P	P	P	P
Dlu 4259	P	P	P	P
Dlu 4276	P	P	P	P
Dlu 4283	P	P	P	P
Dlu 4287	P	P	P	na
Dlu 4296	P	P	P	P
Dlu 4300	P	P	P	P
Dlu 4303	P	P	P	P
Dlu 4307	P	P	P	P
Dlu 4314	P	P	P	P
Dlu 4315	P	P	P	P
Dlu 4338	P	P	P	P
Dlu 4339	P	P	P	P

Table 3. Allele frequencies, F_{IS} , and sample size (N) values for all sucker populations. Samples are identified as ^ashortnose (SNS), largescale (LSS), Lost River (LRS), and smallscale (SSS) suckers from the Lost River (LR), Lower Klamath River (LK), Sprague River (SP), Upper Klamath Lake (UK), Upper Williamson River (UW), and the Rogue River (RR). Alleles are named by base pair sizes.

Locus	Allele	Population											
		sns-lr	sns-lk	sns-sp	sns-uk	lrs-lr	lrs-sp	lrs-uk	lss-lr	lss-sp	lss-uw	sss-lk	sss-rr
Dlu 476	156	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.13	0.00
	158	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	160	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	164	0.02	0.00	0.00	0.03	0.03	0.00	0.00	0.00	0.02	0.00	0.04	0.00
	168	0.00	0.04	0.10	0.06	0.17	0.00	0.06	0.00	0.02	0.17	0.00	0.00
	172	0.02	0.04	0.00	0.03	0.06	0.00	0.22	0.00	0.07	0.28	0.00	0.02
	174	0.00	0.00	0.00	0.00	0.00	0.10	0.00	0.01	0.00	0.00	0.00	0.00
	176	0.00	0.04	0.00	0.03	0.08	0.00	0.11	0.00	0.08	0.11	0.02	0.00
	180	0.05	0.11	0.00	0.06	0.08	0.00	0.08	0.04	0.07	0.00	0.06	0.00
	184	0.14	0.11	0.00	0.03	0.03	0.10	0.06	0.13	0.07	0.00	0.00	0.16
	186	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	188	0.11	0.07	0.10	0.06	0.06	0.00	0.19	0.13	0.05	0.00	0.00	0.13
	190	0.00	0.00	0.00	0.00	0.00	0.10	0.00	0.00	0.00	0.00	0.00	0.00
	192	0.06	0.00	0.10	0.11	0.03	0.00	0.08	0.03	0.08	0.00	0.04	0.11
	196	0.04	0.18	0.10	0.06	0.08	0.00	0.00	0.13	0.02	0.00	0.17	0.11
	200	0.14	0.07	0.10	0.17	0.03	0.00	0.11	0.18	0.10	0.00	0.08	0.13
	204	0.06	0.14	0.10	0.08	0.06	0.30	0.03	0.01	0.10	0.03	0.08	0.07
	208	0.05	0.11	0.00	0.08	0.03	0.10	0.06	0.14	0.03	0.19	0.06	0.04
	212	0.14	0.00	0.20	0.06	0.00	0.00	0.00	0.13	0.08	0.08	0.06	0.04
	216	0.06	0.00	0.10	0.00	0.17	0.00	0.00	0.04	0.07	0.14	0.02	0.07
	220	0.05	0.04	0.00	0.06	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.04
	224	0.05	0.04	0.00	0.06	0.00	0.00	0.00	0.01	0.02	0.00	0.02	0.04
	228	0.02	0.00	0.00	0.03	0.00	0.10	0.00	0.01	0.05	0.00	0.02	0.00
	232	0.01	0.00	0.00	0.03	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.02
	236	0.00	0.00	0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.00
	240	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.07	0.00	0.00	0.02
	244	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
	248	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.02
	252	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00
	256	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	268	0.00	0.00	0.00	0.00	0.00	0.20	0.00	0.00	0.00	0.00	0.00	0.00
N		63	14	5	18	18	5	18	36	30	18	24	28
F_{IS}		0.03	0.00	-0.03	0.12	-0.01	-0.11	-0.06	0.00	0.01	-0.13	-0.03	0.07

Locus	Allele	Population												
		sns-lr	sns-lk	sns-sp	sns-uk	Irs-lr	Irs-sp	Irs-uk	Iss-lr	Iss-sp	Iss uw	sss-lk	sss-rr	
Dlu 488														
	198	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00
	202	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.00	0.00	0.00	0.00	0.00	0.00
	206	0.00	0.03	0.00	0.00	0.00	0.08	0.03	0.00	0.00	0.00	0.00	0.00	0.00
	210	0.00	0.00	0.00	0.00	0.00	0.17	0.03	0.00	0.02	0.00	0.00	0.00	0.00
	214	0.00	0.03	0.00	0.00	0.03	0.08	0.03	0.00	0.00	0.00	0.00	0.00	0.00
	218	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	222	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.00	0.00	0.00	0.00	0.00	0.00
	226	0.02	0.00	0.00	0.04	0.00	0.00	0.03	0.01	0.00	0.00	0.00	0.00	0.02
	228	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	230	0.02	0.00	0.00	0.00	0.03	0.08	0.00	0.03	0.03	0.00	0.00	0.00	0.00
	234	0.02	0.00	0.06	0.02	0.00	0.08	0.06	0.00	0.00	0.00	0.00	0.00	0.00
	238	0.01	0.00	0.06	0.00	0.00	0.00	0.00	0.01	0.00	0.06	0.00	0.00	0.00
	242	0.05	0.03	0.00	0.02	0.24	0.00	0.08	0.06	0.05	0.00	0.02	0.02	0.02
	246	0.07	0.13	0.13	0.11	0.00	0.00	0.00	0.14	0.03	0.00	0.02	0.02	0.06
	250	0.07	0.10	0.06	0.00	0.05	0.08	0.00	0.04	0.03	0.02	0.04	0.07	
	252	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	254	0.16	0.10	0.00	0.00	0.11	0.08	0.03	0.10	0.02	0.02	0.02	0.11	
	258	0.09	0.10	0.13	0.02	0.05	0.00	0.06	0.10	0.12	0.17	0.00	0.04	
	262	0.02	0.07	0.00	0.02	0.03	0.00	0.14	0.06	0.00	0.15	0.04	0.06	
	266	0.00	0.07	0.13	0.02	0.03	0.00	0.06	0.00	0.03	0.07	0.04	0.00	
	270	0.05	0.00	0.00	0.04	0.16	0.08	0.03	0.04	0.05	0.04	0.08	0.00	
	274	0.02	0.00	0.06	0.07	0.08	0.00	0.06	0.03	0.09	0.07	0.08	0.02	
	276	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
	278	0.03	0.07	0.00	0.04	0.05	0.00	0.03	0.01	0.09	0.06	0.10	0.09	
	282	0.07	0.03	0.13	0.07	0.00	0.08	0.00	0.07	0.05	0.13	0.08	0.09	
	286	0.07	0.07	0.06	0.00	0.03	0.08	0.06	0.03	0.05	0.09	0.04	0.07	
	290	0.11	0.00	0.06	0.13	0.00	0.00	0.03	0.13	0.02	0.06	0.06	0.07	
	294	0.03	0.03	0.13	0.11	0.00	0.08	0.06	0.01	0.09	0.00	0.02	0.09	
	296	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	
	298	0.01	0.00	0.00	0.07	0.05	0.00	0.00	0.01	0.00	0.00	0.06	0.07	
	302	0.00	0.00	0.00	0.11	0.03	0.00	0.03	0.00	0.00	0.00	0.00	0.02	
	306	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.07	0.00	0.04	0.04	
	310	0.03	0.00	0.00	0.07	0.00	0.00	0.03	0.06	0.02	0.02	0.06	0.02	
	314	0.01	0.03	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	
	318	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.00	0.00	0.02	0.06	0.02	
	322	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.02	0.02	
	326	0.00	0.03	0.00	0.02	0.00	0.00	0.00	0.00	0.02	0.02	0.00	0.00	
	330	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.02	0.00	
	334	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.03	0.00	0.02	0.00	
	338	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	
	342	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	
N		62	15	8	23	19	6	18	36	29	27	24	27	
F_{IS}		0.03	-0.05	-0.05	0.17	-0.04	-0.02	0.02	0.05	0.03	-0.05	-0.04	0.02	

