

Selektion von *Rhododendron* - Teilbereich III – ARC seibersdorf research

Erfassung der genetischen Vielfalt mittels Mikrosatelliten

Kurzfassung

Zielstellung des Projekts

Von den beiden heimischen *Rhododendron* Wildarten *R. ferrugineum* und *R. hirsutum* gibt es unseres Wissens noch keine in vitro vermehrten Klone. Der Einsatz der in vitro Vermehrung erlaubt eine rasche Selektion und Massenvermehrung praxisrelevanter Klone, die im Gartenbau und in der Begrünung eingesetzt werden können.

Im Vordergrund dieses Projektes steht die in vitro Etablierung und gezielte Selektion von *Rhododendron ferrugineum*, *R. hirsutum* und *R. x intermedium* Klonen aus umfassenden Naturstandorten und postglazialen Reliktbeständen (Österreich, Deutschland, Schweiz, Slowenien).

Es erfolgt somit eine Selektion von *Rhododendron* -Klonen die an bestimmte Boden- und Klimaverhältnisse angepasst sind und dadurch gezielter eingesetzt werden können.

Praxisrelevante Klone werden in der Folge beim Europäischen Sortenschutzamt angemeldet.

Die Erfassung der existierenden genetischen Vielfalt in den natürlichen Beständen - als auch die Zertifizierung spezieller *Rhododendron* -Klone - erfolgt mittels der gut reproduzierbaren Mikrosatellitenanalyse (SSRs). Für die beiden heimischen *Rhododendron* -Wildarten *R. ferrugineum* und *R. hirsutum* werden daher spezielle SSR Primer entwickelt.

1. Arbeitbericht:

1.1 Material

Von der HBLVA Schönbrunn wurde Pflanzenmaterial von 11 unterschiedlichen Naturstandorten und 12 in vitro Kulturen bereitgestellt. Das Material wurde in Form von Blattproben von insgesamt 305 Einzelpflanzen und Sämlinge der Probe 22/1 zur Verfügung gestellt.

Tabelle 1: Aufstellung des Untersuchungsmaterials

| Standort | Spezies | Kennung | Probenanzahl |
|------------------------------|------------|--------------|--------------|
| Populationen | | | |
| A/ Gutenstein-Klostertal | <i>h</i> | 19 | 22 |
| A/ Kirchkogel-Predigtstuhl | <i>f</i> | 20 | 20 |
| SLO/ Trnovski gozd | <i>h</i> | 21 | 21 |
| A/ Patscherkofel | <i>f</i> | 22 | 22 |
| A/ Karwendel-Seegrube | <i>h</i> | 23 | 24 |
| A/Kalkkögel-Saile | <i>f</i> | 24 | 20 |
| A/ Axamer Lizum | <i>i/f</i> | 25 | 20 |
| I/Viote-Trient | | 26 | 20 |
| A/ Großes Walsertal | <i>h</i> | 28 | 20 |
| A/ Fernpass-Blindsee | <i>f/i</i> | 29 | 20 |
| CH/Versam-Station, Chur | <i>h</i> | 30 | 20 |
| Samenherkünfte | | | |
| Churfürsten (CH) | <i>f</i> | 1 | 4 |
| Bot. Garten Frankfurt (D) | <i>f</i> | 2 | 4 |
| Pinzgau (A) | <i>f</i> | 3 | 3 |
| Pongau (A) | <i>f</i> | 5 | 5 |
| Tennengau (A) | <i>h</i> | 8 | 5 |
| Karawanken (A) | <i>h</i> | 11 | 3 |
| Churfürsten (CH) | <i>h</i> | 12 | 8 |
| Koralpe (A) | <i>f</i> | 13 | 8 |
| Karnische Alpen (A) | <i>f</i> | 14 | 6 |
| Karnische Alpen (A) | <i>h</i> | 15 | 5 |
| Steiner Alpen (SLO) | <i>h</i> | 16 | 5 |
| Trnovski gozd-Predmeja (SLO) | <i>h</i> | 17 | 20 |
| Sämlinge | | | |
| A/ Patscherkofel | <i>f</i> | 22 Individ.1 | 50 |
| Summe | | | 355 |

* Legende: *f*: *R. ferrugineum*; *h*: *R. hirsutum*; *i*: *R. x intermedium*
17=21; Herkunft Trnovski gozd-Predmeja (SLO) wurde zweimal beprobt.

DNA-Präparationen:

Das oben beschriebene Pflanzenmaterial wurde zur Isolierung von gesamtgenomischer DNA herangezogen. Die DNA Präparationen, wurden mittels DNeasy Plant Minikit (Qiagen) durchgeführt. Diese DNA liegt in jeweils 2 Fraktionen á 100µl für nachfolgende populationsanalytische Untersuchungen vor. Agarosegeleanalysen dokumentieren die DNA Qualität (Abbildung 1).

Die für die Markerentwicklung benötigte DNA wurde ebenfalls mittels DNeasy Plant Minikit (Qiagen) gewonnen, da andere Protokolle nicht zum Erfolg führten. Zur Herstellung einer ausreichenden DNA-Menge wurden Proben unterschiedlicher Standorte gepoolt.

Abbildung 1

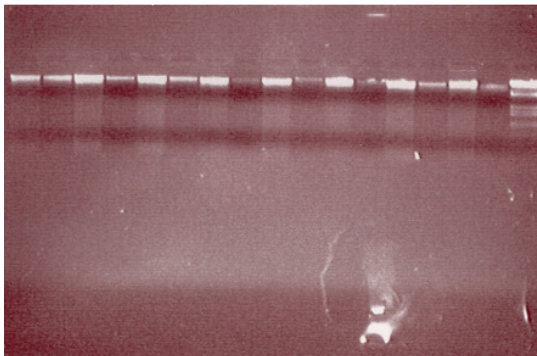


Abb.1 zeigt ein 0,8%, EtBr gefärbtes Agarosegel. In den Lanes 1-16 sind jeweils die erste und zweite Fraktion der DNA-Präparation eines einzelnen Individuums zu sehen. In Lane 17 (re. Aussen) befindet sich der Längenmarker.

2. Microsatellitenanalysen (SSR):

Um auf dem schnellsten Wege zu aussagekräftigen Daten über die genetische Vielfalt in Österreichischen *Rhododendron* -Populationen zu kommen, wurden 2 Ansätze gewählt:

1. Testung heterologer Microsatelliten-Primer, die für *R.metternichii* entwickelt wurden (Lit: K. Naito, Y Isagi, N. Nakagoshi; Isolation and characterisation of microsatellites of *R.metternichii* Sieb. et Zucc.Var. *hondoense* Nakai; 1998; Molecular Ecology, 7, 925-931)
2. Neuentwicklung von *R. ferrugineum* und *R. hirsutum* spezifischen -Microsatellitenprimern

1.2 Ad1) Testung heterologer Primer

Die folgenden sieben, aus der Literatur bekannten Primerpaare (Tabelle 2) wurden auf ihre Einsetzbarkeit bei *R. hirsutum*, *R. x intermedium* und *R. ferrugineum* getestet. Kriterien bei der Testung waren: der Erhalt eines PCR Produktes, sowie dessen Reinheit, und in weiterer Folge die Variabilität der SSR Region in den zu untersuchenden Populationen.

Zur Optimierung der Amplifikations -Konditionen wurden Gradienten -PCRs durchgeführt. Im Zuge dieser Arbeiten stellte sich heraus, dass nur 3 der 7 Primerpaare für die weiterführenden Analysen verwendet werden können. Es handelt sich dabei um RM9D1, RM2D2 und RM9D6, da diese sehr schöne Amplifikationsprodukte ergaben. Die anderen Primerpaare erzeugten in den Vorversuchen kein eindeutiges PCR Fragment (Abbildung 2).

Tabelle 2 Getestete SSRs

| Lokus | Repeat | Sequenz fwd | Sequenz rev | Tm (°C) |
|-------|--------------------|----------------------|----------------------|---------|
| RM3D2 | (GA) ₁₈ | TCAACACATAATAACAAAC | GAAAAGAAGGGCAAGTAAGT | 46,1 |
| RM2D2 | (CT) ₁₆ | ATGTGTTTCGTTGCTACTGT | ATGGGTTGGTTTGTTCCTA | 49,8 |

| | | | | |
|-------|--|-----------------------|----------------------|------|
| RM9D1 | (CT) ₂₁ | TGACCAAGTGCGACCTAATC | TAACCTCAACAACCAAAC | 48,6 |
| RM9D6 | (GA) ₁₆ | CTCGCCTCCCAAAGCAAT | CGTGTCTCACCCCCGTAAC | 55,2 |
| RM2D5 | (CT) ₃₀ | CTCAGCCCTTTGTCCTCT | ATCCCGATTTTATCTGTC | 49,0 |
| RM3D1 | (CT) ₂₁ (AT) ₉ (GT) ₉ | CTCCACAGCAGTCCTTGATAC | GGAAACAGCAACAGAAAACA | 52,2 |
| RM3D4 | (CT) ₇ +(CT) ₁₉ | CTCCCAACAAACAAATCCAT | CACCGAACGAAGACACTCAG | 52,1 |

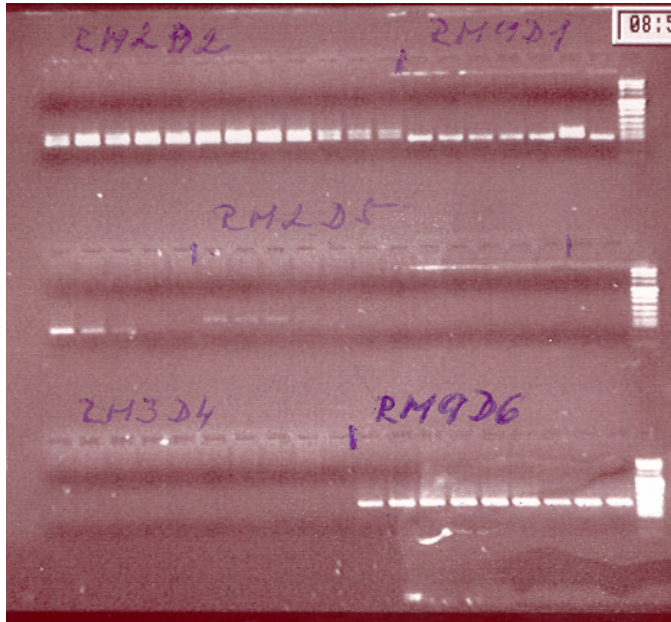


Abbildung 2 zeigt die Produkte einer Gradienten PCR. 5 SSR Primerpaare wurden mit nur einer DNA ausprobiert, um optimale PCR-Bedingungen zu ermitteln. Je Primerpaar wurden 12 idente Ansätze gemacht, die am Agarosegel analysiert wurden. An der Intensität der Banden entlang des Temperaturgradienten kann die optimale T_m ermittelt werden. Temperaturgradient: 47,5°C- 62,5°C (von li. → 47,5 – 47,8 – 48,9 – 50,5 – 52,3 – 54,1 – 55,9 – 57,6 – 59,4 – 61,1 – 62,1 – 62,5)

Tabelle 3 optimierte T_m für selektierte, heterologe SSR Primer

| Primer | T _m |
|--------|----------------|
| RM9D1 | 50 °C |
| RM9D6 | 56 °C |
| RM2D2 | 63 °C |

Für diese 3 Primerpaare wurde jeweils der ‚Forward-Primer‘ mit Fluoreszenzfarbstoff versehen, damit die PCR-Fragmente bei den nachfolgenden automatisierten Analysen am Sequenzierer (AB 3100) detektiert werden können. Die PCR -Reaktionen wurden durchwegs mit HotStar Taq Polymerase (Qiagen), unter Verwendung von 2,5mM MgCl₂ durchgeführt.

1.3 Ad 2) Neuentwicklung spezifischer SSR-Primer

Um neue SSR-Primer für die gegenständliche Fragestellung zu entwickeln, wurde vorerst eine Literatursuche durchgeführt, um Publikationen zu sichten, die über die Entwicklung von SSR -Markern berichten. Ziel war, unterschiedliche Methoden zu evaluieren, und jene für ein weiteres Vorgehen zu wählen, die es am effizientesten erlaubt, SSRs aus angereicherten Genbanken zu isolieren.

Die Wahl fiel auf eine Methode, die für Lachs (*Salmo salar* L.) erstmals beschrieben wurde: Hybridisation capture of microsaellites directly from genomic DNA; (1997) Refseth U, Fagan B, Jakobsen K; Electrophoresis, 18, p1519-1523

Bei dieser Methode werden in Anlehnung an das AFLP -Verfahren die DNA -Fragmente mit Adaptoren versehen, diese Fragmente über magnetische Kügelchen auf die Gegenwart von

SSR-Regionen selektiert, und dieses angereicherte Gemisch zur Erzeugung einer ‚angereicherten Genbank‘ verwendet.

DNA isolation:

DNA was extracted from 6x100mg plant material (code: 22/1, 22/2, 25, 20/19) with the Qiagen Plant Minikit, was collected and further extracted with 1M NaCl, 1% SDS and 1 volume of CHCl₃. The DNA was precipitated with 2.5 volume of EtOH and dissolved in 200µl 5mM Tris Ph8.0. Concentration 113 ng/µl, 22.5µg/200µl.

Partial digestion of the genomic DNA:

5µg genomic DNA was digested in 200µl volume with 4U Sau3A restriction endonuclease. The digestion was made at 37°C with sample collection after 10, 20, 30, 40, 50, 60, 90 and 120 minutes. The samples were checked on 1% agarose gel.

Sample after one hour digestion showed the expected digestion grade, the fragments length between 300bp and 2kb. The fragments were purified with phenol extraction and EtOH precipitation.

Adaptor ligation:

1µg digested genomic DNA (1.5pmol) was ligated at room temperature with 177ng (22.7pmol) Sau3A adaptor for 2 hours in 50µl volume.

The ligation reaction was purified on Qiaquick PCR purification column.

Adaptor sequences:

Sau3AI A Oligo, 5'-GGCCAGAGACCCCAAGCTTCG-3'

Sau3AI B Oligo, 5'PHO-GATCCGAAGCTTGGGGTCTCTGGCC-3'

Amplification of the adapted fragments:

20, 40 and 60ng of fragmented/adapted DNA was amplified in 50µl volume with Sau3AI A adaptor primer.

The PCR product was loaded on 1% agarose gel and amplified fragments between 400bp and 1kb was cut and purified on Qiagen fragment purification kit. The three samples were pooled together. After elution 1,7µg amplified fragments in 170µl volume were obtained (10ng/µl).

PCR:

- 1, 94°C 2'
2. 94°C 1'
3. 68°C 3'
4. go to 2. 30x
5. 72°C 10'

Capture on magnetic beads:

Biotinilated (AG)₁₀ and (CA)₁₀ oligos were used to capture AG or CA repeated sequences from the digested and ligated Rhododendron genomic DNA.

AG₁₀ 5'BIO-AAAAAGAGAGAGAGAGAGAGAGAG-3'

CA₁₀ 5'BIO-AAAACACACACACACACACACA-3'

The basic protocol is written in the publication of Refseth et.al, Electrophoresis 18:1519-1523 Hybridisation capture of microsatellites directly from genomic DNA (1997).

Streptavidin Magnet Particle (Roche, 1 641 778) was used to bind the biotinilated oligoes.

The following modifications were made to the original protocol:

- 1, The selection was made on fragments after amplification with the adaptor primer

2, The capture-oligos were planed with a 5' AAAA starting sequence, to provide space between the magnetic particle and the oligo-captured genomic DNA.

3, The hybridisation procedure was made in two different ways:

A, 50µl beads were washed with 0.2xSSC and suspend in 30µl volume.

About 2µg biotinilated (CA)₁₀ oligo was added to the dynabeads and incubated at room temperature. After 10 minutes the non-bound oligos were washed off the beads by extensive washing with 0.2xSSC. The beads were suspended back in 160µl volume in 6xSSC buffer and 40µl (400ng) adapted fragments were add. After 15 min incubation at room temperature the beads were washed three times with 2xSSC and three times with 1xSSC.

The captured fragments were eluted 2 times in 50µl H₂O at 95 °C with 5min incubation.

In the **B** protocol the 400ng fragments were hybridised first with 2µg biotinilated oligos in 6xSSC then after 15min hybridisation separated on Streptavidin Magnetic Particles.

The washing was performed as described before.

Amplification of the microsatellite-oligos captured, Sau3AI adapted fragments:

PCR amplification with the Sau3AI A adaptor primer with the same program as before.

1 and 5.5µl captured fragments were amplified in 50µl volumes.

The fragments were purified on Qiagen PCR purification kit.

Cloning of the selected microsatellite containing fragments:

2µl of purified amplification product was ligated into TOPO TA cloning vector and 1-2µl of the 10 µl ligatum was transformed into electro-competent E.coli. 20 and 100µl transformed bacteria were plated on Km containing LB-plates.

Altogether 544 clones were analysed by multiplex PCR containing three primers (M13 fw. and rev. and one of the respective oligos CA₁₀ or AG₁₀) to select the microsatellite containing clones.

PC3 reaction: 1: 95 °C 3'; 2: 95 °C 45"; 3: 56 °C 25"; 4: 50 °C 25"; 5: go to 2 35x; 6, 72 °C 10'

The samples were checked on 1% agarose gel; among them 176 showed two (three?) amplification bands (see Fig.1).

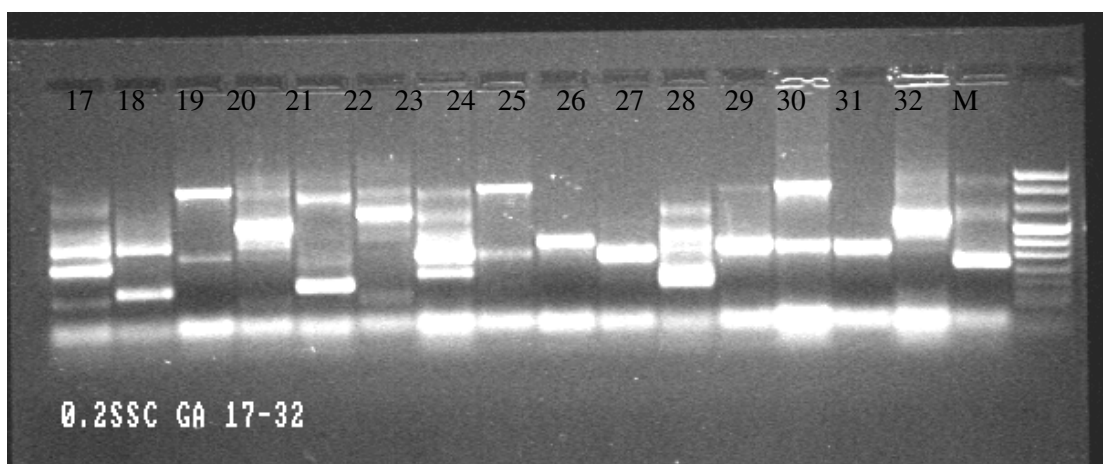


Fig.1 Direct Multiplex PCR from the selected bacterial clones.

Clones 17, 18, 19, 21, 23, 24, 27, 29 show double bands. The bigger band is the amplificatum between the M13 primers, the smaller one between the microsatellite oligo primer and one of the M13 primers, depending on its orientation.

Sequencing of the microsatellite primer containing clones:

176 clones were sequenced from two directions and 27 was found to have really microsatellites.

The other 149 sequence had only small repeats, enough to bind the (AG)₁₀ or (CA)₁₀ primers and amplify the second band.

Primer design based on the microsatellite sequences:

We had designed primers for 25 microsatellite sequences, 2 of them had the microsatellite regions very close to the 5' part of the sequence. In three cases we had planned two 3' primer, one close to the microsatellite regions, the other far away.

The designed primer pairs were tested first with two different Rhododendron genomic DNAs. PCR reactions were tested on 3% agarose gel (see Fig.2).

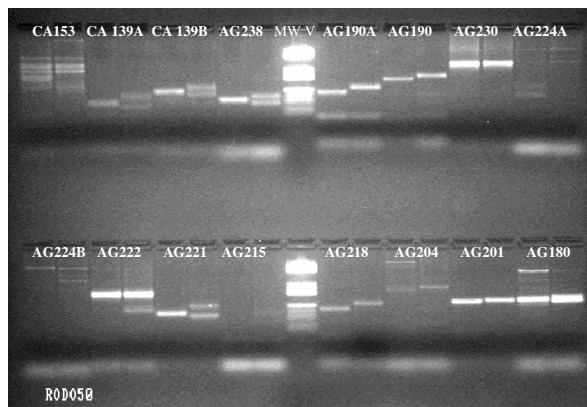


Fig.2 Testing of the Microsatellite primers on 3% agarose gels.

Primers: CA153, CA 139A, CA 139B, AG238, MWM V, AG190A, AG190B, AG230, AG224A, AG224B, AG222, AG221, AG215, AG218, AG204, AG201, AG180

Evaluation of the selected microsatellite primers:

17 of the 25 designed microsatellite primers worked on the two selected genomic DNAs.

For these 17 Primer combinations, one primer was fluorescently labelled with Fam-6 labelled for analysis of the PCR fragments on the automated sequencer. For a first trial study to evaluate the degree of polymorphism existing in the different loci, 8 different genomic DNAs from different populations were tested. The analysis was made on ABI 3100 Sequencer and analysed with the Genotyper program.

The reactions were made on the calculated T_m temperature or an optimal T_m temperature was established with gradient PCR analysis. All of the 17 amplified microsatellite regions were variable, except AG24.

13 primer pairs worked properly on 11 microsatellite sequences, for two microsatellite regions both planned primer pair worked well.

Reactions were made in 25µl volume first with Dynazym, later with Hotstar Taq polymerase (Qiagen).

1µl genomic DNA (30-50ng/µl) and 15pmol primers were used for PCR.

The all analysis result are saved on:G/UL/ULB/Rhododendron: Analysis of putative microsatellite primers.doc.

The best ones are shown on the next pages. The length of the original fragments are in brackets, the planned primer sequences are underlined

The table shows the best working SSR-Primers developed for this Project:

Working Microsat
primers

| Primer name | Fr Length | Tm/oligo | Tm/MWG | Tm used | 5' Primer sequence 5'-3' | 3' Primer seq 5'-3' |
|-----------------|-----------|----------|--------|---------|--------------------------|-------------------------|
| 6CA139 A | 92bp | 55 | 48/50 | 56 | TATCTACAAGCCCAATG FAM | AGCACTCGAGTATGTTG |
| 6AG238 | 94bp | 56 | 52/51 | 59 | CCTGTGCTACAGTTGG FAM | GCAGGTTACCAGTAAAAC |
| 6AG190 A | 133bp | 58 | 51/50 | 50 | GGACCGATGATTACTTCT FAM | GGACCGATGATTACTTCT |
| 6AG190 B | 199bp | 58 | 51/49 | 50 | GGACCGATGATTACTTCT FAM | GAGTTCTTCTGATTCGTT |
| 6AG230 | 308bp | 56 | 51/44 | 56 | GATTGGAAGTGACAAGTC | AGGGTGGTCCAATG FAM |
| 6AG218 | 137bp | 60 | 49/50 | 50 | TTCTTCTGATTCGTTGC | TTTCTTAGGACCGATGATT FAM |
| 6AG201 | 150bp | 57 | 50/50 | 50 | ACTTAAAGAATGCCTCTC | CCCGTTTAGTATGGATG FAM |
| 6AG180 | 165bp | 60 | 55/52 | 65 | CTGTGAGCTTTTGGGTTAC | CAGGTGGGTCTCACA FAM |
| 6AG13 | 131bp | 55 | 50/47 | 49 | GACAAAATAGCTCCTCTAA FAM | GTTCTATTAATGGGGATT |
| 6AG23 | 184bp | 50 | 47/44 | 56 | TATGCATACATACAGACA | TCATTAGCATAACTGC FAM |
| 6AG219 A | 104bp | 51 | 47/39 | 49 | GATCACATGCTTATATGT FAM | CAGCATTTTAAACCA |
| 6AG219 B | 119bp | 51 | 47/40 | 49 | GATCACATGCTTATATGT FAM | AGCTGCCATTGTTA |
| 6AG185 | 210bp | 64 | 57/57 | 65 | GCACAAGGGAGGTATCAAG | GTGGCTCCTGAGACATTC FAM |

Die rot markierten Primerpaare wurden für nachfolgende populations-genetische Untersuchungen verwendet.

1.4 Populationsgenetische Untersuchungen

Bei der Untersuchung der 334 Individuen mit Hilfe der 7 Microsatelliten Regionen, konnten insgesamt 118 verschiedene Allele detektiert werden, wobei die neu entwickelten Primer eine etwas höhere Allelanzahl aufwiesen, als jene Primer, die für *R. meternichii* entwickelt wurden.

| Region | Detektierte Allele |
|--------|--------------------|
| D01 | 12 |
| D02 | 14 |
| D06 | 17 |
| AG13 | 22 |
| AG218 | 17 |
| Ag219 | 26 |
| Ag230 | 10 |

Die Untersuchung der genetischen Vielfalt in den untersuchten 11 natürlichen Populationen zeigte, dass alle einen hohen Grad an Diversität aufweisen. In keiner der Populationen wurde klonales Material festgestellt, was bedeutet, dass jedem der gesammelten Einzelindividuen ein eindeutiger Genotyp zugewiesen werden kann. Die existierende genetische Vielfalt ist relativ hoch, wobei der beobachtete Heterozygotiegrad zumeist dem Erwarteten entspricht. Nur in den Populationen 4 (Versam-Station) und 10 (Kirchkogel) ist eine verminderte genetische Vielfalt zu beobachten.

Bei der Untersuchung des Samenmaterials (50 Sämlinge) eines Einzelindividuums der Population Patscherkofel konnten in jedem Locus die mütterlichen Allele wiedergefunden werden. Jedes dieser Allele machte zumindest 25% bis 50% der detektierten Allele aus. In den meisten Fällen stammten annähernd 100% der detektierten Allele von der Mutterpflanze, nur im Locus 218 konnten ca.30% der gefundenen Allele auf paternalen Ursprung zurückgeführt werden. Bei allen anderen Loci fanden sich nur 1-4% nicht-maternaler Allele. Dieses Ergebnis lässt auf eine hohe Selbstungsrate schließen.

Bei der Analyse der genetischen Distanz zwischen den natürlichen Populationen bildeten sich 2 Cluster (siehe Dendrogramm), wobei aber die verschiedenen Herkünfte genetisch dennoch relativ weit von einander entfernt sind, und kein eindeutiger geografischer Trend ausgemacht werden kann.

Die Untersuchung der bereits in vitro etablierten Samenherkünfte (9) zeigte, dass auch diese Linien zum Grossteil genetisch unterschiedlich sind. Nur bei den Herkünften Tennengau und Pinzgau handelt es sich um identische Pflanzenlinien. Für die Samenherkunft (Trnovski Gozd, Predmeja (SLO) liegen aufgrund labortechnischer Schwierigkeiten nicht genügend genetische Daten vor, weshalb die Proben aus allen populationsgenetischen Analysen ausgeklammert wurden.

Setzt man diese Samenherkünfte, und auch die Sämlinge der Herkunft Patscherkofel miteinander in Beziehung, so zeigt sich wiederum eine Zweiteilung des Dendrogramms in 2 Cluster. In dem einen Cluster finden sich die beiden Samenherkünfte Churfürsten dicht nebeneinander, und auch die Sämlinge (Patscherkofel) clustern mit der natürlichen Population Patscherkofel, von der sie auch abstammen. Im zweiten Cluster finden sich 6 natürliche Populationen sowie 5 Samenherkünfte unterschiedlichen geografischen Ursprungs.

Versucht man, die verschiedenen Spezies anhand ihrer Allelfrequenzen zu unterscheiden, so zeigt sich, dass in allen Loci die Allele in den 3 Spezies annähernd gleich verteilt sind, außer in Locus 219. Hier kann beobachtet werden, dass in *R. ferrugineum* die Allele A (74bp) und D (84bp) beinahe 90% der detektierten Fragmente ausmachen (38%:A, 53%:D),

während genau diese Fragmentlängen in *R. x intermedium* selten (8%:A, 12%:D), in *R. hirsutum* beinahe gar nicht auftreten (0%:A, 3%:D).

1.5 Populationsanalysen der 11 natürlichen Populationen:

Summary of Genetic Variation Statistics for All Loci

| Locus | Sample Size | na* |
|---------|-------------|---------|
| D01 | 422 | 110.000 |
| D02 | 440 | 130.000 |
| D96 | 430 | 180.000 |
| AG13 | 432 | 180.000 |
| AG218 | 416 | 140.000 |
| AG219 | 442 | 240.000 |
| AG230 | 412 | 90.000 |
| Mean | 428 | 152.857 |
| St. Dev | | 50.897 |

* na = Observed number of alleles

Heterozygosity Statistics über alle Loci

| Locus | Sample Size | Obs_Hom | Obs_Het | Exp_Hom | Exp_Het* | Nei** | Ave_Het |
|---------|-------------|---------|---------|---------|----------|--------|---------|
| D01 | 422 | 0.3886 | 0.6114 | 0.2182 | 0.7818 | 0.7800 | 0.5453 |
| D02 | 440 | 0.4136 | 0.5864 | 0.2206 | 0.7794 | 0.7776 | 0.5647 |
| D96 | 430 | 0.3256 | 0.6744 | 0.1266 | 0.8734 | 0.8713 | 0.7290 |
| AG13 | 432 | 0.3148 | 0.6852 | 0.1340 | 0.8660 | 0.8640 | 0.6931 |
| AG218 | 416 | 0.3606 | 0.6394 | 0.1428 | 0.8572 | 0.8551 | 0.6646 |
| AG219 | 442 | 0.4977 | 0.5023 | 0.0996 | 0.9004 | 0.8984 | 0.6417 |
| AG230 | 412 | 0.4466 | 0.5534 | 0.2963 | 0.7037 | 0.7020 | 0.5541 |
| Mean | 428 | 0.3925 | 0.6075 | 0.1769 | 0.8231 | 0.8212 | 0.6275 |
| St. Dev | | 0.0658 | 0.0658 | 0.0700 | 0.0700 | 0.0698 | 0.0733 |

* Expected homozygosity and heterozygosity were computed using Levene (1949)

** Nei's (1973) expected heterozygosity

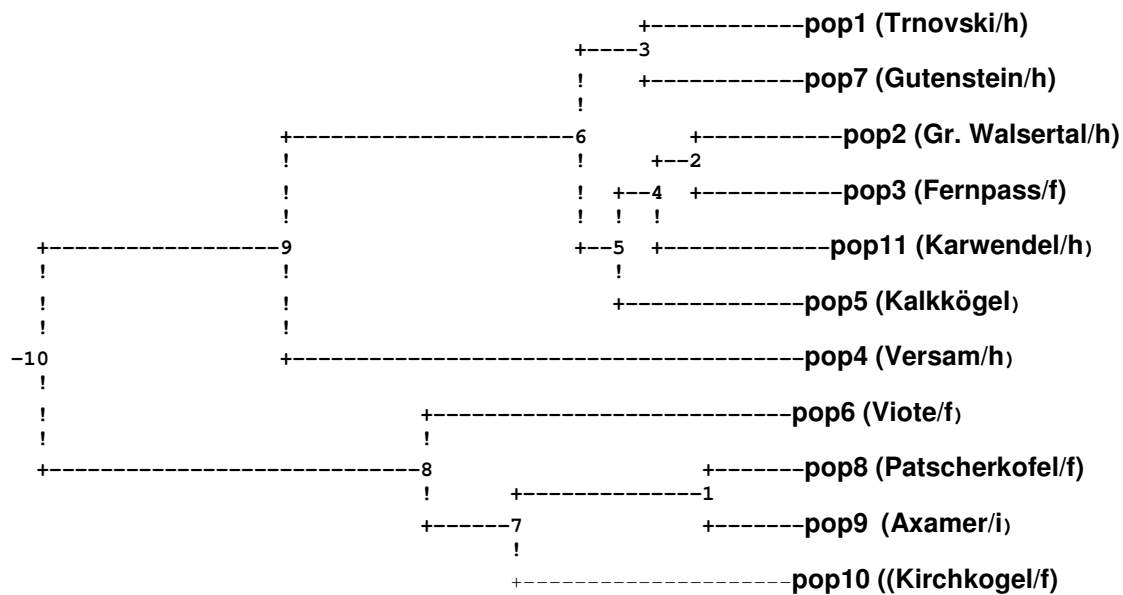
Nei's Original Measures of Genetic Identity and Genetic distance

[See Nei (1972) Am. Nat. 106:283-292]

| pop | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 |
|-----|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| 1 | **** | 0.6226 | 0.6834 | 0.3445 | 0.7141 | 0.2808 | 0.7545 | 0.1321 | 0.3895 | 0.1471 | 0.7148 |
| 2 | 0.4739 | **** | 0.7715 | 0.4182 | 0.6784 | 0.3351 | 0.6165 | 0.2922 | 0.5647 | 0.2304 | 0.7197 |
| 3 | 0.3807 | 0.2594 | **** | 0.4887 | 0.7464 | 0.3925 | 0.6568 | 0.2201 | 0.5344 | 0.2117 | 0.7586 |
| 4 | 10.655 | 0.8719 | 0.7160 | **** | 0.4038 | 0.2425 | 0.4053 | 0.0259 | 0.2556 | 0.0303 | 0.3768 |
| 5 | 0.3367 | 0.3881 | 0.2925 | 0.9068 | **** | 0.5201 | 0.6606 | 0.2720 | 0.5199 | 0.3191 | 0.7339 |
| 6 | 12.703 | 10.934 | 0.9351 | 14.169 | 0.6538 | **** | 0.3560 | 0.4852 | 0.5486 | 0.5270 | 0.4058 |
| 7 | 0.2816 | 0.4837 | 0.4204 | 0.9031 | 0.4147 | 10.328 | **** | 0.2081 | 0.5197 | 0.2583 | 0.6861 |
| 8 | 20.245 | 12.305 | 15.136 | 36.529 | 13.021 | 0.7232 | 15.696 | **** | 0.8396 | 0.6361 | 0.3498 |
| 9 | 0.9429 | 0.5714 | 0.6266 | 13.643 | 0.6541 | 0.6003 | 0.6544 | 0.1748 | **** | 0.5757 | 0.6750 |
| 10 | 19.169 | 14.680 | 15.527 | 34.953 | 11.424 | 0.6405 | 13.536 | 0.4524 | 0.5521 | **** | 0.3130 |
| 11 | 0.3358 | 0.3289 | 0.2763 | 0.9761 | 0.3093 | 0.9018 | 0.3768 | 10.505 | 0.3931 | 11.616 | **** |

Nei's genetic identity (above diagonal) and genetic distance (below diagonal).