Locus	Allele	Population											
		sns-lr	sns-lk	sns-sp	sns-uk	Irs-lr	Irs-sp	Irs-uk	Iss-lr	Iss-sp	Iss uw	sss-lk	sss-rr
Dlu 4105													
	148	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00
	152	0.00	0.00	0.00	0.00	0.00	0.08	0.00	0.00	0.02	0.00	0.00	0.00
	156	0.00	0.00	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.02	0.00	0.00
	160	0.01	0.07	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.04	0.00	0.00
	164	0.01	0.03	0.06	0.00	0.00	0.00	0.06	0.01	0.00	0.00	0.00	0.00
	168	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.03
	172	0.02	0.00	0.00	0.07	0.03	0.00	0.03	0.00	0.02	0.00	0.00	0.00
	176	0.04	0.03	0.13	0.02	0.00	0.00	0.00	0.05	0.03	0.00	0.00	0.03
	180	0.07	0.03	0.00	0.04	0.03	0.00	0.00	0.05	0.02	0.00	0.00	0.07
	184	0.06	0.00	0.00	0.02	0.29	0.08	0.06	0.03	0.05	0.02	0.00	0.02
	188	0.06	0.10	0.00	0.15	0.13	0.08	0.09	0.07	0.03	0.07	0.00	0.07
	192	0.02	0.07	0.06	0.02	0.21	0.00	0.06	0.01	0.07	0.04	0.02	0.05
	196	0.02	0.03	0.13	0.09	0.18	0.17	0.12	0.01	0.05	0.04	0.02	0.10
	200	0.07	0.10	0.06	0.07	0.03	0.17	0.24	0.08	0.03	0.11	0.08	0.05
	204	0.10	0.10	0.06	0.07	0.05	0.08	0.12	0.08	0.16	0.04	0.15	0.07
	208	0.08	0.07	0.00	0.15	0.03	0.00	0.06	0.12	0.05	0.26	0.08	0.07
	212	0.09	0.13	0.00	0.07	0.03	0.17	0.06	0.11	0.10	0.06	0.08	0.07
	216	0.07	0.03	0.13	0.04	0.00	0.00	0.03	0.07	0.12	0.11	0.08	0.02
	220	0.06	0.03	0.25	0.09	0.00	0.00	0.00	0.05	0.09	0.06	0.10	0.05
	224	0.04	0.03	0.00	0.02	0.00	0.00	0.00	0.05	0.03	0.11	0.13	0.09
	228	0.02	0.07	0.06	0.00	0.00	0.00	0.06	0.01	0.10	0.00	0.08	0.05
	232	0.04	0.00	0.00	0.02	0.00	0.00	0.03	0.03	0.02	0.02	0.08	0.02
	236	0.02	0.00	0.06	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.04	0.03
	238	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00
	240	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.02
	244	0.04	0.03	0.00	0.02	0.00	0.00	0.00	0.03	0.00	0.00	0.02	0.05
	248	0.04	0.03	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
	252	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.02
N		64	15	8	23	19	6	17	37	29	27	24	29
F_{IS}		-0.02	0.17	-0.09	0.17	-0.07	-0.05	0.03	-0.06	0.00	0.01	0.01	0.06

Locus	Allele	Population											
		sns-lr	sns-lk	sns-sp	sns-uk	lrs-lr	lrs-sp	lrs-uk	lss-lr	lss-sp	lss uw	sss-lk	sss-rr
Dlu 4139													
	156	0.00	0.00	0.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	160	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00
	162	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	164	0.00	0.00	0.06	0.02	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00
	168	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	172	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	176	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.02	0.07	0.02	0.08
	180	0.05	0.00	0.00	0.00	0.08	0.00	0.00	0.06	0.00	0.02	0.00	0.07
	182	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00
	184	0.09	0.04	0.00	0.04	0.03	0.17	0.00	0.09	0.00	0.02	0.00	0.03
	188	0.09	0.07	0.06	0.00	0.11	0.00	0.08	0.12	0.05	0.00	0.04	0.03
	192	0.04	0.18	0.00	0.06	0.08	0.17	0.08	0.08	0.05	0.02	0.02	0.07
	196	0.11	0.04	0.13	0.06	0.24	0.17	0.00	0.10	0.15	0.03	0.09	0.10
	200	0.08	0.07	0.06	0.14	0.05	0.17	0.17	0.06	0.18	0.21	0.20	0.13
	204	0.10	0.07	0.19	0.16	0.11	0.08	0.14	0.08	0.05	0.10	0.13	0.10
	208	0.06	0.04	0.06	0.10	0.16	0.17	0.22	0.05	0.15	0.16	0.07	0.13
	212	0.09	0.18	0.06	0.12	0.11	0.00	0.08	0.05	0.08	0.16	0.15	0.13
	216	0.10	0.07	0.00	0.06	0.03	0.00	0.11	0.10	0.07	0.07	0.11	0.07
	220	0.03	0.04	0.31	0.04	0.00	0.00	0.03	0.05	0.15	0.14	0.11	0.00
	224	0.06	0.00	0.00	0.08	0.03	0.00	0.03	0.06	0.03	0.00	0.04	0.00
	228	0.07	0.14	0.00	0.02	0.00	0.00	0.03	0.04	0.02	0.00	0.00	0.02
	232	0.00	0.04	0.00	0.04	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.02
	236	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.02
	244	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00
	252	0.00	0.00	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.00	0.00
N		64	14	8	25	19	6	18	39	30	29	23	30
F_{IS}		-0.01	-0.09	0.01	0.05	0.18	-0.09	-0.06	-0.04	-0.01	-0.14	-0.11	-0.05

Locus	Allele	Population											
		sns-lr	sns-lk	sns-sp	sns-uk	Irs-lr	Irs-sp	Irs-uk	Iss-lr	Iss-sp	Iss-uw	sss-lk	sss-rr
Dlu 4283													
	98	0.02	0.00	0.06	0.00	0.03	0.00	0.03	0.01	0.00	0.00	0.02	0.00
	102	0.00	0.00	0.00	0.02	0.03	0.17	0.03	0.00	0.00	0.00	0.00	0.00
	104	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00
	106	0.00	0.07	0.06	0.16	0.21	0.33	0.25	0.00	0.11	0.00	0.08	0.00
	110	0.01	0.07	0.13	0.08	0.18	0.50	0.14	0.01	0.05	0.00	0.10	0.00
	114	0.05	0.07	0.13	0.24	0.24	0.00	0.08	0.03	0.23	0.03	0.08	0.00
	118	0.20	0.07	0.13	0.08	0.32	0.00	0.06	0.20	0.19	0.00	0.33	0.05
	122	0.24	0.20	0.00	0.04	0.00	0.00	0.11	0.40	0.07	0.00	0.10	0.17
	126	0.06	0.17	0.00	0.06	0.00	0.00	0.00	0.05	0.03	0.32	0.13	0.17
	127	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00
	130	0.07	0.07	0.13	0.04	0.00	0.00	0.03	0.03	0.02	0.07	0.06	0.10
	134	0.06	0.07	0.13	0.06	0.00	0.00	0.06	0.04	0.11	0.38	0.02	0.02
	138	0.09	0.07	0.06	0.08	0.00	0.00	0.06	0.04	0.02	0.00	0.00	0.03
	142	0.03	0.10	0.00	0.08	0.00	0.00	0.03	0.04	0.02	0.13	0.00	0.02
	146	0.03	0.03	0.06	0.02	0.00	0.00	0.06	0.05	0.03	0.00	0.00	0.08
	150	0.02	0.03	0.06	0.02	0.00	0.00	0.03	0.05	0.03	0.00	0.04	0.10
	154	0.03	0.00	0.06	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.15
	158	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.02	0.02	0.00	0.05
	162	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.01	0.00	0.03	0.00	0.02
	166	0.01	0.00	0.00	0.00	0.00	0.00	0.06	0.01	0.05	0.02	0.00	0.00
	170	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	178	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
	196	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00
	202	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	206	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
	214	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
N		65	15	8	25	19	6	18	38	31	30	24	30
F_{IS}		-0.01	0.13	0.09	-0.03	0.13	-0.28	-0.05	0.08	0.20	0.24	-0.13	0.00