Dendrogramm aller natürlichen Populationen:



Based Nei's (1972) Genetic distance: Method = UPGMA
 --Modified from NEIGHBOR procedure of PHYLIP Version 3.5

| Herkunf | Spezies | Bezeichnung |
|----------------------|---------------|-------------|
| SLO/Trnovski/21 | R.hirsutum | Pop 1 |
| A/Gr. Walsertal/28 | R.hirsutum | Pop 2 |
| A/Fernpass/29 | alle | Pop3 |
| CH/Versam-Station/30 | R.hirsutum | Pop4 |
| A/Kalkkögel/24 | R.hirsutum | Pop 5 |
| I/Viote/26 | R.ferrugineum | Pop 6 |
| A/Gutenstein/19 | R.hirsutum | Pop 7 |
| A/Patscherkofel/22 | R.ferrugineum | Pop 8 |
| A/Axamer L./25 | alle | Pop 9 |
| A/Kirchkogel/20 | R.ferrugineum | Pop 10 |
| A/Karwendel/23 | R.hirsutum | Pop 11 |

1.6 Populationsgenetische Analyse aller untersuchten Individuen

Summary of Genetic Variation Statistics for All Loci

| Locus | Sample Size | na* |
|---------|-------------|---------|
| D01 | 618 | 120.000 |
| D02 | 652 | 140.000 |
| D96 | 624 | 180.000 |
| AG13 | 620 | 180.000 |
| AG218 | 620 | 150.000 |
| AG219 | 650 | 250.000 |
| AG230 | 624 | 90.000 |
| Mean | 630 | 158.571 |
| St. Dev | | 51.455 |

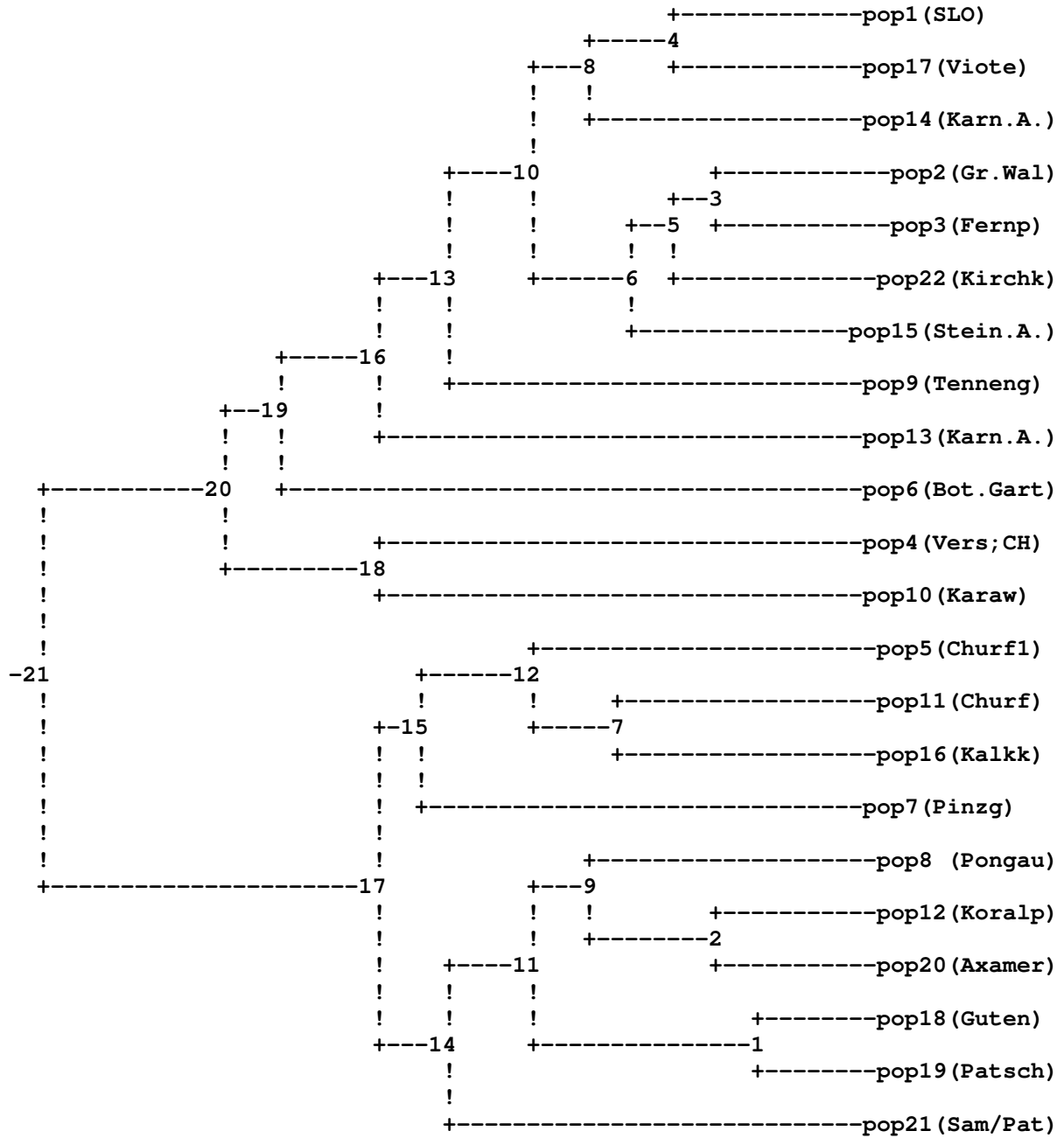
* na = Observed number of alleles

Tabelle der Nei's Original Measures of Genetic Identity and Genetic distance

| pop ID | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 |
|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| 1 | **** | 0.6228 | 0.8894 | 0.3445 | 0.3219 | 0.4579 | 0.3448 | 0.4818 | 0.4819 | 0.4446 | 0.4121 | 0.3102 | 0.5850 | 0.6940 | 0.7141 | 0.2803 | 0.7545 | 0.1321 | 0.3995 | 0.2872 | 0.1471 |
| 2 | 0.4739 | **** | 0.7715 | 0.4182 | 0.3416 | 0.4420 | 0.2972 | 0.3925 | 0.4630 | 0.4222 | 0.3793 | 0.3186 | 0.5425 | 0.4476 | 0.6784 | 0.3951 | 0.6165 | 0.2822 | 0.6947 | 0.2865 | 0.2304 |
| 3 | 0.3807 | 0.2594 | **** | 0.4887 | 0.3213 | 0.4585 | 0.2159 | 0.3410 | 0.4854 | 0.5157 | 0.3894 | 0.3475 | 0.5470 | 0.4882 | 0.7484 | 0.3925 | 0.6558 | 0.2201 | 0.6394 | 0.2804 | 0.2117 |
| 4 | 10.065 | 0.8719 | 0.7160 | **** | 0.1722 | 0.1735 | 0.1168 | 0.2570 | 0.3760 | 0.4878 | 0.1584 | 0.1301 | 0.3078 | 0.3159 | 0.4088 | 0.2125 | 0.4053 | 0.0259 | 0.2585 | 0.1441 | 0.0308 |
| 5 | 11.336 | 10.740 | 11.354 | 17.588 | **** | 0.2404 | 0.4887 | 0.5162 | 0.3717 | 0.2888 | 0.5418 | 0.4039 | 0.2770 | 0.2429 | 0.4084 | 0.6773 | 0.4084 | 0.4284 | 0.4854 | 0.4905 | 0.4627 |
| 6 | 0.7396 | 0.8166 | 15.382 | 17.513 | 14.256 | **** | 0.5166 | 0.4074 | 0.2131 | 0.3288 | 0.4625 | 0.3347 | 0.4486 | 0.5521 | 0.5266 | 0.3882 | 0.3941 | 0.1775 | 0.3274 | 0.2103 | 0.2385 |
| 7 | 10.018 | 12.183 | 15.382 | 21.488 | 0.7763 | 0.6804 | **** | 0.6367 | 0.2816 | 0.3291 | 0.6784 | 0.5189 | 0.3783 | 0.3450 | 0.4684 | 0.4603 | 0.4265 | 0.3794 | 0.4092 | 0.4763 | 0.5130 |
| 8 | 0.7302 | 0.9362 | 10.789 | 13.588 | 0.6831 | 0.9128 | 0.6241 | **** | 0.3732 | 0.3221 | 0.6820 | 0.6730 | 0.5313 | 0.4823 | 0.5888 | 0.4894 | 0.4265 | 0.5430 | 0.5584 | 0.6162 | 0.5287 |
| 9 | 0.7289 | 0.7919 | 0.7024 | 11.841 | 0.9896 | 15.988 | 14.489 | 0.9867 | **** | 0.4197 | 0.3771 | 0.3076 | 0.3221 | 0.6110 | 0.7080 | 0.4220 | 0.6627 | 0.2179 | 0.4171 | 0.3770 | 0.2891 |
| 10 | 0.8705 | 0.8623 | 0.6823 | 0.7179 | 12.285 | 11.784 | 11.115 | 11.329 | 0.8882 | **** | 0.3201 | 0.3229 | 0.4288 | 0.4842 | 0.6676 | 0.3775 | 0.3763 | 0.1735 | 0.3086 | 0.3630 | 0.1832 |
| 11 | 0.8885 | 11.416 | 11.290 | 18.553 | 0.6129 | 0.7980 | 0.3809 | 0.4276 | 0.9752 | 11.391 | **** | 0.5825 | 0.4607 | 0.3859 | 0.5488 | 0.6802 | 0.3919 | 0.4280 | 0.4402 | 0.5803 | 0.6287 |
| 12 | 11.705 | 11.501 | 10.569 | 20.388 | 0.8942 | 10.947 | 0.6889 | 0.3691 | 11.988 | 11.306 | 0.5405 | **** | 0.4865 | 0.2009 | 0.4888 | 0.4267 | 0.2873 | 0.6808 | 0.6943 | 0.7880 | 0.5777 |
| 13 | 0.5709 | 0.6116 | 0.6033 | 11.980 | 12.888 | 0.7994 | 0.9801 | 0.6324 | 11.327 | 0.8467 | 0.7749 | 0.7008 | **** | 0.4402 | 0.7162 | 0.2881 | 0.4022 | 0.2253 | 0.3882 | 0.4609 | 0.2188 |
| 14 | 0.3798 | 0.8088 | 0.7212 | 11.427 | 14.149 | 0.5941 | 10.642 | 0.8386 | 0.6714 | 0.7253 | 0.9267 | 16.047 | 0.8206 | **** | 0.6064 | 0.3770 | 0.6681 | 0.0885 | 0.3297 | 0.2205 | 0.1366 |
| 15 | 0.3367 | 0.3881 | 0.2825 | 0.9088 | 0.8854 | 0.6413 | 0.7819 | 0.6783 | 0.3453 | 0.4192 | 0.6001 | 0.7199 | 0.3339 | 0.5001 | **** | 0.5201 | 0.6606 | 0.2720 | 0.5799 | 0.4678 | 0.3191 |
| 16 | 12.703 | 10.984 | 0.9851 | 14.189 | 0.3887 | 0.9463 | 0.7871 | 0.6883 | 0.8828 | 0.6741 | 0.3884 | 0.8518 | 12.102 | 11.487 | 0.6888 | **** | 0.3680 | 0.4852 | 0.6185 | 0.4128 | 0.5270 |
| 17 | 0.2816 | 0.4887 | 0.4204 | 0.9081 | 0.8856 | 0.9311 | 12.204 | 0.8845 | 0.4677 | 0.8775 | 0.9547 | 13.165 | 0.9109 | 0.4184 | 0.4147 | 10.328 | **** | 0.2081 | 0.6797 | 0.2908 | 0.2883 |
| 18 | 20.215 | 12.305 | 15.136 | 36.529 | 0.8477 | 17.286 | 0.9797 | 0.6706 | 15.236 | 17.402 | 0.8534 | 0.3882 | 14.903 | 28.071 | 13.021 | 0.7232 | 15.696 | **** | 0.8895 | 0.7088 | 0.6361 |
| 19 | 0.9429 | 0.5714 | 0.6286 | 13.643 | 0.7228 | 11.168 | 0.8884 | 0.5883 | 0.8743 | 11.793 | 0.8205 | 0.4395 | 0.9882 | 11.037 | 0.6641 | 0.6008 | 0.6644 | 0.7748 | **** | 0.6047 | 0.5757 |
| 20 | 12.477 | 12.500 | 12.383 | 19.376 | 0.7122 | 15.583 | 0.7411 | 0.4942 | 0.9755 | 10.412 | 0.5793 | 0.2282 | 0.7748 | 15.116 | 0.7732 | 0.8847 | 12.359 | 0.3513 | 0.6780 | **** | 0.4811 |
| 21 | 19.189 | 14.880 | 15.527 | 34.983 | 0.7708 | 13.527 | 0.6675 | 0.6573 | 14.310 | 18.757 | 0.4841 | 0.5489 | 15.389 | 19.634 | 11.424 | 0.6405 | 13.536 | 0.4624 | 0.6621 | 0.7318 | **** |
| 22 | 0.3389 | 0.3289 | 0.2763 | 0.9761 | 0.9881 | 0.6894 | 13.053 | 0.8026 | 0.4898 | 0.6787 | 10.208 | 0.8721 | 0.6889 | 0.4689 | 0.3093 | 0.9018 | 0.3768 | 10.505 | 0.3681 | 11.067 | 11.616 |

Nei's genetic identity (above diagonal) and genetic distance (below diagonal).