Locus	Allele	Population											
		sns-lr	sns-lk	sns-sp	sns-uk	lrs-lr	lrs-sp	lrs-uk	lss-lr	lss-sp	lss uw	sss-lk	sss-rr
Dlu 4153													
	108	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.07	0.00	0.04	0.00
	116	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00
	120	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00
	124	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.13	0.03
	128	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.07	0.03
	132	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.09	0.05
	136	0.15	0.00	0.00	0.02	0.00	0.00	0.00	0.13	0.00	0.00	0.07	0.15
	140	0.02	0.07	0.00	0.02	0.00	0.00	0.00	0.03	0.02	0.02	0.02	0.22
	144	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.07	0.13	0.08
	148	0.07	0.00	0.00	0.08	0.00	0.08	0.00	0.04	0.14	0.02	0.20	0.08
	152	0.01	0.10	0.00	0.10	0.24	0.00	0.00	0.01	0.03	0.00	0.04	0.00
	156	0.05	0.03	0.13	0.13	0.05	0.17	0.08	0.05	0.10	0.02	0.02	0.07
	158	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	160	0.03	0.17	0.31	0.10	0.11	0.00	0.08	0.05	0.02	0.27	0.04	0.05
	164	0.08	0.07	0.13	0.06	0.05	0.08	0.17	0.11	0.07	0.04	0.02	0.02
	168	0.14	0.20	0.13	0.17	0.11	0.42	0.06	0.11	0.10	0.09	0.00	0.02
	172	0.21	0.03	0.00	0.06	0.00	0.00	0.11	0.20	0.17	0.34	0.00	0.03
	176	0.14	0.03	0.00	0.04	0.16	0.17	0.08	0.11	0.07	0.02	0.00	0.08
	180	0.01	0.07	0.06	0.00	0.11	0.00	0.03	0.03	0.00	0.05	0.00	0.00
	184	0.02	0.03	0.06	0.00	0.00	0.00	0.08	0.04	0.09	0.04	0.00	0.03
	188	0.03	0.03	0.00	0.00	0.03	0.00	0.03	0.05	0.00	0.02	0.00	0.02
	192	0.00	0.07	0.00	0.04	0.00	0.00	0.14	0.04	0.00	0.00	0.04	0.00
	194	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	196	0.00	0.00	0.19	0.02	0.05	0.00	0.06	0.00	0.00	0.00	0.00	0.02
	200	0.00	0.00	0.00	0.02	0.03	0.00	0.06	0.00	0.03	0.00	0.00	0.00
	204	0.00	0.03	0.00	0.00	0.00	0.08	0.03	0.00	0.00	0.02	0.00	0.02
	208	0.00	0.00	0.00	0.04	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	212	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	216	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	224	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	228	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00
	240	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00
	244	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
N		63	15	8	24	19	6	18	38	29	28	23	30
F_{IS}		0.03	-0.01	-0.17	0.06	-0.06	0.20	-0.08	-0.07	0.02	-0.20	0.06	0.01

Locus	Allele	Population												
		sns-lr	sns-lk	sns-sp	sns-uk	Irs-lr	Irs-sp	Irs-uk	Iss-lr	Iss-sp	Iss-uw	sss-lk	sss-rr	
Dlu 4296														
	156	0.00	0.03	0.07	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	160	0.01	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	164	0.00	0.03	0.00	0.00	0.03	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00
	168	0.00	0.07	0.00	0.02	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00
	172	0.02	0.03	0.00	0.02	0.03	0.00	0.00	0.03	0.03	0.00	0.00	0.00	0.00
	176	0.01	0.03	0.00	0.00	0.00	0.00	0.00	0.01	0.03	0.00	0.00	0.00	0.00
	180	0.01	0.00	0.07	0.00	0.00	0.00	0.06	0.00	0.02	0.02	0.00	0.00	0.03
	182	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00
	184	0.04	0.00	0.00	0.06	0.11	0.17	0.06	0.00	0.00	0.13	0.00	0.00	0.02
	188	0.03	0.03	0.00	0.06	0.03	0.00	0.06	0.00	0.03	0.27	0.00	0.00	0.02
	189	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00
	192	0.05	0.07	0.00	0.04	0.05	0.00	0.06	0.04	0.08	0.13	0.06	0.06	0.02
	196	0.02	0.00	0.14	0.04	0.05	0.08	0.08	0.03	0.05	0.28	0.02	0.03	
	200	0.05	0.03	0.00	0.04	0.16	0.00	0.06	0.05	0.05	0.00	0.02	0.00	0.00
	204	0.04	0.07	0.07	0.06	0.00	0.33	0.00	0.06	0.03	0.03	0.04	0.00	0.00
	208	0.05	0.07	0.14	0.08	0.00	0.25	0.19	0.10	0.03	0.00	0.04	0.10	
	212	0.05	0.07	0.07	0.14	0.05	0.08	0.08	0.13	0.10	0.00	0.08	0.03	
	216	0.13	0.03	0.00	0.10	0.08	0.00	0.08	0.09	0.05	0.05	0.04	0.07	
	220	0.07	0.07	0.07	0.10	0.11	0.08	0.03	0.04	0.17	0.02	0.06	0.03	
	224	0.05	0.07	0.14	0.04	0.05	0.00	0.14	0.05	0.10	0.02	0.06	0.18	
	228	0.11	0.00	0.00	0.08	0.16	0.00	0.06	0.10	0.05	0.00	0.08	0.05	
	232	0.09	0.17	0.00	0.02	0.03	0.00	0.03	0.09	0.03	0.00	0.06	0.03	
	236	0.06	0.03	0.00	0.04	0.00	0.00	0.00	0.03	0.00	0.00	0.02	0.13	
	240	0.03	0.03	0.14	0.02	0.00	0.00	0.00	0.04	0.02	0.00	0.06	0.03	
	244	0.02	0.00	0.07	0.02	0.03	0.00	0.03	0.05	0.00	0.00	0.04	0.08	
	248	0.01	0.03	0.00	0.02	0.00	0.00	0.00	0.01	0.05	0.00	0.06	0.05	
	252	0.01	0.03	0.00	0.00	0.03	0.00	0.00	0.00	0.02	0.00	0.02	0.05	
	256	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.02	
	260	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.02	0.00	0.00	0.02	
	264	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.02	0.00	
	268	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	
	276	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	
	280	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	
	292	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	
	296	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00	
	300	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	
	312	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	
	324	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	
N		65	15	7	25	19	6	18	39	30	30	24	30	
F_{IS}		-0.05	-0.04	-0.05	-0.02	-0.02	-0.20	-0.02	0.10	0.08	-0.02	-0.03	0.03	

Locus	Allele	Population											
		sns-lr	sns-lk	sns-sp	sns-uk	lrs-lr	lrs-sp	lrs-uk	lss-lr	lss-sp	lss uw	sss-lk	sss-rr
Dlu 4184													
	160	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	164	0.00	0.00	0.00	0.00	0.00	0.08	0.06	0.00	0.00	0.00	0.00	0.00
	168	0.00	0.00	0.07	0.00	0.00	0.00	0.03	0.01	0.00	0.00	0.00	0.00
	170	0.00	0.00	0.00	0.00	0.05	0.08	0.06	0.00	0.00	0.00	0.00	0.00
	172	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00
	174	0.00	0.00	0.00	0.02	0.00	0.00	0.06	0.00	0.00	0.00	0.00	0.00
	176	0.00	0.00	0.00	0.02	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	180	0.01	0.00	0.07	0.02	0.18	0.08	0.00	0.01	0.03	0.00	0.00	0.00
	182	0.01	0.00	0.00	0.00	0.03	0.00	0.00	0.03	0.00	0.00	0.00	0.00
	184	0.05	0.00	0.00	0.02	0.03	0.25	0.06	0.09	0.08	0.00	0.00	0.00
	188	0.02	0.03	0.00	0.02	0.05	0.08	0.08	0.04	0.02	0.00	0.08	0.00
	192	0.02	0.07	0.00	0.04	0.00	0.08	0.03	0.01	0.03	0.12	0.04	0.00
	196	0.06	0.00	0.07	0.04	0.03	0.00	0.11	0.03	0.16	0.12	0.04	0.00
	200	0.12	0.13	0.00	0.06	0.03	0.17	0.03	0.13	0.16	0.08	0.15	0.05
	204	0.06	0.10	0.14	0.04	0.03	0.08	0.03	0.03	0.03	0.45	0.06	0.05
	208	0.09	0.03	0.07	0.08	0.26	0.00	0.03	0.06	0.11	0.07	0.00	0.17
	212	0.12	0.07	0.14	0.10	0.11	0.00	0.08	0.10	0.03	0.02	0.00	0.20
	216	0.08	0.07	0.21	0.14	0.03	0.08	0.08	0.03	0.02	0.00	0.06	0.25
	220	0.06	0.07	0.07	0.06	0.08	0.00	0.08	0.05	0.00	0.02	0.00	0.05
	224	0.10	0.07	0.00	0.08	0.00	0.00	0.00	0.08	0.05	0.03	0.04	0.12
	228	0.02	0.13	0.00	0.08	0.05	0.00	0.08	0.03	0.07	0.07	0.00	0.07
	232	0.02	0.00	0.07	0.02	0.03	0.00	0.00	0.05	0.03	0.03	0.02	0.03
	236	0.05	0.07	0.07	0.02	0.00	0.00	0.03	0.10	0.03	0.00	0.02	0.00
	240	0.02	0.00	0.00	0.04	0.00	0.00	0.00	0.05	0.07	0.00	0.10	0.00
	244	0.02	0.10	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.04	0.02
	248	0.09	0.03	0.00	0.04	0.00	0.00	0.06	0.05	0.03	0.00	0.06	0.00
	252	0.01	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00
	256	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.00
	260	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.02	0.00
	264	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.03	0.00	0.04	0.00
	268	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00
	270	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	284	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00
	292	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00
	296	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00
N		65	15	7	25	19	6	18	39	31	30	24	30
F_{IS}		-0.03	0.01	-0.06	0.08	-0.01	0.12	0.02	0.07	0.02	-0.14	-0.01	-0.13

Locus	Allele	Population											
		sns-lr	sns-lk	sns-sp	sns-uk	Irs-lr	Irs-sp	Irs-uk	Iss-lr	Iss-sp	Iss uw	sss-lk	sss-rr
Dlu 4235													
	150	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00
	152	0.00	0.00	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.00	0.00
	164	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.02	0.00
	168	0.01	0.07	0.00	0.02	0.03	0.00	0.03	0.00	0.00	0.00	0.04	0.00
	172	0.00	0.00	0.00	0.00	0.00	0.08	0.03	0.00	0.00	0.00	0.00	0.00
	176	0.00	0.00	0.00	0.00	0.03	0.08	0.09	0.00	0.02	0.00	0.00	0.00
	177	0.00	0.00	0.13	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	180	0.00	0.00	0.06	0.00	0.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	184	0.00	0.03	0.00	0.06	0.13	0.00	0.06	0.00	0.00	0.04	0.02	0.00
	188	0.01	0.03	0.00	0.04	0.00	0.08	0.09	0.01	0.11	0.05	0.02	0.00
	189	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.09	0.00	0.00
	192	0.05	0.03	0.00	0.00	0.16	0.00	0.00	0.05	0.04	0.18	0.04	0.00
	194	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00
	196	0.10	0.03	0.00	0.08	0.08	0.00	0.00	0.16	0.02	0.00	0.09	0.00
	200	0.08	0.20	0.00	0.02	0.11	0.00	0.16	0.04	0.15	0.02	0.04	0.00
	204	0.05	0.13	0.13	0.02	0.03	0.00	0.03	0.16	0.11	0.09	0.07	0.00
	208	0.19	0.03	0.06	0.06	0.05	0.00	0.00	0.12	0.11	0.05	0.07	0.08
	212	0.06	0.00	0.13	0.08	0.03	0.17	0.03	0.12	0.09	0.02	0.09	0.08
	216	0.09	0.10	0.00	0.06	0.05	0.00	0.19	0.05	0.04	0.02	0.00	0.05
	217	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
	220	0.02	0.03	0.06	0.13	0.05	0.08	0.03	0.04	0.02	0.09	0.00	0.07
	224	0.10	0.13	0.19	0.06	0.05	0.17	0.00	0.00	0.09	0.05	0.09	0.13
	228	0.06	0.00	0.06	0.06	0.03	0.08	0.03	0.07	0.07	0.05	0.02	0.10
	232	0.06	0.00	0.00	0.13	0.00	0.00	0.09	0.07	0.00	0.00	0.11	0.07
	236	0.03	0.10	0.00	0.04	0.00	0.00	0.03	0.04	0.02	0.04	0.11	0.05
	238	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	240	0.05	0.00	0.13	0.04	0.00	0.08	0.00	0.03	0.02	0.20	0.02	0.17
	244	0.02	0.00	0.06	0.00	0.00	0.08	0.03	0.05	0.02	0.02	0.00	0.02
	248	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.02	0.00	0.09	0.03
	252	0.00	0.03	0.00	0.02	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.03
	256	0.01	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.07
	260	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.02
	264	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.02
	268	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00
N		65	15	8	24	19	6	16	38	23	28	23	30
F_{IS}		0.06	-0.09	0.08	0.03	0.02	0.15	-0.01	0.17	0.17	-0.03	-0.01	0.06

Locus	Allele	Population											
		sns-lr	sns-lk	sns-sp	sns-uk	Irs-lr	Irs-sp	Irs-uk	Iss-lr	Iss-sp	Iss uw	sss-lk	sss-rr
<i>Dlu 4259</i>													
	102	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	138	0.08	0.04	0.08	0.02	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00
	142	0.00	0.04	0.00	0.02	0.00	0.00	0.00	0.00	0.03	0.02	0.02	0.00
	146	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.12	0.04	0.00
	150	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.03	0.02	0.00	0.00
	154	0.01	0.07	0.00	0.00	0.00	0.00	0.03	0.03	0.07	0.00	0.02	0.00
	156	0.01	0.00	0.00	0.00	0.03	0.00	0.03	0.00	0.00	0.00	0.02	0.00
	158	0.01	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.00
	160	0.00	0.00	0.00	0.02	0.00	0.00	0.06	0.00	0.00	0.00	0.00	0.00
	162	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.02	0.05
	163	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
	166	0.03	0.04	0.00	0.04	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.07
	168	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.02	0.00	0.00	0.00
	170	0.08	0.00	0.00	0.09	0.21	0.08	0.06	0.05	0.05	0.00	0.02	0.03
	174	0.05	0.04	0.17	0.04	0.13	0.08	0.11	0.04	0.05	0.00	0.00	0.00
	178	0.17	0.04	0.08	0.15	0.03	0.08	0.00	0.15	0.08	0.03	0.15	0.05
	182	0.23	0.11	0.08	0.02	0.03	0.25	0.08	0.21	0.21	0.00	0.15	0.10
	186	0.07	0.07	0.00	0.11	0.16	0.08	0.11	0.09	0.07	0.17	0.10	0.13
	190	0.01	0.04	0.17	0.07	0.00	0.00	0.11	0.09	0.05	0.12	0.06	0.07
	194	0.08	0.07	0.08	0.07	0.18	0.00	0.06	0.13	0.11	0.25	0.04	0.13
	198	0.09	0.07	0.17	0.07	0.11	0.00	0.14	0.06	0.03	0.18	0.04	0.13
	202	0.04	0.04	0.00	0.04	0.00	0.17	0.06	0.01	0.02	0.10	0.06	0.05
	206	0.03	0.04	0.00	0.02	0.00	0.17	0.06	0.05	0.05	0.00	0.02	0.10
	210	0.03	0.07	0.00	0.07	0.11	0.08	0.08	0.04	0.00	0.00	0.10	0.02
	214	0.00	0.04	0.08	0.04	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00
	216	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00
	218	0.00	0.00	0.00	0.04	0.00	0.00	0.03	0.00	0.00	0.00	0.08	0.05
	222	0.01	0.07	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.02	0.00
	230	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	232	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00
	238	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00
	262	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	266	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
N		60	14	6	23	19	6	18	39	31	30	24	30
F_{IS}		-0.03	-0.03	-0.05	-0.06	0.04	-0.09	-0.07	-0.07	-0.03	-0.05	-0.10	-0.03

Locus	Allele	Population											
		sns-lr	sns-lk	sns-sp	sns-uk	lrs-lr	lrs-sp	lrs-uk	lss-lr	lss-sp	lss uw	sss-lk	sss-rr
Dlu 4314													
	208	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.00	0.00	0.00	0.00	0.00
	212	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00
	214	0.00	0.00	0.00	0.00	0.00	0.17	0.00	0.00	0.00	0.00	0.00	0.00
	216	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00
	220	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	224	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00
	228	0.00	0.07	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.05	0.00
	230	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	232	0.00	0.00	0.00	0.02	0.00	0.00	0.03	0.01	0.00	0.00	0.05	0.00
	234	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	236	0.01	0.03	0.00	0.00	0.00	0.00	0.06	0.03	0.02	0.00	0.03	0.00
	240	0.06	0.07	0.06	0.08	0.08	0.08	0.06	0.06	0.02	0.09	0.03	0.00
	244	0.09	0.07	0.00	0.02	0.11	0.00	0.03	0.11	0.08	0.02	0.05	0.00
	248	0.14	0.07	0.19	0.00	0.19	0.00	0.06	0.17	0.07	0.00	0.00	0.00
	252	0.10	0.07	0.00	0.04	0.03	0.08	0.14	0.04	0.05	0.00	0.10	0.02
	256	0.05	0.03	0.06	0.04	0.17	0.08	0.08	0.04	0.03	0.04	0.00	0.04
	260	0.08	0.13	0.19	0.25	0.28	0.17	0.17	0.08	0.13	0.18	0.10	0.02
	264	0.08	0.10	0.06	0.17	0.00	0.17	0.14	0.01	0.08	0.20	0.08	0.07
	268	0.13	0.10	0.13	0.10	0.00	0.00	0.03	0.08	0.17	0.07	0.13	0.06
	272	0.08	0.00	0.13	0.15	0.06	0.08	0.08	0.11	0.10	0.02	0.05	0.02
	276	0.03	0.03	0.06	0.00	0.00	0.17	0.03	0.08	0.03	0.00	0.08	0.11
	280	0.03	0.13	0.00	0.02	0.00	0.00	0.00	0.01	0.02	0.07	0.08	0.13
	284	0.04	0.03	0.00	0.00	0.03	0.00	0.03	0.06	0.02	0.04	0.03	0.06
	288	0.04	0.00	0.06	0.06	0.03	0.00	0.00	0.04	0.08	0.05	0.03	0.09
	292	0.02	0.00	0.06	0.00	0.00	0.00	0.00	0.01	0.05	0.04	0.08	0.07
	296	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.09
	300	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.09
	304	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.05	0.00	0.06
	308	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.02
	312	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.09	0.03	0.04
	316	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
	324	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00
N		60	15	8	24	18	6	18	36	30	28	20	27
F_{IS}		0.17	0.16	0.21	0.20	0.16	0.31	0.04	0.10	0.14	0.30	0.00	-0.07