Dendrogramm aller untersuchten Populationen



| Herkunft | Spezies | Bezeichnung |
|------------------------|----------------|-------------|
| A/Kalkkogel/24 | R. hirsutum | Pop 16 |
| I/Viote / Trient/26 | R.ferrugineum | Pop 17 |
| A/Patscherkofel/22 | R.ferrugineum | Pop 19 |
| A/Kirchkogel/20 | R.ferrugineum | Pop 22 |
| A/Karwendel/23 | R.hirsutum | Pop 23 |
| SLO/Trnovski/21 | R.hirsutum | Pop01 |
| A/Gr. Walsertal/28 | R.hirsutum | Pop02 |
| A/Fernpass/29 | alle | Pop03 |
| CH/Versam/30 | R.hirsutum | Pop04 |
| Churfürsten (CH)1/Gw | R. ferrugineum | Pop05 |
| Bot.Garten Frankfurt | R. ferrugineum | Pop06 |
| Pinzgau/Gw | R. ferrugineum | Pop07 |
| Pongau (A)/GW | R. ferrugineum | Pop08 |
| Tennengau (A)/Gw | R.hirsutum | Pop09 |
| Karawanken (A)/Gw | R.hirsutum | Pop10 |
| Churfürsten (CH)/Gw | R. hirsutum | Pop11 |
| Koralpe (A)/Gw | R. ferrugineum | Pop12 |
| Karnische Alpen (A)/Gw | R. ferrugineum | Pop13 |
| Karnische Alpen (A)/Gw | R. hirsutum | Pop14 |
| Steiner Aplen (SLO)/Gw | R. hirsutum | Pop15 |
| A/Gutenstein/19 | R.hirsutum | Pop18 |
| A/Axamer L./25 | alle | Pop20 |
| Samen/Patscherk/1 | R.ferrugineum | Pop21 |

Tabellen zur Zweisung der Allelgrößen zu Buchstabencodes für Popgen Analysen

D6

| | | |
|---------------|-----|---|
| 176,0 - 176,9 | 176 | A |
| 178,0 - 178,8 | 178 | B |
| 182 | 182 | C |
| 184 - 185 | 184 | D |
| 186 - 187,7 | 186 | E |
| 188 - 188,6 | 188 | F |
| 189,3-190,7 | 190 | G |
| 191,9 - 192,5 | 192 | H |
| 194 - 194,5 | 194 | I |
| 196 - 196,5 | 196 | J |
| 197,8 - 198,2 | 198 | K |
| 203,5 - 204,5 | 204 | L |
| 208 - 209 | 208 | M |
| 210 - 210,5 | 210 | N |
| 215 - 216 | 216 | O |
| 217 - 217,8 | 218 | P |
| 219,81 | 220 | Q |

D1

| | | |
|----------------|-----|---|
| 108,4 - 109,5 | 108 | A |
| 111,49 | 110 | B |
| 112 - 113,4 | 112 | C |
| 113,5 - 114,6 | 114 | D |
| 115 - 116,5 | 116 | E |
| 118,4 - 119,4 | 118 | F |
| 120,4 - 121,62 | 120 | G |
| 122,4 - 123,4 | 122 | H |
| 124,4 - 125,2 | 124 | I |
| 126,7 - 127,3 | 126 | J |
| 130 - 131,2 | 130 | K |
| 134,79 | 134 | L |

D2

| | | |
|----------------|-----|---|
| 115,85 | 116 | A |
| 118,6 - 118,8 | 118 | B |
| 120,5 - 120,9 | 120 | C |
| 122 - 123,55 | 122 | D |
| 123,7 - 124,95 | 124 | E |
| | | F |
| 126 - 127 | 126 | G |
| 128,1 - 129,1 | 128 | H |
| 130,2 -131 | 130 | I |
| 132,9 - 133,2 | 133 | J |
| 136,92 | 137 | K |
| 140,42 - 141,5 | 141 | L |
| 147,1 - 149,7 | 148 | M |
| 154,9 - 155 | 155 | N |
| 173,8 - 174,2 | 174 | O |

AG 218

| | | |
|----------------|-----|---|
| 107,6 - 109,1 | 108 | A |
| 109,6 - 111,84 | 110 | B |
| 112 - 113,35 | 112 | C |
| 114,5 - 115,1 | 114 | D |
| 116,1 - 117,5 | 116 | E |
| 118,6 - 119,3 | 118 | F |
| 119,7 - 121,2 | 120 | G |
| 122,6 - 123 | 122 | H |
| 124,1 - 125,4 | 124 | I |
| 126,3 - 127,3 | 126 | J |
| 128,5 - 129 | 128 | K |
| 130,3 - 132 | 130 | L |
| 132,3 - 133,2 | 132 | M |
| 134,5 - 134,8 | 134 | N |
| 143,5 - 143,7 | 143 | O |

AG 230

| | | |
|----------------|-----|---|
| 278,7 - 278,9 | 278 | A |
| 292,7 | 292 | B |
| 294,1 - 294,99 | 294 | C |
| 295,7 - 297 | 296 | D |
| 300,2 - 300,9 | 300 | E |
| 304 - 305 | 304 | F |
| 306,96 | 306 | G |
| 307,7 - 309,4 | 308 | H |
| 309,8 - 311 | 310 | I |
| 312 - 312,5 | 312 | J |

AG 219

| | | |
|----------------|-----|---|
| 74,8 - 75 | 74 | A |
| 76,7 - 77,4 | 76 | B |
| 78,6 - 78,8 | 78 | C |
| 83,2-83,8 | 84 | D |
| 85,3 - 86,2 | 86 | E |
| 87,4 - 87,8 | 87 | F |
| 89,6 - 90,2 | 89 | G |
| 91,1 - 92,2 | 91 | H |
| 93,8 - 94,7 | 94 | I |
| 96 - 97 | 96 | J |
| 98,2 - 98,7 | 98 | K |
| 100,4 - 101 | 100 | L |
| 102,4 - 102,7 | 102 | M |
| 104,4 - 104,9 | 104 | N |
| 106,3 - 106,8 | 106 | O |
| 108,3 - 108,8 | 108 | P |
| 110,1 - 110,8 | 110 | Q |
| 112,3 - 112,5 | 112 | R |
| 114,4 - 114,7 | 114 | S |
| 116,4 - 116,7 | 116 | T |
| 118,4 | 118 | U |
| 120 - 120,6 | 120 | V |
| 122,3 - 122,6 | 122 | W |
| 124 - 124,7 | 124 | X |
| 126,2 - 126,8 | 126 | Y |
| 129,2 - 129, 6 | 129 | Z |

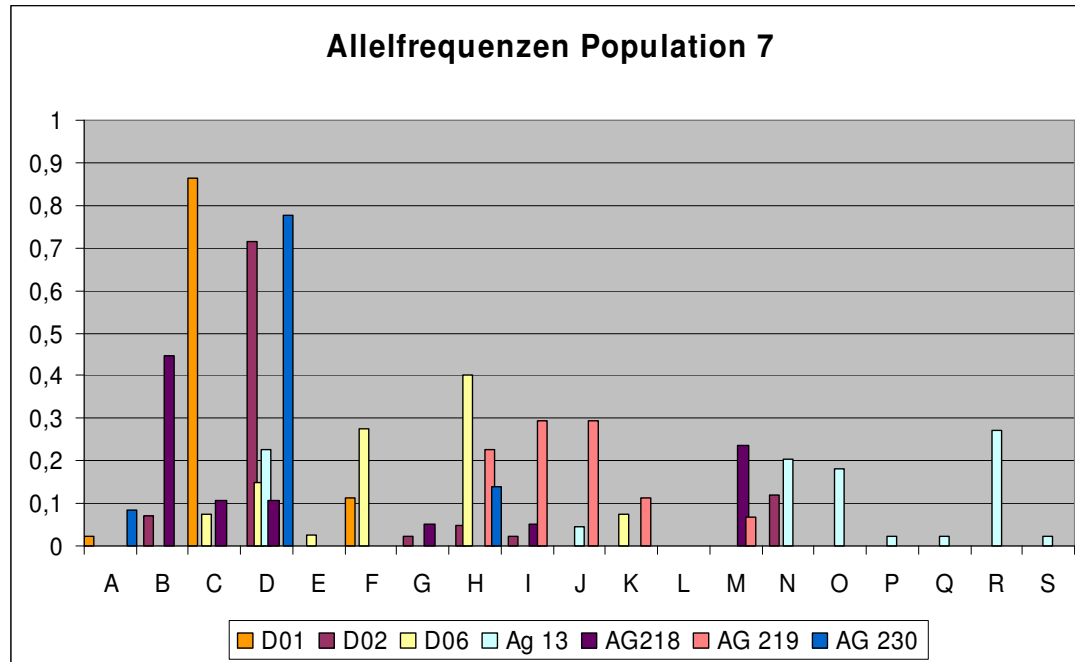
AG 13

| | | |
|----------------|-----|---|
| 122,85 | 122 | A |
| 124,6 - 125,02 | 124 | B |
| 126,9 - 127 | 126 | C |
| 128,8 - 129,4 | 138 | D |
| 130,9 - 131 | 131 | E |
| 150 - 151 | 151 | F |
| 152,6 - 152,9 | 153 | G |
| 157,9 - 158,2 | 158 | H |
| 159,6 - 160,9 | 160 | I |
| 164,9 - 165,4 | 165 | J |
| 166,9 - 167,4 | 167 | K |
| 169 - 169,9 | 169 | L |
| 171,2 - 171,9 | 171 | M |
| 173 - 174 | 173 | N |
| 175 - 176,1 | 175 | O |
| 177 - 177,9 | 177 | P |
| 179,2 - 179,7 | 179 | Q |
| 181 - 181,9 | 181 | R |
| 183,2 - 184 | 183 | S |
| 185,2 - 185,9 | 185 | T |
| 186,4 - 187,8 | 187 | U |
| 189,3 - 190 | 189 | V |

1.7 Analysen zur genetischen Vielfalt in den natürlichen Populationen:

Nummerierungsschlüssel

| Herkunft | Spezies | Bezeichnung |
|---------------------|---------------|-------------|
| SLO/Trnovski/21 | R.hirsutum | Pop 1 |
| A/Gr. Walsertal/28 | R.hirsutum | Pop 2 |
| A/Fernpass/29 | alle | Pop3 |
| CH/Versam/30 | R.hirsutum | Pop4 |
| A/Kalkkögel/24 | R. hirsutum | Pop 5 |
| I/Viote / Trient/26 | R.ferrugineum | Pop 6 |
| A/Gutenstein/19 | R.hirsutum | Pop 7 |
| A/Patscherkofel/22 | R.ferrugineum | Pop 8 |
| A/Axamer L./25 | alle | Pop9 |
| A/Kirchkogel/20 | R.ferrugineum | Pop 10 |
| A/Karwendel/23 | R.hirsutum | Pop 11 |

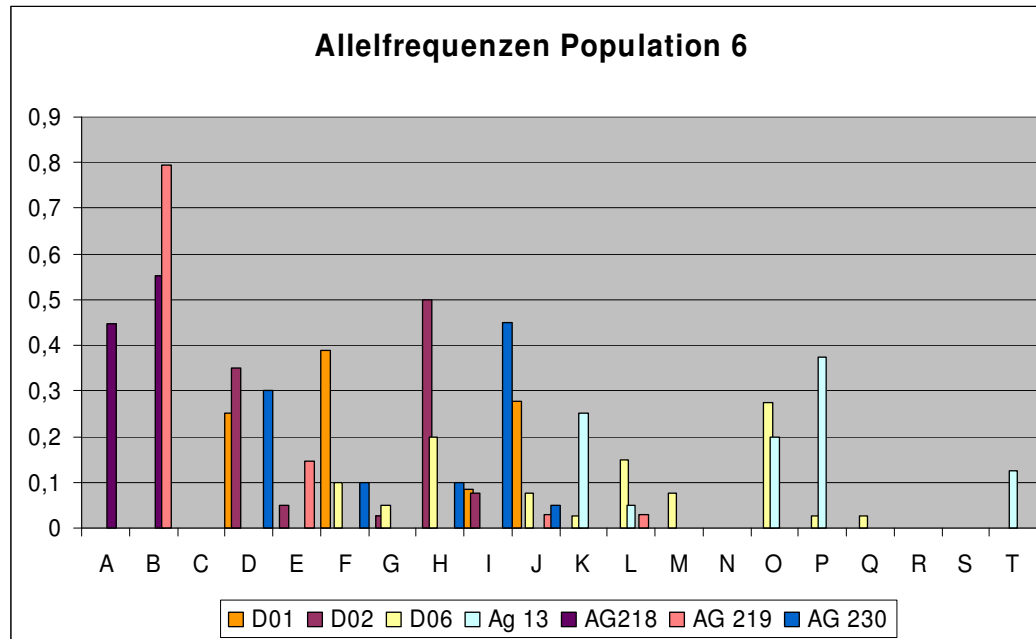


| | Locus | D01 | D02 | D96 | AG13 | AG218 | AG219 | AG230 |
|--------|-------|--------|--------|-------|--------|--------|--------|--------|
| Allele | | | | | | | | |
| A | | 0,0227 | | | | | | 0,0833 |
| B | | | 0,0714 | | | 0,4474 | | |
| C | | 0,8636 | | 0,075 | | 0,1053 | | |
| D | | | 0,7143 | 0,15 | 0,2273 | 0,1053 | | 0,7778 |
| E | | | | 0,025 | | | | |
| F | | 0,1136 | | 0,275 | | | | |
| G | | | 0,0238 | | | 0,0526 | | |
| H | | | 0,0476 | 0,4 | | | 0,2273 | 0,1389 |
| I | | | 0,0238 | | | 0,0526 | 0,2955 | |
| J | | | | | 0,0455 | | 0,2955 | |
| K | | | | 0,075 | | | 0,1136 | |
| L | | | | | | | | |
| M | | | | | | 0,2368 | 0,0682 | |
| N | | | 0,119 | | 0,2045 | | | |
| O | | | | | 0,1818 | | | |
| P | | | | | 0,0227 | | | |
| Q | | | | | 0,0227 | | | |
| R | | | | | 0,2727 | | | |
| S | | | | | 0,0227 | | | |

Summary of Heterozygosity Statistics for All Loci

| Locus | Sample Size | Obs_Hom | Obs_Het | Exp_Hom* | Exp_Het* | Nei** | Ave_Het |
|---------|-------------|---------|---------|----------|----------|--------|---------|
| D01 | 44 | 0.7273 | 0.2727 | 0.7537 | 0.2463 | 0.2407 | 0.5453 |
| D02 | 42 | 0.6667 | 0.3333 | 0.5215 | 0.4785 | 0.4671 | 0.5647 |
| D96 | 40 | 0.6000 | 0.4000 | 0.2513 | 0.7487 | 0.7300 | 0.7290 |
| AG13 | 44 | 0.2273 | 0.7727 | 0.1860 | 0.8140 | 0.7955 | 0.6931 |
| AG218 | 38 | 0.4211 | 0.5789 | 0.2646 | 0.7354 | 0.7161 | 0.6646 |
| AG219 | 44 | 0.7727 | 0.2273 | 0.2262 | 0.7738 | 0.7562 | 0.6417 |
| AG230 | 36 | 0.5556 | 0.4444 | 0.6206 | 0.3794 | 0.3688 | 0.5541 |
| Mean | 41 | 0.5672 | 0.4328 | 0.4034 | 0.5966 | 0.5821 | 0.6275 |
| St. Dev | | 0.1897 | 0.1897 | 0.2254 | 0.2254 | 0.2202 | 0.0733 |

Expected homozygosity and heterozygosity were computed using Levene (1949)
 ** Nei's (1973) expected heterozygosity



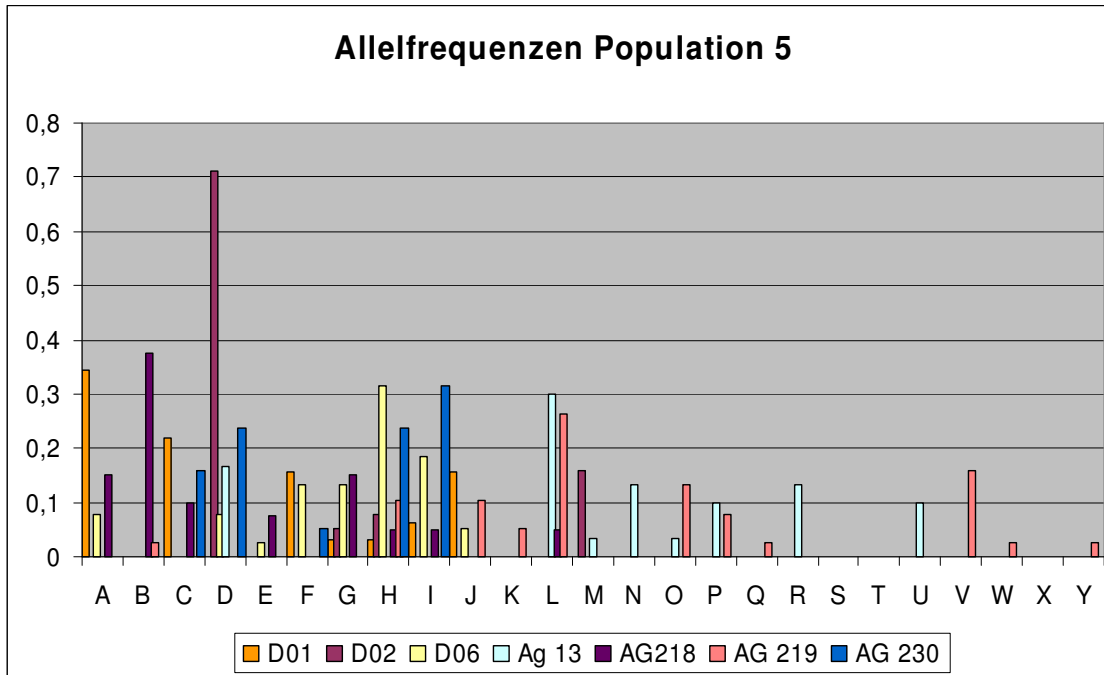
| | Locus | D01 | D02 | D96 | AG13 | AG218 | AG219 | AG230 |
|--------|-------|--------|-------|-------|-------|--------|--------|-------|
| Allele | | | | | | | | |
| A | | | | | | 0,4474 | | |
| B | | | | | | 0,5526 | 0,7941 | |
| C | | | | | | | | |
| D | | 0,25 | 0,35 | | | | | 0,3 |
| E | | | 0,05 | | | | 0,1471 | |
| F | | 0,3889 | | 0,1 | | | | 0,1 |
| G | | | 0,025 | 0,05 | | | | |
| H | | | 0,5 | 0,2 | | | | 0,1 |
| I | | 0,0833 | 0,075 | | | | | 0,45 |
| J | | 0,2778 | | 0,075 | | | 0,0294 | 0,05 |
| K | | | | 0,025 | 0,25 | | | |
| L | | | | 0,15 | 0,05 | | 0,0294 | |
| M | | | | 0,075 | | | | |
| N | | | | | | | | |
| O | | | | 0,275 | 0,2 | | | |
| P | | | | 0,025 | 0,375 | | | |
| Q | | | | 0,025 | | | | |
| R | | | | | | | | |
| S | | | | | | | | |
| T | | | | | 0,125 | | | |