Locus	Allele	Population											
		sns-lr	sns-lk	sns-sp	sns-uk	Irs-lr	Irs-sp	Irs-uk	Iss-lr	Iss-sp	Iss uw	sss-lk	sss-rr
Dlu 461													
	133	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00
	185	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00
	189	0.00	0.08	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.02	0.00	0.00
	193	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.15	0.00	0.00
	197	0.02	0.00	0.00	0.00	0.03	0.00	0.03	0.06	0.02	0.00	0.00	0.00
	201	0.07	0.00	0.00	0.00	0.00	0.00	0.06	0.08	0.05	0.00	0.00	0.00
	205	0.05	0.04	0.13	0.04	0.28	0.30	0.06	0.06	0.00	0.04	0.00	0.00
	209	0.11	0.04	0.00	0.08	0.09	0.00	0.03	0.13	0.03	0.19	0.00	0.00
	213	0.13	0.04	0.19	0.10	0.13	0.20	0.24	0.11	0.03	0.02	0.02	0.00
	217	0.10	0.00	0.13	0.10	0.13	0.30	0.12	0.06	0.07	0.02	0.02	0.00
	221	0.12	0.04	0.06	0.08	0.03	0.10	0.03	0.13	0.03	0.00	0.05	0.00
	225	0.09	0.17	0.06	0.02	0.06	0.00	0.06	0.14	0.12	0.00	0.02	0.00
	229	0.04	0.04	0.13	0.06	0.00	0.00	0.03	0.06	0.12	0.04	0.05	0.03
	233	0.00	0.21	0.00	0.02	0.13	0.00	0.00	0.03	0.02	0.02	0.02	0.02
	237	0.07	0.08	0.13	0.06	0.13	0.00	0.06	0.03	0.07	0.04	0.07	0.03
	241	0.06	0.00	0.06	0.10	0.00	0.00	0.09	0.03	0.10	0.23	0.11	0.03
	245	0.05	0.08	0.06	0.00	0.00	0.00	0.03	0.03	0.05	0.17	0.05	0.18
	249	0.04	0.08	0.00	0.08	0.00	0.00	0.06	0.03	0.00	0.04	0.09	0.07
	253	0.02	0.00	0.00	0.13	0.00	0.00	0.06	0.00	0.03	0.00	0.07	0.07
	257	0.00	0.04	0.06	0.00	0.00	0.00	0.00	0.01	0.03	0.00	0.14	0.07
	261	0.00	0.00	0.00	0.00	0.00	0.10	0.00	0.00	0.02	0.00	0.02	0.13
	265	0.01	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.03	0.00	0.02	0.10
	269	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.01	0.00	0.00	0.05	0.08
	273	0.01	0.00	0.00	0.04	0.00	0.00	0.00	0.03	0.02	0.00	0.09	0.08
	277	0.02	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.03	0.00	0.02	0.03
	281	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.02	0.02
	285	0.01	0.04	0.00	0.02	0.00	0.00	0.00	0.00	0.02	0.00	0.02	0.02
	289	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.03
	301	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
N		63	12	8	24	16	5	17	36	29	24	22	30
F_{IS}		0.02	0.01	-0.07	0.11	-0.01	-0.21	-0.02	0.04	0.09	0.09	-0.01	0.10

Locus	Allele	Population											
		sns-lr	sns-lk	sns-sp	sns-uk	Irs-lr	Irs-sp	Irs-uk	Iss-lr	Iss-sp	Iss uw	sss-lk	sss-rr
Dlu 4123													
	137	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
	139	0.00	0.03	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.21
	143	0.00	0.00	0.00	0.02	0.05	0.00	0.03	0.00	0.02	0.00	0.00	0.09
	147	0.00	0.00	0.29	0.09	0.05	0.00	0.03	0.01	0.02	0.02	0.06	0.28
	151	0.02	0.03	0.07	0.02	0.05	0.25	0.08	0.04	0.10	0.04	0.19	0.19
	155	0.01	0.10	0.07	0.04	0.11	0.08	0.11	0.03	0.00	0.02	0.06	0.09
	159	0.22	0.13	0.14	0.13	0.37	0.17	0.11	0.28	0.14	0.00	0.06	0.03
	163	0.16	0.10	0.21	0.07	0.05	0.00	0.19	0.13	0.26	0.39	0.04	0.05
	167	0.09	0.07	0.07	0.15	0.00	0.00	0.17	0.03	0.10	0.14	0.04	0.00
	171	0.10	0.13	0.07	0.09	0.03	0.25	0.03	0.11	0.09	0.00	0.02	0.02
	175	0.14	0.17	0.00	0.09	0.03	0.00	0.06	0.14	0.07	0.02	0.15	0.03
	179	0.17	0.10	0.00	0.07	0.03	0.00	0.03	0.14	0.09	0.02	0.08	0.00
	183	0.03	0.03	0.07	0.11	0.00	0.17	0.08	0.01	0.09	0.10	0.06	0.00
	187	0.03	0.03	0.00	0.02	0.03	0.00	0.03	0.03	0.03	0.06	0.08	0.00
	191	0.00	0.00	0.00	0.00	0.13	0.00	0.00	0.04	0.00	0.12	0.08	0.00
	195	0.00	0.07	0.00	0.04	0.08	0.00	0.03	0.00	0.00	0.10	0.04	0.00
	199	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00
	203	0.00	0.00	0.00	0.02	0.00	0.08	0.00	0.00	0.00	0.00	0.00	0.00
	207	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00
	215	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	219	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	223	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00
N		59	15	7	23	19	6	18	36	29	26	24	29
F_{IS}		-0.12	-0.09	0.04	0.02	0.12	-0.15	0.03	0.10	-0.10	0.05	0.05	-0.07

Locus	Allele	Population											
		sns-lr	sns-lk	sns-sp	sns-uk	Irs-lr	Irs-sp	Irs-uk	Iss-lr	Iss-sp	Iss-uw	sss-lk	sss-rr
Dlu 466													
	232	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.02	0.00
	236	0.01	0.00	0.00	0.00	0.00	0.08	0.06	0.00	0.05	0.00	0.07	0.00
	240	0.16	0.25	0.38	0.19	0.13	0.17	0.00	0.19	0.10	0.30	0.31	0.20
	244	0.19	0.08	0.06	0.25	0.21	0.08	0.12	0.09	0.25	0.04	0.19	0.43
	248	0.07	0.00	0.06	0.06	0.08	0.33	0.06	0.06	0.08	0.41	0.07	0.05
	252	0.08	0.08	0.13	0.13	0.18	0.25	0.44	0.18	0.08	0.15	0.10	0.07
	256	0.04	0.04	0.13	0.06	0.11	0.08	0.12	0.02	0.02	0.00	0.10	0.25
	260	0.05	0.21	0.06	0.04	0.13	0.00	0.06	0.04	0.10	0.07	0.12	0.00
	264	0.03	0.08	0.00	0.04	0.13	0.00	0.03	0.00	0.10	0.04	0.00	0.00
	268	0.02	0.08	0.00	0.15	0.00	0.00	0.09	0.03	0.08	0.00	0.00	0.00
	272	0.05	0.08	0.06	0.02	0.00	0.00	0.00	0.06	0.03	0.00	0.02	0.00
	276	0.13	0.04	0.00	0.02	0.00	0.00	0.03	0.16	0.07	0.00	0.00	0.00
	280	0.13	0.04	0.06	0.04	0.03	0.00	0.00	0.13	0.00	0.00	0.00	0.00
	284	0.04	0.00	0.06	0.00	0.00	0.00	0.00	0.03	0.02	0.00	0.00	0.00
	288	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00
	N	59	12	8	24	19	6	17	34	30	27	21	28
	F_{IS}	0.01	0.07	0.13	0.19	0.10	-0.20	-0.06	-0.03	0.03	0.24	-0.02	0.31

Locus	Allele	Population												
		sns-lr	sns-lk	sns-sp	sns-uk	Irs-lr	Irs-sp	Irs-uk	Iss-lr	Iss-sp	Iss-uw	sss-lk	sss-rr	
Dlu 4183	150	0.00	0.00	0.00	0.00	0.00	0.08	0.06	0.01	0.00	0.00	0.05	0.00	
	154	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	
	158	0.00	0.00	0.06	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.11	0.00	
	162	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
	170	0.01	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.18	0.38	0.30	0.05	
	174	0.00	0.00	0.06	0.02	0.03	0.08	0.00	0.00	0.00	0.00	0.02	0.04	
	176	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	
	178	0.02	0.00	0.00	0.00	0.08	0.00	0.08	0.00	0.00	0.00	0.07	0.30	
	180	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	
	182	0.04	0.13	0.00	0.04	0.00	0.00	0.00	0.01	0.02	0.02	0.00	0.11	
	186	0.02	0.04	0.00	0.02	0.06	0.25	0.19	0.06	0.02	0.00	0.00	0.14	
	188	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	
	190	0.03	0.00	0.25	0.00	0.03	0.00	0.06	0.06	0.04	0.00	0.02	0.04	
	194	0.02	0.04	0.06	0.08	0.08	0.08	0.08	0.03	0.02	0.00	0.00	0.00	
	198	0.02	0.00	0.00	0.02	0.08	0.08	0.11	0.04	0.04	0.00	0.00	0.00	
	200	0.00	0.00	0.00	0.06	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	
	202	0.04	0.13	0.06	0.02	0.11	0.17	0.03	0.06	0.05	0.24	0.02	0.00	
	206	0.04	0.21	0.13	0.02	0.08	0.00	0.08	0.03	0.13	0.09	0.05	0.00	
	210	0.14	0.13	0.00	0.04	0.11	0.00	0.08	0.11	0.02	0.00	0.02	0.00	
	214	0.08	0.08	0.00	0.04	0.14	0.08	0.06	0.04	0.09	0.00	0.05	0.00	
	218	0.06	0.00	0.00	0.06	0.03	0.00	0.03	0.10	0.04	0.02	0.00	0.07	
	222	0.11	0.00	0.00	0.10	0.03	0.00	0.03	0.08	0.04	0.05	0.05	0.02	
	224	0.00	0.00	0.00	0.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
	226	0.11	0.04	0.00	0.12	0.03	0.08	0.00	0.07	0.04	0.00	0.05	0.00	
	230	0.07	0.08	0.06	0.02	0.06	0.00	0.06	0.07	0.02	0.00	0.07	0.00	
	232	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
	234	0.04	0.00	0.13	0.00	0.03	0.00	0.03	0.06	0.00	0.00	0.02	0.04	
	238	0.00	0.04	0.00	0.06	0.03	0.00	0.00	0.01	0.13	0.00	0.05	0.00	
	240	0.01	0.00	0.00	0.04	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	
	242	0.00	0.00	0.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.02	
	246	0.02	0.00	0.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
	250	0.01	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.02	0.00	0.05	0.00	
	252	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	
	254	0.04	0.00	0.00	0.02	0.00	0.00	0.00	0.03	0.05	0.00	0.00	0.00	
	258	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.04	
	262	0.02	0.04	0.00	0.00	0.00	0.00	0.00	0.01	0.02	0.00	0.00	0.00	
	266	0.00	0.00	0.06	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	
	274	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.02	0.00	0.00	0.00	
	278	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	
	282	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	
	284	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	
	286	0.01	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
	288	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.12	0.00	0.00	
	290	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
	292	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.02	0.00	0.02	
	296	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	
	308	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	
	312	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	
N		60	12	8	25	188	6	18	36	28	29	22	28	
F _{IS}		0.04	0.10	0.07	0.12	0.18	0.12	0.05	0.04	0.08	0.34	-0.02	0.60	

Table 4. Pairwise matrix of $(\delta\mu)^2$ genetic distance (top) and R_{ST} (bottom). Values in bold are not significant ($P < 0.05$ after Bonferroni adjustment and 1000 permutations).

	sns-lr	sns-lk	sns-sp	sns-uk	lrs-lr	lrs-sp	lrs-uk	sss-lk	sss-rr	lss-lr	lss-sp	lss uw
sns-lr	*	0.066	0.115	0.100	0.333	0.573	0.269	0.504	0.645	0.012	0.072	0.229
sns-lk	0.017	*	0.109	0.074	0.227	0.498	0.143	0.487	0.656	0.065	0.055	0.180
sns-sp	0.022	0.004	*	0.078	0.233	0.359	0.173	0.557	0.485	0.091	0.061	0.200
sns-uk	0.035	0.006	-0.002	*	0.293	0.474	0.225	0.375	0.519	0.084	0.037	0.172
lrs-lr	0.154	0.098	0.083	0.136	*	0.219	0.071	0.927	1.131	0.271	0.271	0.350
lrs-sp	0.181	0.146	0.098	0.156	0.056	*	0.315	1.118	1.252	0.519	0.485	0.575
lrs-uk	0.125	0.040	0.042	0.085	0.030	0.073	*	0.830	0.950	0.222	0.205	0.254
sss-lk	0.177	0.146	0.156	0.114	0.295	0.260	0.225	*	0.446	0.518	0.404	0.719
sss-rr	0.229	0.224	0.172	0.189	0.355	0.326	0.310	0.137	*	0.688	0.490	0.678
lss-lr	-0.003	0.012	0.007	0.028	0.138	0.172	0.106	0.173	0.235	*	0.068	0.236
lss-sp	0.025	0.000	-0.008	-0.001	0.130	0.149	0.073	0.118	0.189	0.019	*	0.145
lss uw	0.097	0.068	0.056	0.085	0.168	0.173	0.115	0.207	0.230	0.099	0.062	*

Table 5. Pairwise matrix of Nei's genetic distance (top) and F_{ST} (bottom). Values in bold are not significant ($P < 0.05$ after Bonferroni adjustment and 6600 permutations).

	sns-lr	sns-lk	sns-sp	sns-uk	lrs-lr	lrs-sp	lrs-uk	sss-lk	sss-rr	lss-lr	lss-sp	lss-uw
sns-lr	*	0.042	0.103	0.042	0.108	0.187	0.110	0.067	0.090	0.009	0.034	0.105
sns-lk	0.010	*	0.110	0.051	0.103	0.178	0.088	0.056	0.113	0.032	0.047	0.117
sns-sp	0.018	0.009	*	0.084	0.150	0.171	0.154	0.083	0.146	0.102	0.079	0.131
sns-uk	0.013	0.007	0.002	*	0.071	0.109	0.041	0.071	0.054	0.044	0.023	0.095
lrs-lr	0.037	0.030	0.028	0.026	*	0.136	0.090	0.116	0.184	0.107	0.069	0.176
lrs-sp	0.040	0.030	0.026	0.019	0.038	*	0.163	0.184	0.159	0.194	0.143	0.265
lrs-uk	0.027	0.017	0.017	0.011	0.030	0.020	*	0.124	0.130	0.082	0.059	0.126
sss-lk	0.024	0.015	0.018	0.013	0.046	0.042	0.034	*	0.091	0.047	0.071	0.148
sss-rr	0.035	0.031	0.025	0.028	0.060	0.055	0.042	0.029	*	0.095	0.124	0.155
lss-lr	0.001	0.010	0.017	0.017	0.040	0.041	0.027	0.025	0.040	*	0.031	0.118
lss-sp	0.013	0.010	0.008	0.007	0.031	0.031	0.018	0.012	0.037	0.018	*	0.101
lss-uw	0.068	0.056	0.052	0.056	0.089	0.089	0.064	0.062	0.081	0.074	0.052	*

Figure 1. Factor analysis of $(\delta\mu)^2$ genetic distance values using the Maximum Likelihood extraction method.