Summary of Heterozygosity Statistics for All Loci

| Locus | Sample Size | Obs_Hom | Obs_Het | Exp_Hom* | Exp_Het* | Nei** | Ave_Het |
|---------|-------------|---------|---------|----------|----------|--------|---------|
| D01 | 36 | 0.0000 | 10.000 | 0.2778 | 0.7222 | 0.7022 | 0.5453 |
| D02 | 40 | 0.0500 | 0.9500 | 0.3654 | 0.6346 | 0.6188 | 0.5647 |
| D96 | 40 | 0.2500 | 0.7500 | 0.1423 | 0.8577 | 0.8362 | 0.7290 |
| AG13 | 40 | 0.2500 | 0.7500 | 0.2423 | 0.7577 | 0.7388 | 0.6931 |
| AG218 | 38 | 0.6316 | 0.3684 | 0.4922 | 0.5078 | 0.4945 | 0.6646 |
| AG219 | 34 | 0.8824 | 0.1176 | 0.6435 | 0.3565 | 0.3460 | 0.6417 |
| AG230 | 20 | 0.0000 | 10.000 | 0.2789 | 0.7211 | 0.6850 | 0.5541 |
| Mean | 35 | 0.2948 | 0.7052 | 0.3489 | 0.6511 | 0.6316 | 0.6275 |
| St. Dev | | 0.3407 | 0.3407 | 0.1691 | 0.1691 | 0.1642 | 0.0733 |

* Expected homozygosity and heterozygosity were computed using Levene (1949)

** Nei's (1973) expected heterozygosity



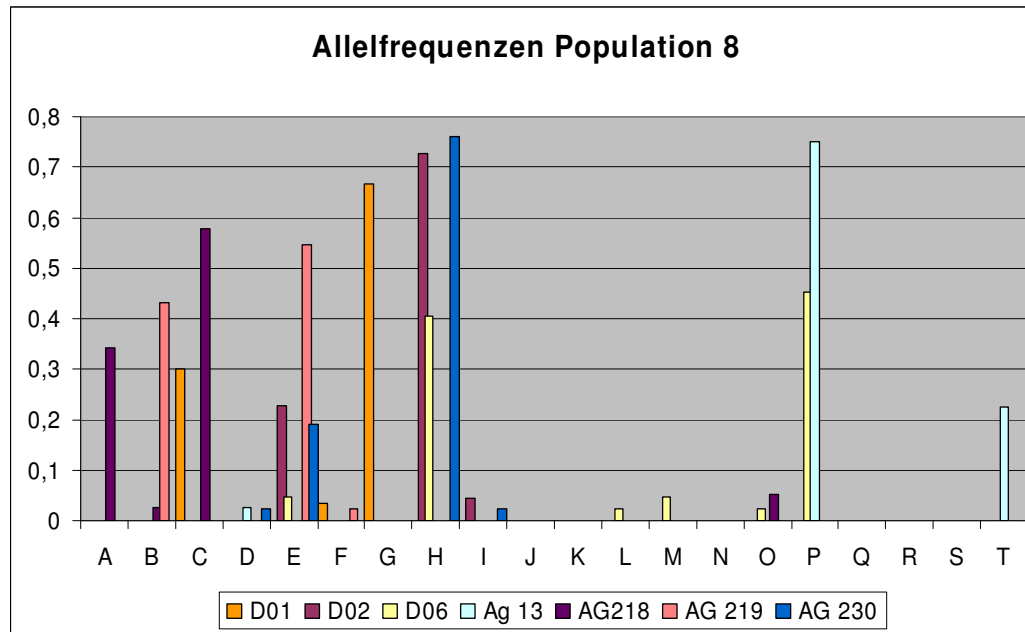
| | Locus | D01 | D02 | D96 | AG13 | AG218 | AG219 | AG230 |
|--------|-------|--------|--------|--------|--------|-------|--------|--------|
| Allele | | | | | | | | |
| A | | 0,3438 | | 0,0789 | | 0,15 | | |
| B | | | | | | 0,375 | 0,0263 | |
| C | | 0,2188 | | | | 0,1 | | 0,1579 |
| D | | | 0,7105 | 0,0789 | 0,1667 | | | 0,2368 |
| E | | | | 0,0263 | | 0,075 | | |
| F | | 0,1562 | | 0,1316 | | | | 0,0526 |
| G | | 0,0312 | 0,0526 | 0,1316 | | 0,15 | | |
| H | | 0,0312 | 0,0789 | 0,3158 | | 0,05 | 0,1053 | 0,2368 |
| I | | 0,0625 | | 0,1842 | | 0,05 | | 0,3158 |
| J | | 0,1562 | | 0,0526 | | | 0,1053 | |
| K | | | | | | | 0,0526 | |
| L | | | | | 0,3 | 0,05 | 0,2632 | |
| M | | | 0,1579 | | 0,0333 | | | |
| N | | | | | 0,1333 | | | |
| O | | | | | 0,0333 | | 0,1316 | |
| P | | | | | 0,1 | | 0,0789 | |
| Q | | | | | | | 0,0263 | |
| R | | | | | 0,1333 | | | |
| S | | | | | | | | |
| T | | | | | | | | |
| U | | | | | 0,1 | | | |
| V | | | | | | | 0,1579 | |
| W | | | | | | | 0,0263 | |
| X | | | | | | | | |
| Y | | | | | | | 0,0263 | |

Summary of Heterozygosity Statistics for All Loci (Pop5)

| Locus | Sample Size | Obs_Hom | Obs_Het | Exp_Hom* | Exp_Het* | Nei** | Ave_Het |
|---------|-------------|---------|---------|----------|----------|--------|---------|
| D01 | 32 | 0.0000 | 10.000 | 0.1956 | 0.8044 | 0.7793 | 0.5453 |
| D02 | 38 | 0.5263 | 0.4737 | 0.5263 | 0.4737 | 0.4612 | 0.5647 |
| D96 | 38 | 0.2105 | 0.7895 | 0.1622 | 0.8378 | 0.8158 | 0.7290 |
| AG13 | 30 | 0.1333 | 0.8667 | 0.1471 | 0.8529 | 0.8244 | 0.6931 |
| AG218 | 40 | 0.2500 | 0.7500 | 0.1885 | 0.8115 | 0.7913 | 0.6646 |
| AG219 | 38 | 0.2632 | 0.7368 | 0.1223 | 0.8777 | 0.8546 | 0.6417 |
| AG230 | 38 | 0.2632 | 0.7368 | 0.2191 | 0.7809 | 0.7604 | 0.5541 |
| Mean | 36 | 0.2352 | 0.7648 | 0.2230 | 0.7770 | 0.7553 | 0.6275 |
| St. Dev | | 0.1596 | 0.1596 | 0.1376 | 0.1376 | 0.1333 | 0.0733 |

* Expected homozygosity and heterozygosity were computed using Levene (1949)

** Nei's (1973) expected heterozygosity



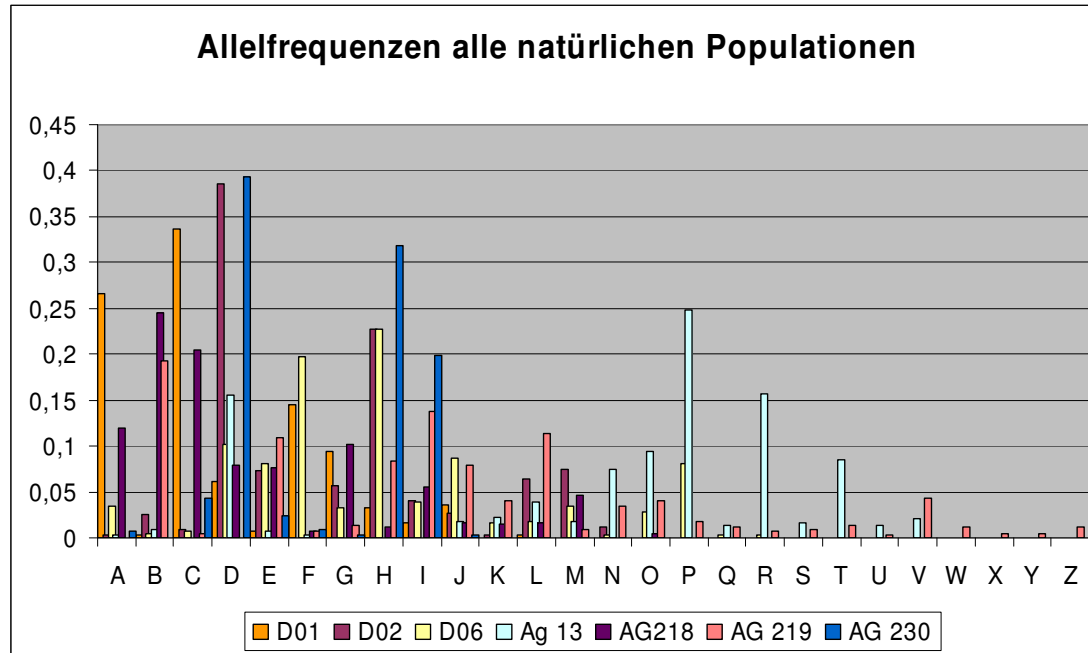
| | Locus | D01 | D02 | D96 | AG13 | AG218 | AG219 | AG230 |
|--------|-------|--------|--------|--------|-------|--------|--------|--------|
| Allele | | | | | | | | |
| A | | | | | | 0,3421 | | |
| B | | | | | | 0,0263 | 0,4318 | |
| C | | 0,3 | | | | 0,5789 | | |
| D | | | | | 0,025 | | | 0,0238 |
| E | | | 0,2273 | 0,0476 | | | 0,5455 | 0,1905 |
| F | | 0,0333 | | | | | 0,0227 | |
| G | | 0,6667 | | | | | | |
| H | | | 0,7273 | 0,4048 | | | | 0,7619 |
| I | | | 0,0455 | | | | | 0,0238 |
| J | | | | | | | | |
| K | | | | | | | | |
| L | | | | 0,0238 | | | | |
| M | | | | 0,0476 | | | | |
| N | | | | | | | | |
| O | | | | 0,0238 | | 0,0526 | | |
| P | | | | 0,4524 | 0,75 | | | |
| Q | | | | | | | | |
| R | | | | | | | | |
| S | | | | | | | | |
| T | | | | | | 0,225 | | |

Summary of Heterozygosity Statistics for All Loci

| Locus | Sample Size | Obs_Hom | Obs_Het | Exp_Hom* | Exp_Het* | Nei** | Ave_Het |
|---------|-------------|---------|---------|----------|----------|--------|---------|
| D01 | 30 | 0.6667 | 0.3333 | 0.5195 | 0.4805 | 0.4644 | 0.5453 |
| D02 | 44 | 0.7273 | 0.2727 | 0.5729 | 0.4271 | 0.4174 | 0.5647 |
| D96 | 42 | 0.5238 | 0.4762 | 0.3589 | 0.6411 | 0.6259 | 0.7290 |
| AG13 | 40 | 0.6500 | 0.3500 | 0.6038 | 0.3962 | 0.3862 | 0.6931 |
| AG218 | 38 | 0.5789 | 0.4211 | 0.4410 | 0.5590 | 0.5443 | 0.6646 |
| AG219 | 44 | 0.5000 | 0.5000 | 0.4725 | 0.5275 | 0.5155 | 0.6417 |
| AG230 | 42 | 0.5714 | 0.4286 | 0.6086 | 0.3914 | 0.3821 | 0.5541 |
| Mean | 40 | 0.6026 | 0.3974 | 0.5110 | 0.4890 | 0.4765 | 0.6275 |
| St. Dev | | 0.0818 | 0.0818 | 0.0927 | 0.0927 | 0.0905 | 0.0733 |

* Expected homozygosity and heterozygosity were computed using Levene (1949)

** Nei's (1973) expected heterozygosity



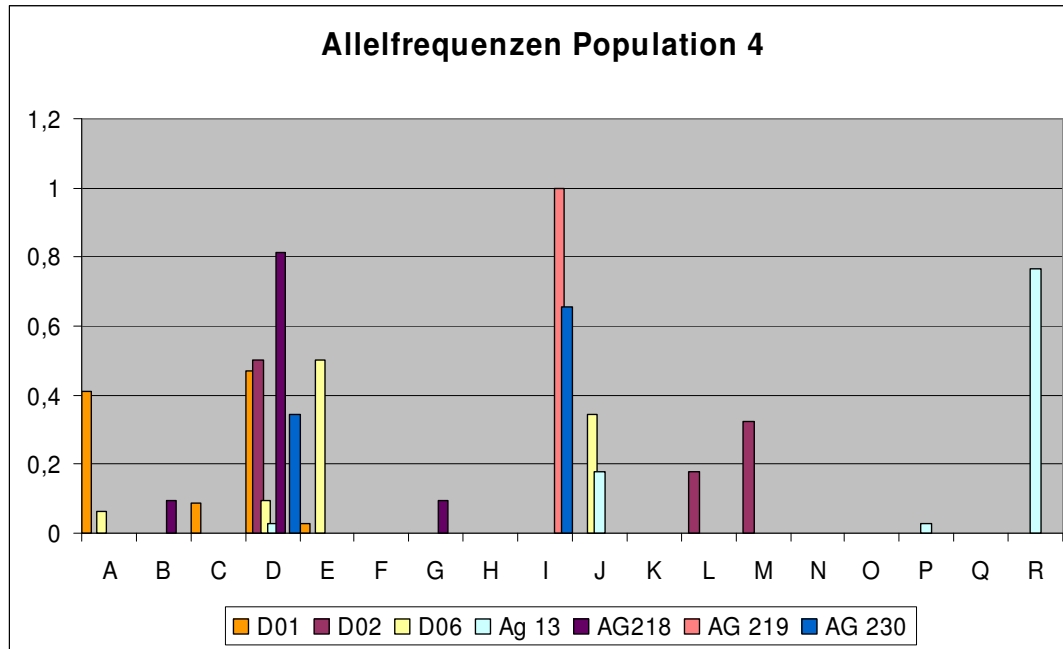
| | Locus | D01 | D02 | D96 | AG13 | AG218 | AG219 | AG230 |
|--------|-------|--------|--------|--------|--------|--------|--------|--------|
| Allele | | | | | | | | |
| A | | 0,2654 | 0,0023 | 0,0349 | 0,0023 | 0,1202 | | 0,0073 |
| B | | 0,0024 | 0,025 | 0,0047 | 0,0093 | 0,2452 | 0,1923 | |
| C | | 0,3365 | 0,0091 | 0,007 | | 0,2043 | 0,0045 | 0,0437 |
| D | | 0,0616 | 0,3864 | 0,1023 | 0,1551 | 0,0793 | | 0,3932 |
| E | | 0,0071 | 0,0727 | 0,0814 | 0,0069 | 0,0769 | 0,1086 | 0,0243 |
| F | | 0,1445 | | 0,1977 | 0,0023 | 0,0072 | 0,0068 | 0,0097 |
| G | | 0,0948 | 0,0568 | 0,0326 | | 0,101 | 0,0136 | 0,0024 |
| H | | 0,0332 | 0,2273 | 0,2279 | | 0,012 | 0,0837 | 0,318 |
| I | | 0,0166 | 0,0409 | 0,0395 | | 0,0553 | 0,138 | 0,199 |
| J | | 0,0355 | 0,0273 | 0,086 | 0,0185 | 0,0168 | 0,0792 | 0,0024 |
| K | | | 0,0023 | 0,0163 | 0,0231 | 0,0144 | 0,0407 | |
| L | | 0,0024 | 0,0636 | 0,0186 | 0,0394 | 0,0168 | 0,1131 | |
| M | | | 0,075 | 0,0349 | 0,0185 | 0,0457 | 0,009 | |
| N | | | 0,0114 | 0,0023 | 0,0741 | | 0,0339 | |
| O | | | | 0,0279 | 0,0949 | 0,0048 | 0,0407 | |
| P | | | | 0,0814 | 0,2477 | | 0,0181 | |
| Q | | | | 0,0023 | 0,0139 | | 0,0113 | |
| R | | | | 0,0023 | 0,1574 | | 0,0068 | |
| S | | | | | 0,0162 | | 0,009 | |
| T | | | | | 0,0856 | | 0,0136 | |
| U | | | | | 0,0139 | | 0,0023 | |
| V | | | | | 0,0208 | | 0,043 | |
| W | | | | | | | 0,0113 | |
| X | | | | | | | 0,0045 | |
| Y | | | | | | | 0,0045 | |
| Z | | | | | | | 0,0113 | |

| Locus | Sample Size | Obs_Hom | Obs_Het | Exp_Hom* | Exp_Het* | Nei** | Ave_Het |
|---------|-------------|---------|---------|----------|----------|--------|---------|
| D01 | 422 | 0.3886 | 0.6114 | 0.2182 | 0.7818 | 0.7800 | 0.5453 |
| D02 | 440 | 0.4136 | 0.5864 | 0.2206 | 0.7794 | 0.7776 | 0.5647 |
| D96 | 430 | 0.3256 | 0.6744 | 0.1266 | 0.8734 | 0.8713 | 0.7290 |
| AG13 | 432 | 0.3148 | 0.6852 | 0.1340 | 0.8660 | 0.8640 | 0.6931 |
| AG218 | 416 | 0.3606 | 0.6394 | 0.1428 | 0.8572 | 0.8551 | 0.6646 |
| AG219 | 442 | 0.4977 | 0.5023 | 0.0996 | 0.9004 | 0.8984 | 0.6417 |
| AG230 | 412 | 0.4466 | 0.5534 | 0.2963 | 0.7037 | 0.7020 | 0.5541 |
| Mean | 428 | 0.3925 | 0.6075 | 0.1769 | 0.8231 | 0.8212 | 0.6275 |
| St. Dev | | 0.0658 | 0.0658 | 0.0700 | 0.0700 | 0.0698 | 0.0733 |