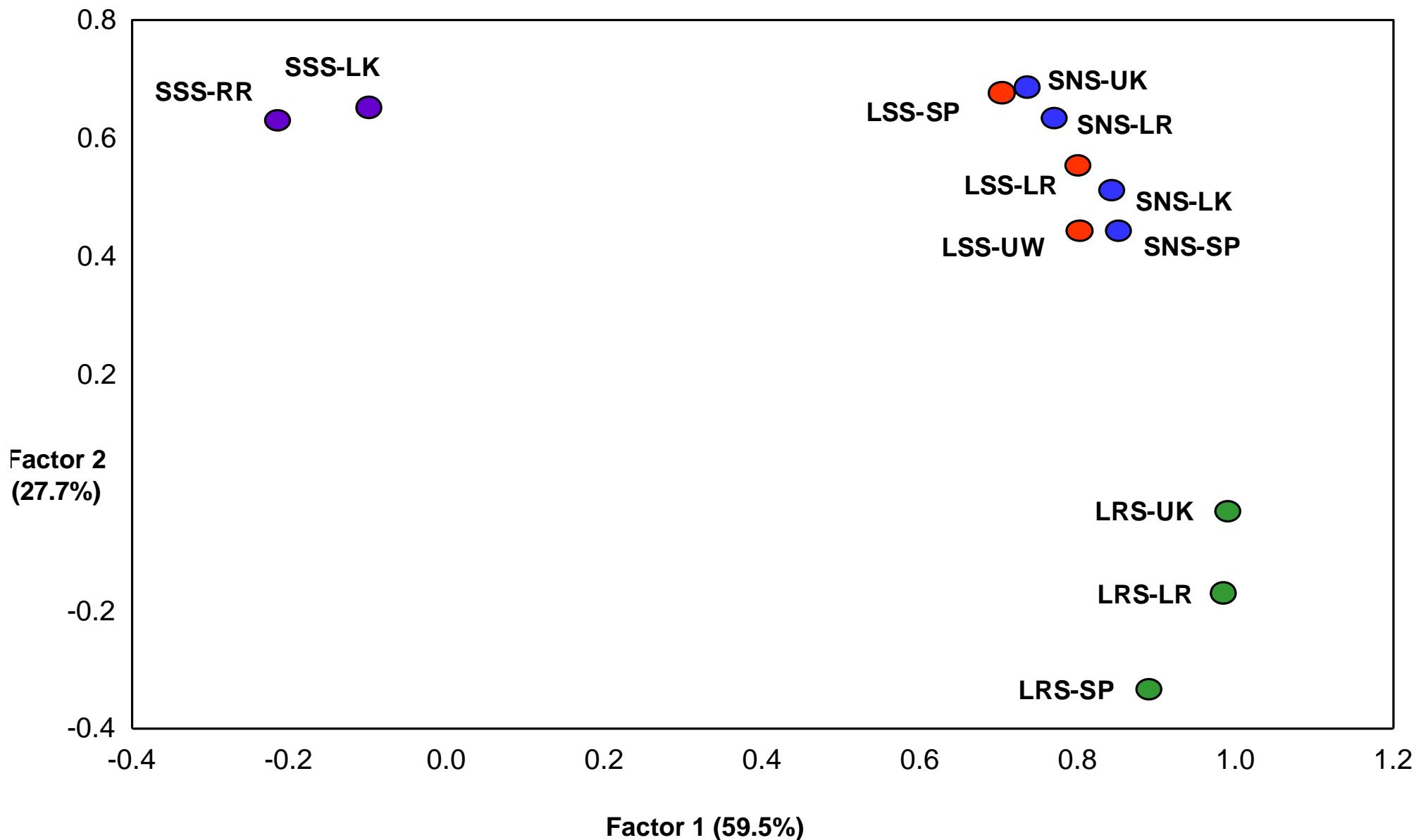


Figure 2. Factor analysis of Nei's genetic distance values using the Maximum Likelihood extraction method.

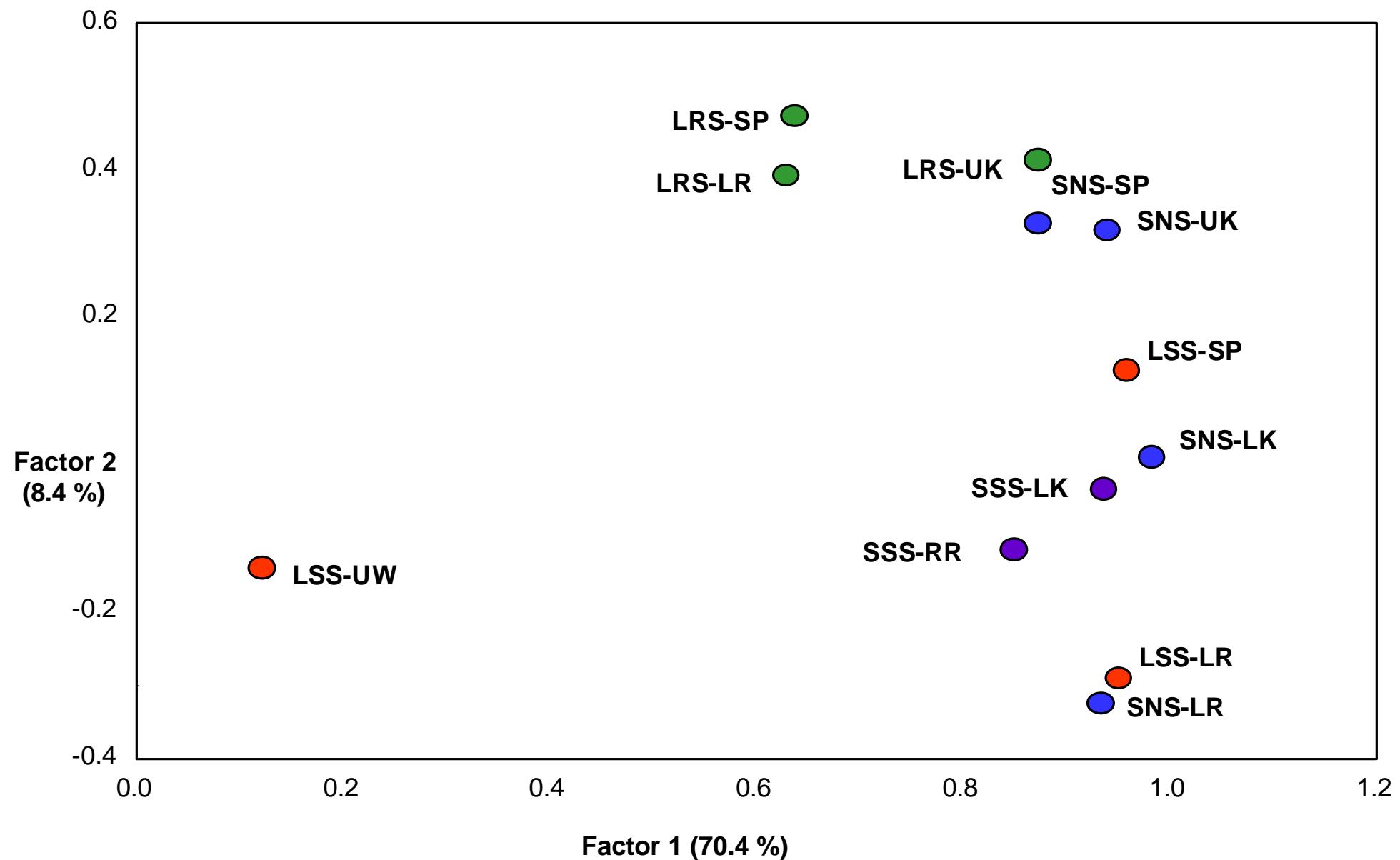


Figure 3. Factor analysis of pairwise R_{xy} values using the Principal Components extraction method. Samples are from the Lost River Basin.

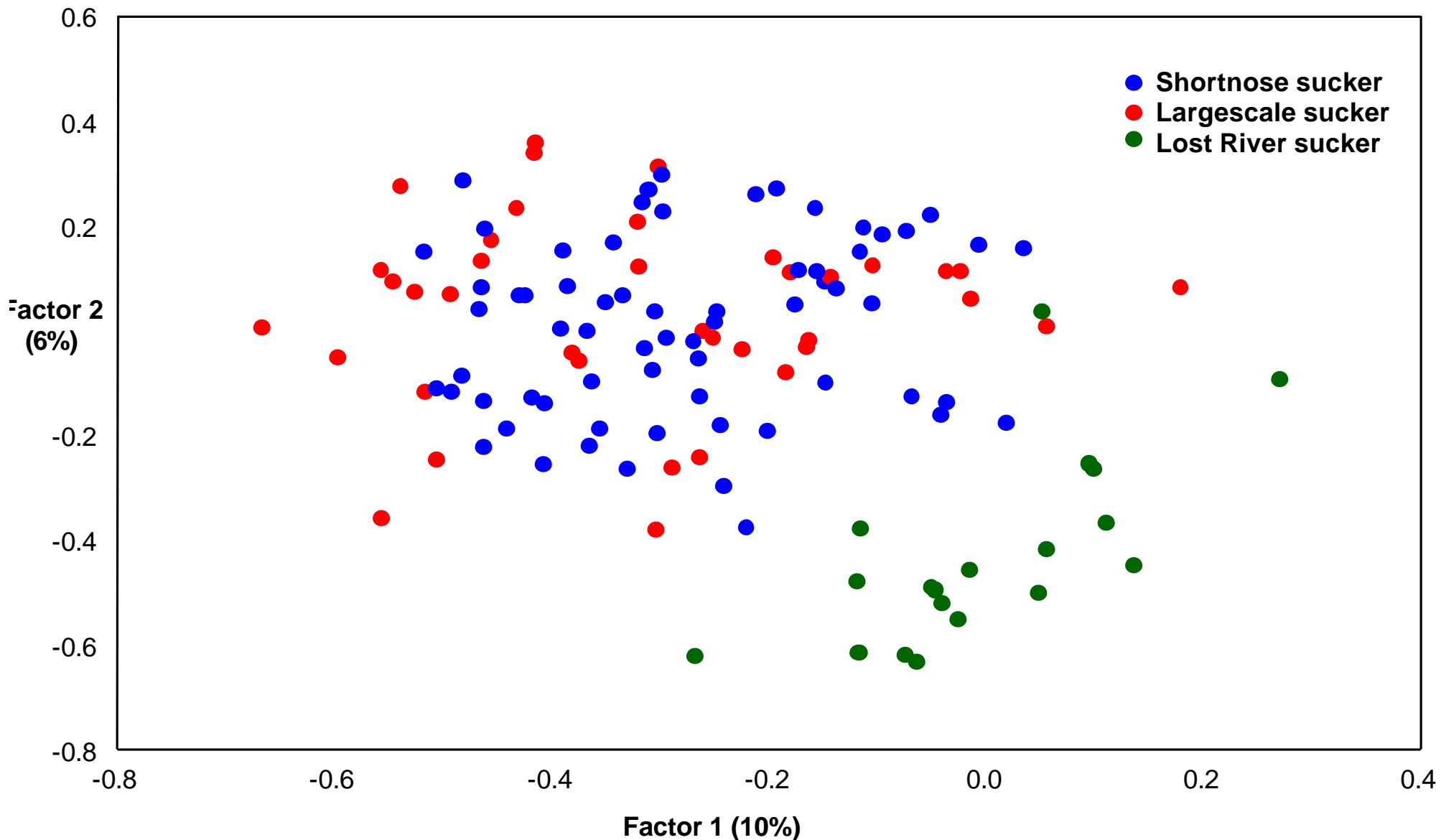


Figure 4. Factor analysis of pairwise R_{xy} values using the Principal Components extraction method. Samples are from Upper Klamath Lake.

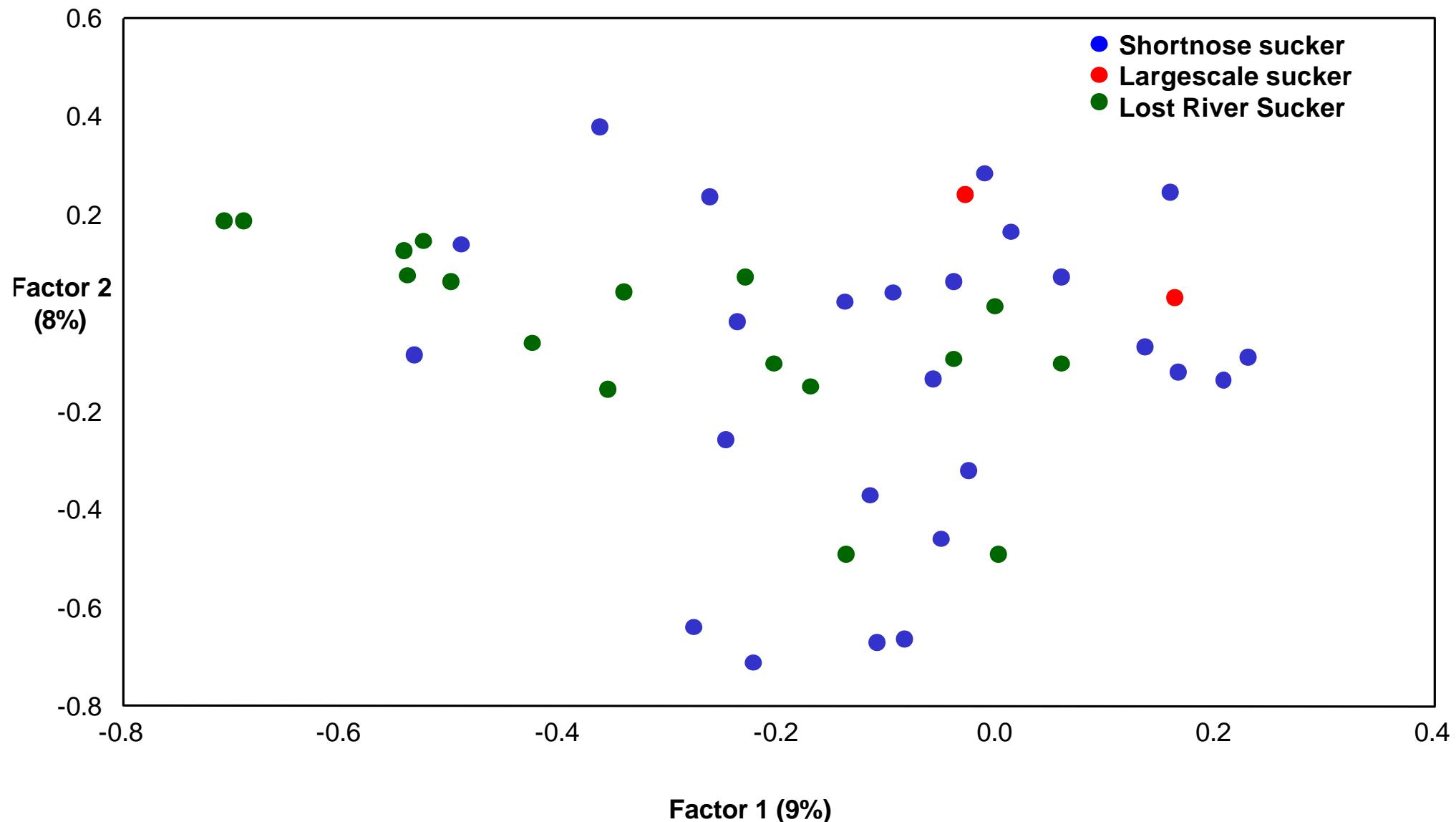


Figure 5. Factor analysis of pairwise R_{xy} values using the Principal Components extraction method. Samples are from the Sprague River Basin.

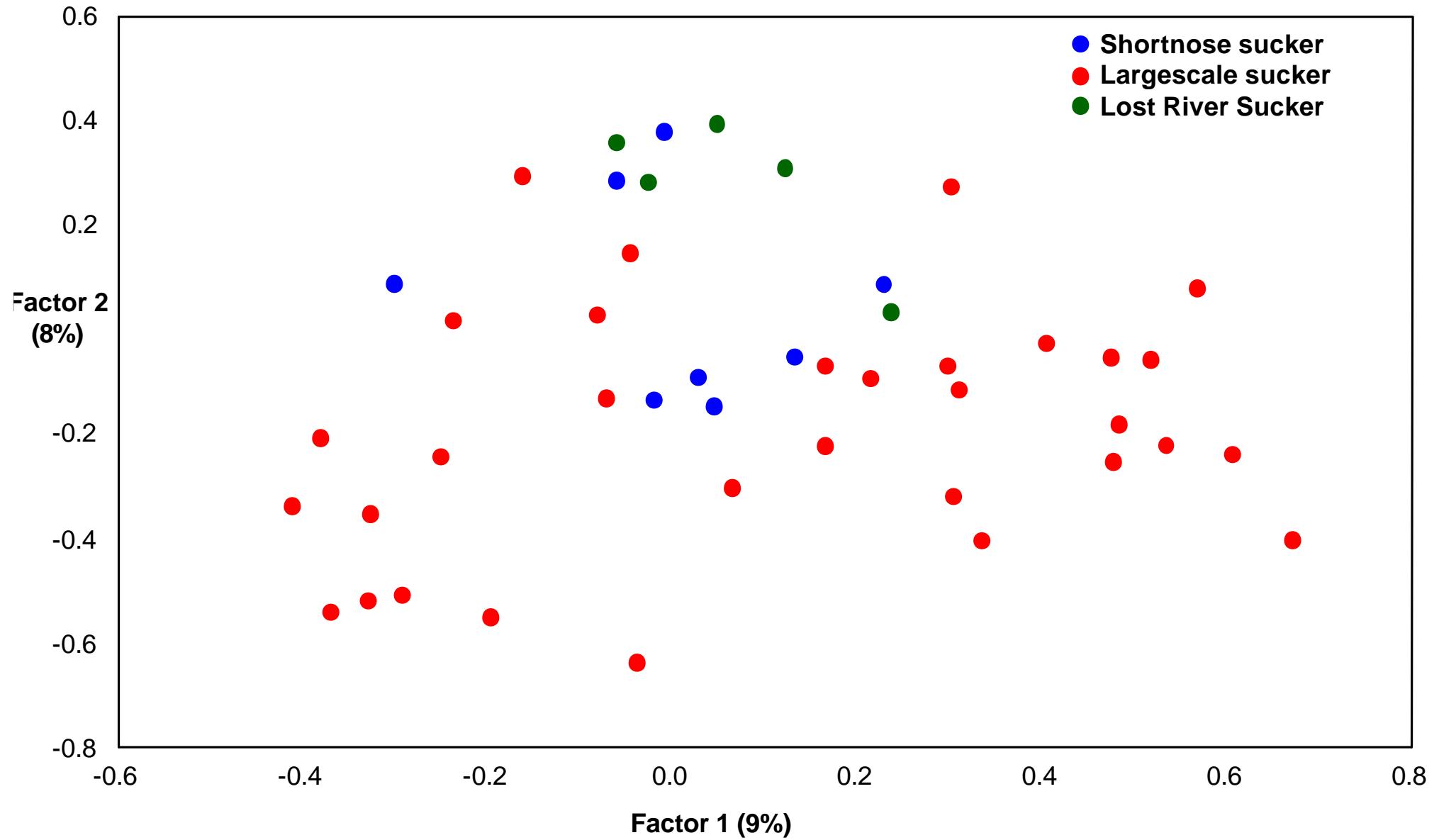


Figure 6. Factor analysis of pairwise R_{xy} values using the Principal Components extraction method. Samples are from Upper Klamath Lake, Sprague River Basin, and the Upper Williamson River.