Summary of Heterozygosity Statistics for All Loci

* Expected homozygosity and heterozygosity were computed using Levene (1949)

** Nei's (1973) expected heterozygosity



| Allele | Locus | D01 | D02 | D96 | AG13 | AG218 | AG219 | AG230 |
|--------|-------|--------|--------|--------|--------|--------|-------|--------|
| A | | 0,4118 | | 0,0625 | | | | |
| B | | | | | | 0,0938 | | |
| C | | 0,0882 | | | | | | |
| D | | 0,4706 | 0,5 | 0,0938 | 0,0294 | 0,8125 | | 0,3438 |
| E | | 0,0294 | | 0,5 | | | | |
| F | | | | | | | | |
| G | | | | | | 0,0938 | | |
| H | | | | | | | | |
| I | | | | | | | 1 | 0,6562 |
| J | | | | 0,3438 | 0,1765 | | | |
| K | | | | | | | | |
| L | | | 0,1765 | | | | | |
| M | | | 0,3235 | | | | | |
| N | | | | | | | | |
| O | | | | | | | | |
| P | | | | | 0,0294 | | | |
| Q | | | | | | | | |
| R | | | | | 0,7647 | | | |

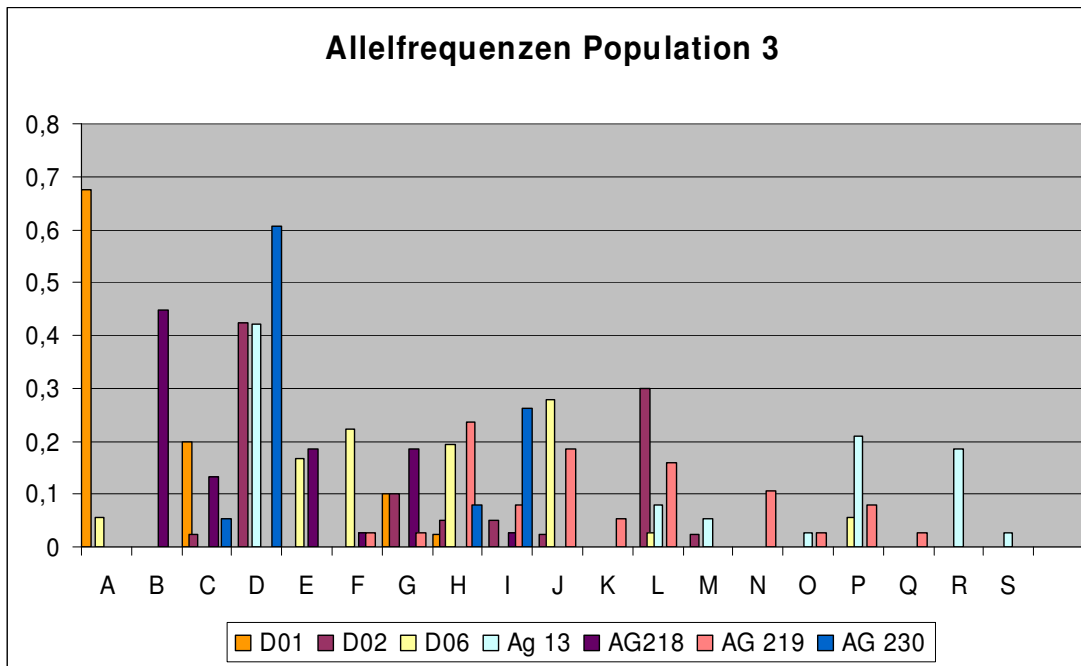
| Locus | Sample Size | Obs_Hom | Obs_Het | Exp_Hom* | Exp_Het* | Nei** | Ave_Het |
|---------|-------------|---------|---------|----------|----------|--------|---------|
| D01 | 34 | 0.0000 | 10.000 | 0.3815 | 0.6185 | 0.6003 | 0.5453 |
| D02 | 34 | 0.0000 | 10.000 | 0.3672 | 0.6328 | 0.6142 | 0.5647 |
| D96 | 32 | 0.0000 | 10.000 | 0.3609 | 0.6391 | 0.6191 | 0.7290 |
| AG13 | 34 | 0.5882 | 0.4118 | 0.6061 | 0.3939 | 0.3824 | 0.6931 |
| AG218 | 32 | 0.6250 | 0.3750 | 0.6673 | 0.3327 | 0.3223 | 0.6646 |
| AG219 | 34 | 10.000 | 0.0000 | 10.000 | 0.0000 | 0.0000 | 0.6417 |
| AG230 | 32 | 0.3125 | 0.6875 | 0.5343 | 0.4657 | 0.4512 | 0.5541 |
| Mean | 33 | 0.3608 | 0.6392 | 0.5596 | 0.4404 | 0.4271 | 0.6275 |
| St. Dev | | 0.3922 | 0.3922 | 0.2297 | 0.2297 | 0.2228 | 0.0733 |

Summary of Heterozygosity Statistics for All Loci

**

* Expected homozygosity and heterozygosity were computed using Levene (1949)

** Nei's (1973) expected heterozygosity



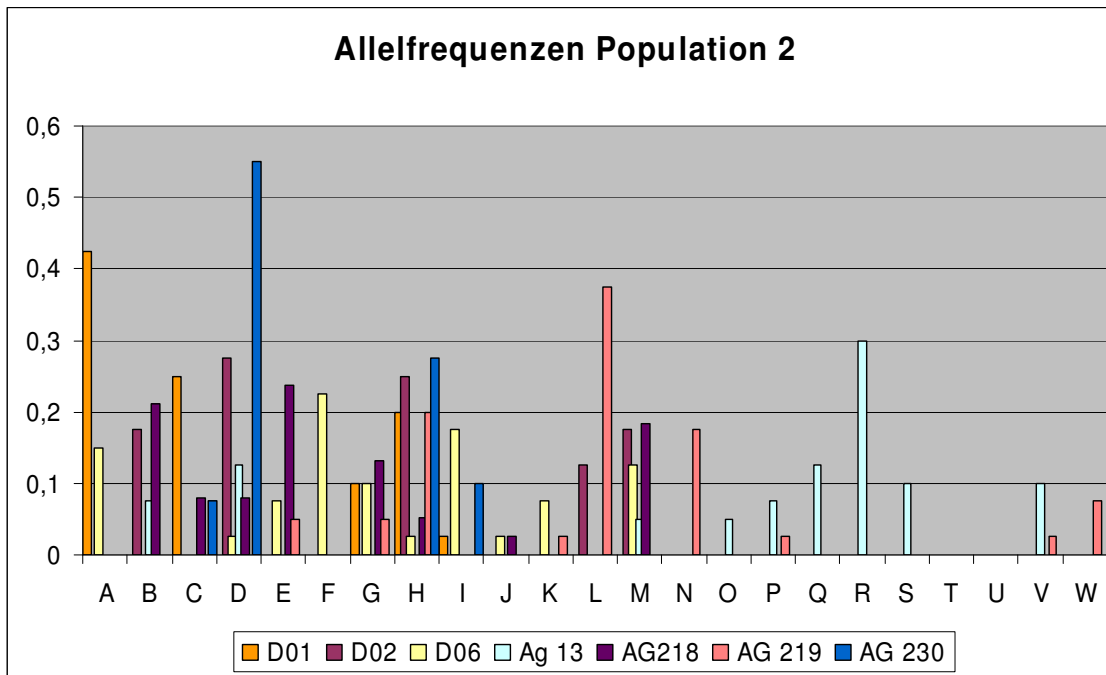
| | Locus | D01 | D02 | D96 | AG13 | AG218 | AG219 | AG230 |
|--------|-------|-------|-------|--------|--------|--------|--------|--------|
| Allele | | | | | | | | |
| A | | 0,675 | | 0,0556 | | | | |
| B | | | | | | 0,4474 | | |
| C | | 0,2 | 0,025 | | | 0,1316 | | 0,0526 |
| D | | | 0,425 | | 0,4211 | | | 0,6053 |
| E | | | | 0,1667 | | 0,1842 | | |
| F | | | | 0,2222 | | 0,0263 | 0,0263 | |
| G | | 0,1 | 0,1 | | | 0,1842 | 0,0263 | |
| H | | 0,025 | 0,05 | 0,1944 | | | 0,2368 | 0,0789 |
| I | | | 0,05 | | | 0,0263 | 0,0789 | 0,2632 |
| J | | | 0,025 | 0,2778 | | | 0,1842 | |
| K | | | | | | | 0,0526 | |
| L | | | 0,3 | 0,0278 | 0,0789 | | 0,1579 | |
| M | | | 0,025 | | 0,0526 | | | |
| N | | | | | | | 0,1053 | |
| O | | | | | 0,0263 | | 0,0263 | |
| P | | | | 0,0556 | 0,2105 | | 0,0789 | |
| Q | | | | | | | 0,0263 | |
| R | | | | | 0,1842 | | | |
| S | | | | | 0,0263 | | | |
| T | | | | | | | | |

Summary of Heterozygosity Statistics for All Loci

| Locus | Sample Size | Obs_Hom | Obs_Het | Exp_Hom* | Exp_Het* | Nei** | Ave_Het |
|---------|-------------|---------|---------|----------|----------|--------|---------|
| D01 | 40 | 0.5500 | 0.4500 | 0.4936 | 0.5064 | 0.4937 | 0.5453 |
| D02 | 40 | 0.4000 | 0.6000 | 0.2692 | 0.7308 | 0.7125 | 0.5647 |
| D96 | 36 | 0.2778 | 0.7222 | 0.1762 | 0.8238 | 0.8009 | 0.7290 |
| AG13 | 38 | 0.2105 | 0.7895 | 0.2461 | 0.7539 | 0.7341 | 0.6931 |
| AG218 | 38 | 0.3158 | 0.6842 | 0.2674 | 0.7326 | 0.7133 | 0.6646 |
| AG219 | 38 | 0.1579 | 0.8421 | 0.1209 | 0.8791 | 0.8560 | 0.6417 |
| AG230 | 38 | 0.4211 | 0.5789 | 0.4296 | 0.5704 | 0.5554 | 0.5541 |
| Mean | 38 | 0.3333 | 0.6667 | 0.2861 | 0.7139 | 0.6951 | 0.6275 |
| St. Dev | | 0.1344 | 0.1344 | 0.1324 | 0.1324 | 0.1286 | 0.0733 |

* Expected homozygosity and heterozygosity were computed using Levene (1949)

** Nei's (1973) expected heterozygosity



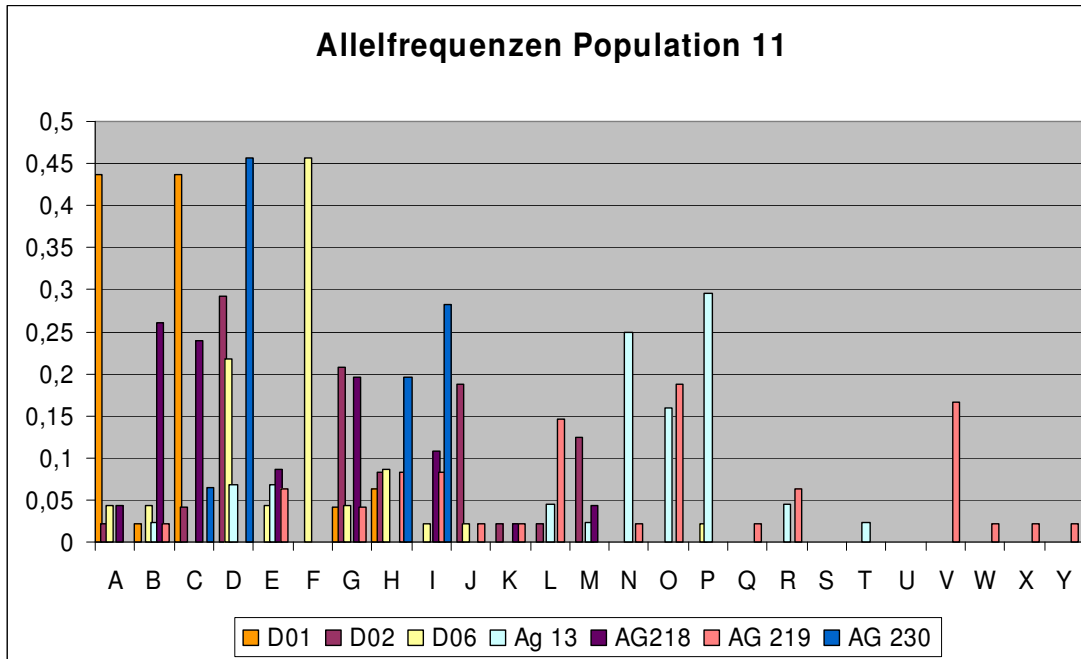
| Allele | Locus | D01 | D02 | D96 | AG13 | AG218 | AG219 | AG230 |
|--------|-------|-------|-------|-------|-------|--------|-------|-------|
| A | | 0,425 | | 0,15 | | | | |
| B | | | 0,175 | | 0,075 | 0,2105 | | |
| C | | 0,25 | | | | 0,0789 | | 0,075 |
| D | | | 0,275 | 0,025 | 0,125 | 0,0789 | | 0,55 |
| E | | | | 0,075 | | 0,2368 | 0,05 | |
| F | | | | 0,225 | | | | |
| G | | 0,1 | | 0,1 | | 0,1316 | 0,05 | |
| H | | 0,2 | 0,25 | 0,025 | | 0,0526 | 0,2 | 0,275 |
| I | | 0,025 | | 0,175 | | | | 0,1 |
| J | | | | 0,025 | | 0,0263 | | |
| K | | | | 0,075 | | | 0,025 | |
| L | | | 0,125 | | | | 0,375 | |
| M | | | 0,175 | 0,125 | 0,05 | 0,1842 | | |
| N | | | | | | | 0,175 | |
| O | | | | | 0,05 | | | |
| P | | | | | 0,075 | | 0,025 | |
| Q | | | | | 0,125 | | | |
| R | | | | | 0,3 | | | |
| S | | | | | 0,1 | | | |
| T | | | | | | | | |
| U | | | | | | | | |
| V | | | | | 0,1 | | 0,025 | |
| W | | | | | | | 0,075 | |

Summary of Heterozygosity Statistics for All Loci

| Locus | Sample Size | Obs_Hom | Obs_Het | Exp_Hom* | Exp_Het* | NeI** | Ave_Het |
|---------|-------------|---------|---------|----------|----------|--------|---------|
| D01 | 40 | 0.3500 | 0.6500 | 0.2756 | 0.7244 | 0.7063 | 0.5453 |
| D02 | 40 | 0.2500 | 0.7500 | 0.1949 | 0.8051 | 0.7850 | 0.5647 |
| D96 | 40 | 0.1500 | 0.8500 | 0.1205 | 0.8795 | 0.8575 | 0.7290 |
| AG13 | 40 | 0.1000 | 0.9000 | 0.1359 | 0.8641 | 0.8425 | 0.6931 |
| AG218 | 38 | 0.1579 | 0.8421 | 0.1451 | 0.8549 | 0.8324 | 0.6646 |
| AG219 | 40 | 0.2500 | 0.7500 | 0.2038 | 0.7962 | 0.7762 | 0.6417 |
| AG230 | 40 | 0.5000 | 0.5000 | 0.3782 | 0.6218 | 0.6062 | 0.5541 |
| Mean | 40 | 0.2511 | 0.7489 | 0.2077 | 0.7923 | 0.7723 | 0.6275 |
| St. Dev | | 0.1375 | 0.1375 | 0.0918 | 0.0918 | 0.0894 | 0.0733 |

* Expected homozygosity and heterozygosity were computed using Levene (1949)

** Nei's (1973) expected heterozygosity

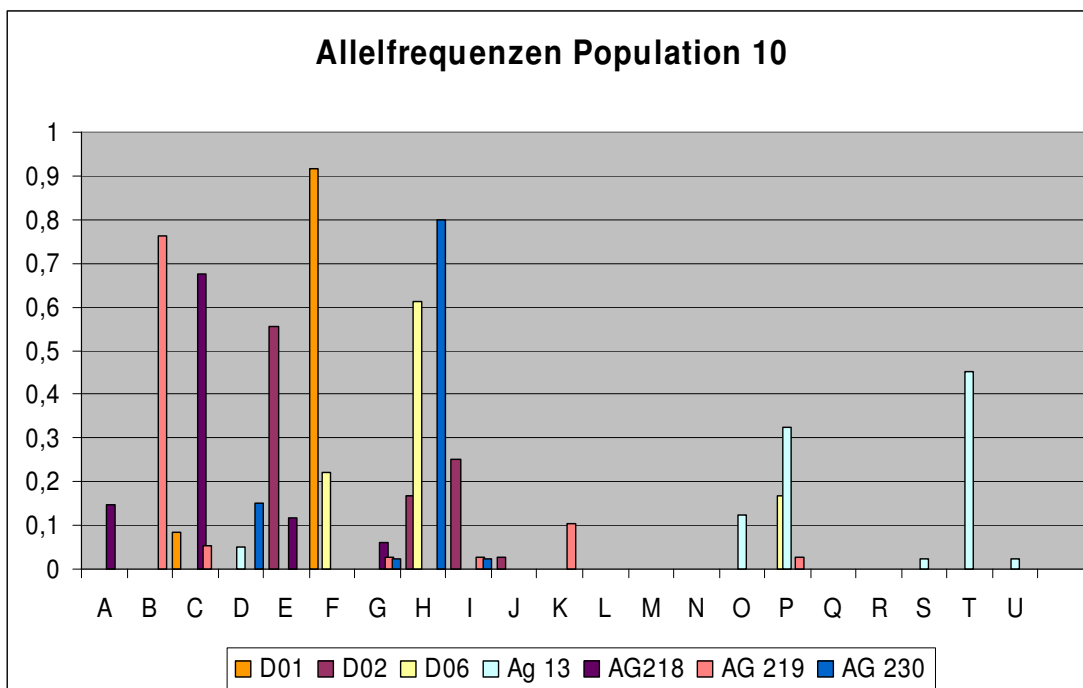


| | Locus | D01 | D02 | D96 | AG13 | AG218 | AG219 | AG230 |
|--------|-------|--------|--------|--------|--------|--------|--------|--------|
| Allele | | | | | | | | |
| A | | 0,4375 | 0,0208 | 0,0435 | | 0,0435 | | |
| B | | 0,0208 | | 0,0435 | 0,0227 | 0,2609 | 0,0208 | |
| C | | 0,4375 | 0,0417 | | | 0,2391 | | 0,0652 |
| D | | | 0,2917 | 0,2174 | 0,0682 | | | 0,4565 |
| E | | | | 0,0435 | 0,0682 | 0,087 | 0,0625 | |
| F | | | | 0,4565 | | | | |
| G | | 0,0417 | 0,2083 | 0,0435 | | 0,1957 | 0,0417 | |
| H | | 0,0625 | 0,0833 | 0,087 | | | 0,0833 | 0,1957 |
| I | | | | 0,0217 | | 0,1087 | 0,0833 | 0,2826 |
| J | | | 0,1875 | 0,0217 | | | 0,0208 | |
| K | | | 0,0208 | | | 0,0217 | 0,0208 | |
| L | | | 0,0208 | | 0,0455 | | 0,1458 | |
| M | | | 0,125 | | 0,0227 | 0,0435 | | |
| N | | | | | 0,25 | | 0,0208 | |
| O | | | | | 0,1591 | | 0,1875 | |
| P | | | | 0,0217 | 0,2955 | | | |
| Q | | | | | | | 0,0208 | |
| R | | | | | 0,0455 | | 0,0625 | |
| S | | | | | | | | |
| T | | | | | 0,0227 | | | |
| U | | | | | | | | |
| V | | | | | | | 0,1667 | |
| W | | | | | | | 0,0208 | |
| X | | | | | | | 0,0208 | |
| Y | | | | | | | 0,0208 | |

Summary of Heterozygosity Statistics for All Loci

| Locus | Sample Size | Obs_Hom | Obs_Het | Exp_Hom* | Exp_Het* | Nei** | Ave_Het |
|---------|-------------|---------|---------|----------|----------|--------|---------|
| D01 | 48 | 0.3333 | 0.6667 | 0.3759 | 0.6241 | 0.6111 | 0.5453 |
| D02 | 48 | 0.0833 | 0.9167 | 0.1720 | 0.8280 | 0.8108 | 0.5647 |
| D96 | 46 | 0.4348 | 0.5652 | 0.2560 | 0.7440 | 0.7278 | 0.7290 |
| AG13 | 44 | 0.2727 | 0.7273 | 0.1712 | 0.8288 | 0.8099 | 0.6931 |
| AG218 | 46 | 0.0870 | 0.9130 | 0.1691 | 0.8309 | 0.8129 | 0.6646 |
| AG219 | 48 | 0.3333 | 0.6667 | 0.0922 | 0.9078 | 0.8889 | 0.6417 |
| AG230 | 46 | 0.3043 | 0.6957 | 0.3159 | 0.6841 | 0.6692 | 0.5541 |
| Mean | 47 | 0.2641 | 0.7359 | 0.2218 | 0.7782 | 0.7615 | 0.6275 |
| St. Dev | | 0.1320 | 0.1320 | 0.0986 | 0.0986 | 0.0965 | 0.0733 |

* Expected homozygosity and heterozygosity were computed using Levene (1949)



** Nei's (1973) expected heterozygosity

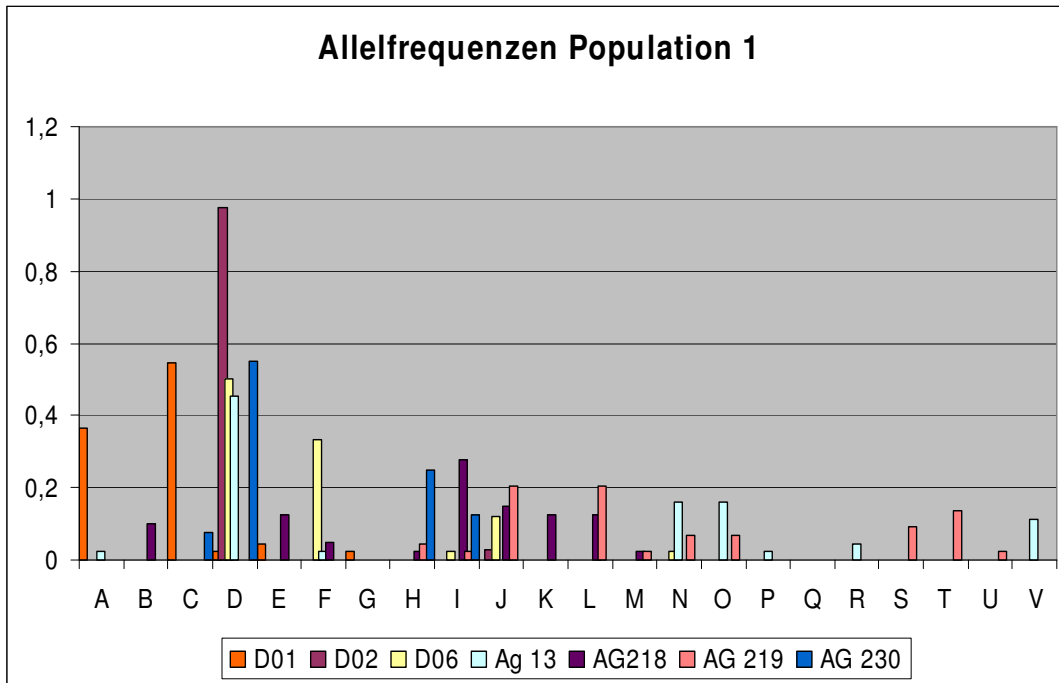
| Allele | Locus | D01 | D02 | D96 | AG13 | AG218 | AG219 | AG230 |
|--------|-------|--------|--------|--------|-------|--------|--------|-------|
| A | | | | | | 0,1471 | | |
| B | | | | | | | 0,7632 | |
| C | | 0,0833 | | | | 0,6765 | 0,0526 | |
| D | | | | | | 0,05 | | 0,15 |
| E | | | 0,5556 | | | 0,1176 | | |
| F | | 0,9167 | | 0,2222 | | | | |
| G | | | | | | 0,0588 | 0,0263 | 0,025 |
| H | | | 0,1667 | 0,6111 | | | | 0,8 |
| I | | | 0,25 | | | | 0,0263 | 0,025 |
| J | | | 0,0278 | | | | | |
| K | | | | | | | 0,1053 | |
| L | | | | | | | | |
| M | | | | | | | | |
| N | | | | | | | | |
| O | | | | | | 0,125 | | |
| P | | | | 0,1667 | 0,325 | | 0,0263 | |
| Q | | | | | | | | |
| R | | | | | | | | |
| S | | | | | | 0,025 | | |
| T | | | | | | 0,45 | | |
| U | | | | | | 0,025 | | |

Summary of Heterozygosity Statistics for All Loci

| Locus | Sample Size | Obs_Hom | Obs_Het | Exp_Hom* | Exp_Het* | Nei** | Ave_Het |
|---------|-------------|---------|---------|----------|----------|--------|---------|
| D01 | 36 | 0.8333 | 0.1667 | 0.8429 | 0.1571 | 0.1528 | 0.5453 |
| D02 | 36 | 0.3889 | 0.6111 | 0.3825 | 0.6175 | 0.6003 | 0.5647 |
| D96 | 36 | 0.5556 | 0.4444 | 0.4349 | 0.5651 | 0.5494 | 0.7290 |
| AG13 | 40 | 0.3500 | 0.6500 | 0.3103 | 0.6897 | 0.6725 | 0.6931 |
| AG218 | 34 | 0.7059 | 0.2941 | 0.4813 | 0.5187 | 0.5035 | 0.6646 |
| AG219 | 38 | 0.6842 | 0.3158 | 0.5875 | 0.4125 | 0.4017 | 0.6417 |
| AG230 | 40 | 0.6500 | 0.3500 | 0.6551 | 0.3449 | 0.3362 | 0.5541 |
| Mean | 37 | 0.5954 | 0.4046 | 0.5278 | 0.4722 | 0.4595 | 0.6275 |
| St. Dev | | 0.1752 | 0.1752 | 0.1818 | 0.1818 | 0.1769 | 0.0733 |

* Expected homozygosity and heterozygosity were computed using Levene (1949)

** Nei's (1973) expected heterozygosity



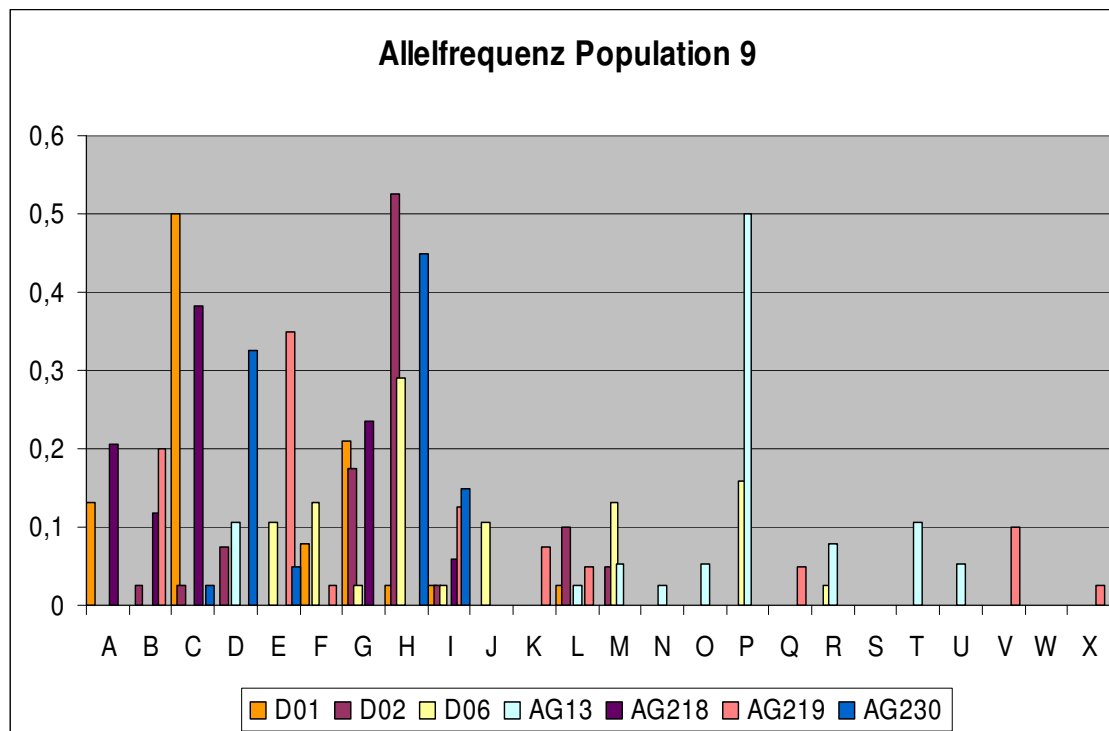
| | Locus | D01 | D02 | D96 | AG13 | AG218 | AG219 | AG230 |
|--------|-------|--------|--------|--------|--------|-------|--------|-------|
| Allele | | | | | | | | |
| A | | 0,3636 | | | 0,0227 | | | |
| B | | | | | | 0,1 | | |
| C | | 0,5455 | | | | | | 0,075 |
| D | | 0,0227 | 0,9737 | 0,5 | 0,4545 | | | 0,55 |
| E | | 0,0455 | | | | 0,125 | | |
| F | | | | 0,3333 | 0,0227 | 0,05 | | |
| G | | 0,0227 | | | | | | |
| H | | | | | | 0,025 | 0,0455 | 0,25 |
| I | | | | 0,0238 | | 0,275 | 0,0227 | 0,125 |
| J | | | 0,0263 | 0,119 | | 0,15 | 0,2045 | |
| K | | | | | | 0,125 | | |
| L | | | | | | 0,125 | 0,2045 | |
| M | | | | | | 0,025 | 0,0227 | |
| N | | | | 0,0238 | 0,1591 | | 0,0682 | |
| O | | | | | 0,1591 | | 0,0682 | |
| P | | | | | 0,0227 | | | |
| Q | | | | | | | | |
| R | | | | | 0,0455 | | | |
| S | | | | | | | 0,0909 | |
| T | | | | | | | 0,1364 | |
| U | | | | | | | 0,0227 | |
| V | | | | | 0,1136 | | | |
| W | | | | | | | | |
| X | | | | | | | | |
| Y | | | | | | | | |
| Z | | | | | | | 0,1136 | |

| Locus | Sample Size | Obs_Hom | Obs_Het | Exp_Hom* | Exp_Het* | Nei** | Ave_Het |
|---------|-------------|---------|---------|----------|----------|--------|---------|
| D01 | 44 | 0.4545 | 0.5455 | 0.4197 | 0.5803 | 0.5671 | 0.5453 |
| D02 | 38 | 0.9474 | 0.0526 | 0.9474 | 0.0526 | 0.0512 | 0.5647 |
| D96 | 42 | 0.2381 | 0.7619 | 0.3612 | 0.6388 | 0.6236 | 0.7290 |
| AG13 | 44 | 0.3182 | 0.6818 | 0.2569 | 0.7431 | 0.7262 | 0.6931 |
| AG218 | 40 | 0.1000 | 0.9000 | 0.1372 | 0.8628 | 0.8413 | 0.6646 |
| AG219 | 44 | 0.3182 | 0.6818 | 0.1163 | 0.8837 | 0.8636 | 0.6417 |
| AG230 | 40 | 0.5000 | 0.5000 | 0.3705 | 0.6295 | 0.6138 | 0.5541 |
| Mean | 42 | 0.4109 | 0.5891 | 0.3727 | 0.6273 | 0.6124 | 0.6275 |
| St. Dev | | 0.2712 | 0.2712 | 0.2791 | 0.2791 | 0.2725 | 0.0733 |

Summary of Heterozygosity Statistics for All Loci

* Expected homozygosity and heterozygosity were computed using Levene (1949)

** Nei's (1973) expected heterozygosity



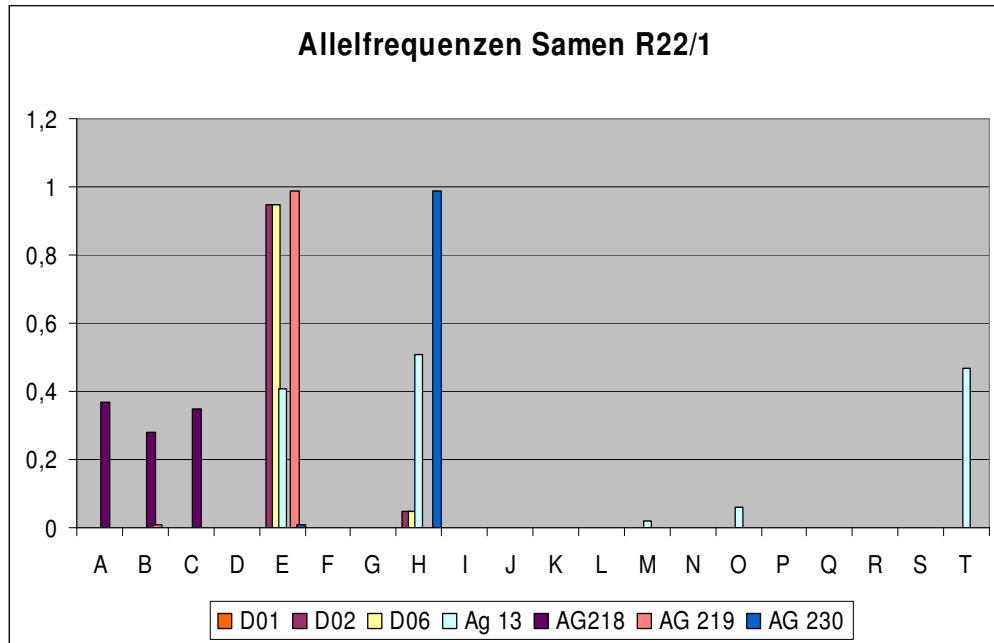
| | Locus | D01 | D02 | D96 | AG13 | AG218 | AG219 | AG230 |
|--------|-------|--------|-------|--------|--------|--------|-------|-------|
| Allele | | | | | | | | |
| A | | 0,1316 | | | | 0,2059 | | |
| B | | | 0,025 | | | 0,1176 | 0,2 | |
| C | | 0,5 | 0,025 | | | 0,3824 | | 0,025 |
| D | | | 0,075 | | 0,1053 | | | 0,325 |
| E | | | | 0,1053 | | | 0,35 | 0,05 |
| F | | 0,0789 | | 0,1316 | | | 0,025 | |
| G | | 0,2105 | 0,175 | 0,0263 | | 0,2353 | | |
| H | | 0,0263 | 0,525 | 0,2895 | | | | 0,45 |
| I | | 0,0263 | 0,025 | 0,0263 | | 0,0588 | 0,125 | 0,15 |
| J | | | | 0,1053 | | | | |
| K | | | | | | | 0,075 | |
| L | | 0,0263 | 0,1 | | 0,0263 | | 0,05 | |
| M | | | 0,05 | 0,1316 | 0,0526 | | | |
| N | | | | | 0,0263 | | | |
| O | | | | | 0,0526 | | | |
| P | | | | 0,1579 | 0,5 | | | |
| Q | | | | | | | 0,05 | |
| R | | | | 0,0263 | 0,0789 | | | |
| S | | | | | | | | |
| T | | | | | 0,1053 | | | |
| U | | | | | 0,0526 | | | |
| V | | | | | | | 0,1 | |
| W | | | | | | | | |
| X | | | | | | | 0,025 | |

Summary of Heterozygosity Statistics for All Loci

| Locus | Sample Size | Obs_Hom | Obs_Het | Exp_Hom* | Exp_Het* | Nei** | Ave_Het |
|---------|-------------|---------|---------|----------|----------|--------|---------|
| D01 | 38 | 0.2632 | 0.7368 | 0.3016 | 0.6984 | 0.6801 | 0.5453 |
| D02 | 40 | 0.5000 | 0.5000 | 0.3090 | 0.6910 | 0.6738 | 0.5647 |
| D96 | 38 | 0.2632 | 0.7368 | 0.1451 | 0.8549 | 0.8324 | 0.7290 |
| AG13 | 38 | 0.3684 | 0.6316 | 0.2688 | 0.7312 | 0.7119 | 0.6931 |
| AG218 | 34 | 0.2353 | 0.7647 | 0.2389 | 0.7611 | 0.7388 | 0.6646 |
| AG219 | 40 | 0.4500 | 0.5500 | 0.1795 | 0.8205 | 0.8000 | 0.6417 |
| AG230 | 40 | 0.6000 | 0.4000 | 0.3167 | 0.6833 | 0.6663 | 0.5541 |
| Mean | 38 | 0.3829 | 0.6171 | 0.2514 | 0.7486 | 0.7290 | 0.6275 |
| St. Dev | | 0.1391 | 0.1391 | 0.0671 | 0.0671 | 0.0652 | 0.0733 |

* Expected homozygosity and heterozygosity were computed using Levene (1949)

** Nei's (1973) expected heterozygosity



| Allele | Locus | D01 | D02 | D96 | AG13 | AG218 | AG219 | AG230 |
|--------|-------|-----|------|--------|--------|-------|-------|-------|
| A | | | | | | 0,37 | | |
| B | | | | | | 0,28 | 0,01 | |
| C | | | | | | 0,35 | | |
| D | | | | | | | | |
| E | | | 0,95 | 0,41 | | | 0,99 | 0,01 |
| F | | | | | | | | |
| G | | 0,5 | | | | | | |
| H | | | 0,05 | 0,51 | | | | 0,99 |
| I | | | | | | | | |
| J | | 0,5 | | | | | | |
| K | | | | | | | | |
| L | | | | | | | | |
| M | | | | 0,02 | | | | |
| N | | | | | | | | |
| O | | | | 0,06 | | | | |
| P | | | | | 0,5306 | | | |
| Q | | | | | | | | |
| R | | | | | | | | |
| S | | | | | | | | |
| T | | | | 0,4694 | | | | |

| | D01 | D02 | D06 | AG13 | Ag 218 | AG 219 | AG 230 |
|---------|-----|-----|-----|------|--------|--------|--------|
| Mutter: | GG | EH | EH | PT | AC | EE | HH |

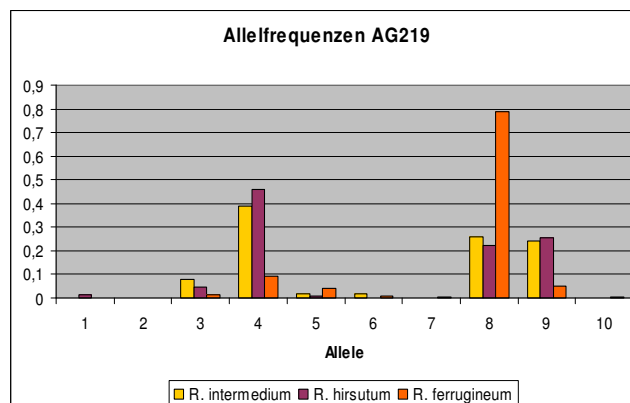
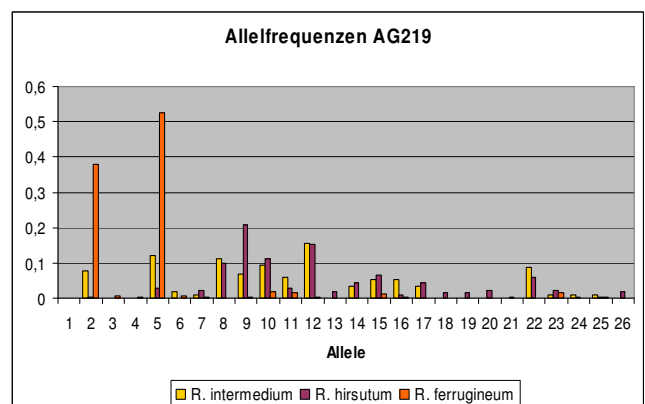
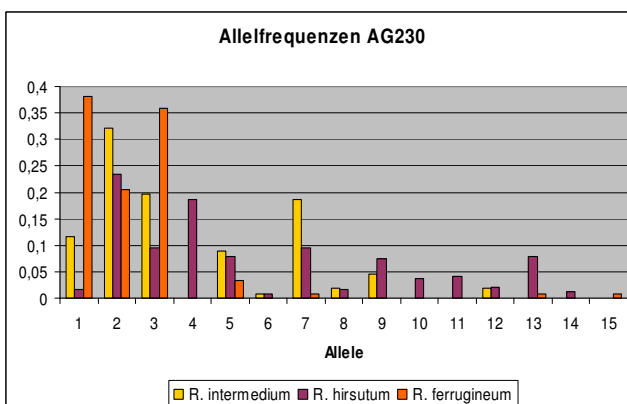
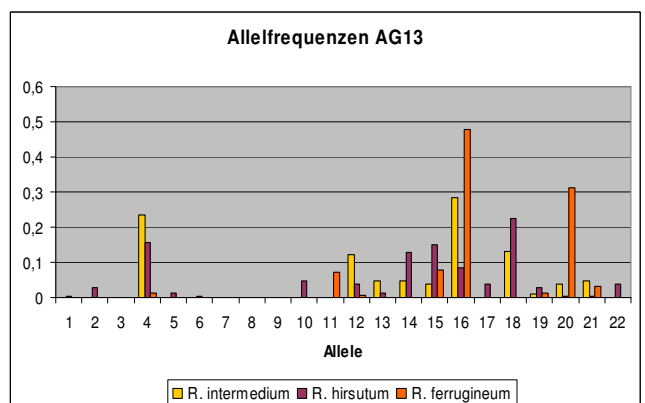
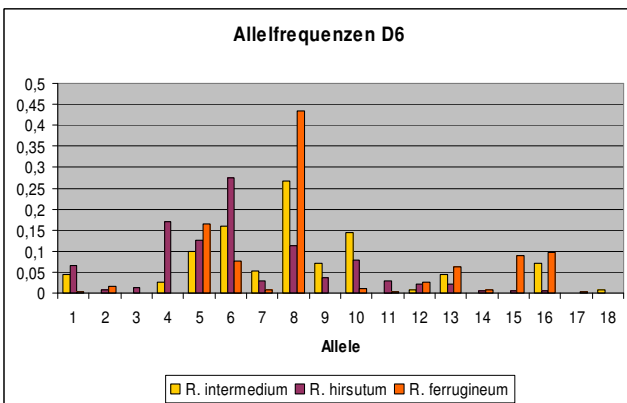
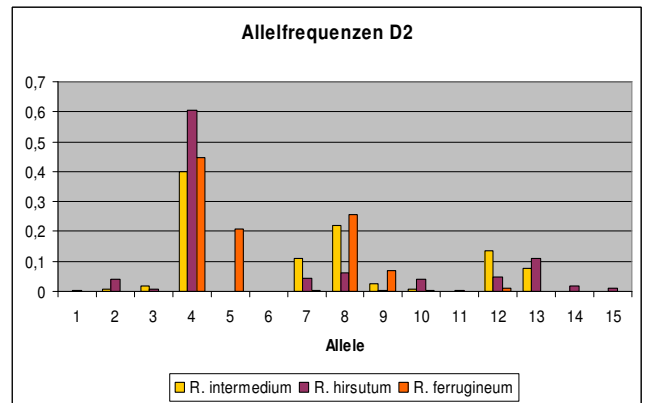
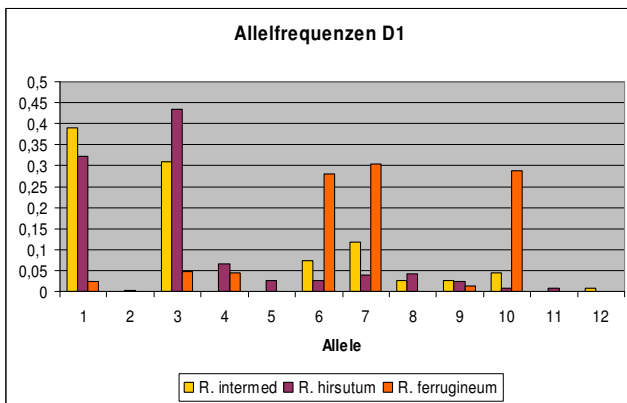
Vergleich der Allelfrequenz der 3 Spezies R.ferrugineum, hirsutum und intermed.

| Locus | D1 | | | D2 | | | D8 | | | AG13 | | | AG218 | | | AG219 | | | AG230 | | | | |
|----------|------|------|------|------|------|------|------|------|------|------|------|------|-------|------|------|-------|------|------|-------|------|------|------|--|
| | G3 | G1 | G2 | G3 | G1 | G2 | G3 | G1 | G2 | G3 | G1 | G2 | G3 | G1 | G2 | G3 | G1 | G2 | G3 | G1 | G2 | | |
| Allele A | 0,39 | 0,32 | 0,02 | | 0 | | 0,04 | 0,07 | 0 | 0 | 0,12 | 0,02 | 0,38 | 0,12 | 0,02 | 0,38 | 0,08 | 0 | 0,38 | 0,08 | 0,05 | 0,02 | |
| Allele B | 0 | | | 0,01 | 0,04 | | | 0,01 | 0,01 | 0,03 | | | 0,32 | 0,23 | 0,21 | 0,08 | 0 | 0,38 | 0,08 | 0,05 | 0,02 | | |
| Allele C | 0,31 | 0,43 | 0,06 | 0,02 | 0,01 | | | 0,01 | | 0,03 | 0,2 | 0,1 | 0,36 | 0,2 | 0,1 | 0,36 | | 0,01 | 0,08 | 0,05 | 0,02 | | |
| Allele D | | 0,07 | 0,04 | 0,4 | 0,8 | 0,45 | 0,03 | 0,17 | 0,24 | 0,16 | 0,19 | 0,19 | | 0,19 | 0,08 | 0,03 | 0,12 | 0,03 | 0,53 | 0,02 | 0,01 | 0,04 | |
| Allele E | | 0,03 | | | | 0,21 | 0,1 | 0,13 | 0,01 | 0,01 | | | 0,08 | 0,08 | 0,03 | 0,12 | 0,03 | 0,53 | 0,02 | 0,01 | 0,04 | | |
| Allele F | 0,07 | 0,03 | 0,28 | | | | 0,16 | 0,28 | 0,08 | 0 | 0,01 | 0,01 | | 0,01 | 0,01 | 0,02 | 0,02 | 0,01 | 0,02 | | 0,01 | 0,01 | |
| Allele G | 0,12 | 0,04 | 0,3 | 0,11 | 0,04 | 0 | 0,05 | 0,03 | 0,01 | | 0,19 | 0,1 | 0,01 | 0,19 | 0,1 | 0,01 | 0,01 | 0,02 | 0 | | | 0 | |
| Allele H | 0,03 | 0,04 | | 0,22 | 0,08 | 0,28 | 0,27 | 0,11 | 0,43 | | 0,02 | 0,02 | | 0,02 | 0,02 | | 0,11 | 0,1 | 0,28 | 0,22 | 0,78 | | |
| Allele I | 0,03 | 0,02 | 0,01 | 0,03 | 0 | 0,07 | 0,07 | 0,04 | | | 0,04 | 0,08 | | 0,04 | 0,08 | | 0,07 | 0,21 | 0 | 0,24 | 0,25 | 0,05 | |
| Allele J | 0,05 | 0,01 | 0,29 | 0,01 | 0,04 | 0 | 0,14 | 0,08 | 0,01 | 0,05 | 0 | 0,04 | | 0 | 0,04 | | 0,09 | 0,11 | 0,02 | | | 0 | |
| Allele K | | 0,01 | | | 0 | | | 0,03 | 0 | | | | | 0 | 0,04 | | 0,08 | 0,03 | 0,01 | | | | |
| Allele L | 0,01 | | | 0,14 | 0,05 | 0,01 | 0,01 | 0,02 | 0,03 | 0,12 | 0,04 | 0,01 | 0,02 | 0,02 | 0,02 | | 0,18 | 0,15 | 0 | | | | |
| Allele M | | | | 0,08 | 0,11 | | 0,04 | 0,02 | 0,08 | 0,05 | 0,01 | | 0,08 | 0,08 | 0,01 | | 0 | 0,02 | | | | | |
| Allele N | | | | | 0,02 | | | 0 | 0,01 | 0,05 | 0,13 | | 0,01 | | | | 0,03 | 0,04 | | | | | |
| Allele O | | | | | 0,01 | | | 0 | 0,09 | 0,04 | 0,15 | 0,08 | | | 0,01 | | 0,05 | 0,07 | 0,01 | | | | |
| Allele P | | | | | | | 0,07 | 0 | 0,1 | 0,28 | 0,08 | 0,48 | | | | | 0,05 | 0,01 | 0 | | | | |
| Allele Q | | | | | | | | | 0 | 0,04 | | | | | | 0,03 | 0,04 | | | | | | |
| Allele R | | | | | | | 0,01 | | | 0,13 | 0,23 | | | | | 0,03 | 0,04 | | | | | | |
| Allele S | | | | | | | | | | 0,01 | 0,03 | 0,01 | | | | | 0,01 | 0,02 | | | | | |
| Allele T | | | | | | | | | | 0,04 | 0 | 0,31 | | | | | 0,02 | 0,02 | | | | | |
| Allele U | | | | | | | | | 0,05 | 0 | 0,03 | | | | | | 0 | 0 | | | | | |
| Allele V | | | | | | | | | | | 0,04 | | | | | 0,09 | 0,08 | | | | | | |
| Allele W | | | | | | | | | | | | | | | | 0,01 | 0,02 | 0,01 | | | | | |
| Allele X | | | | | | | | | | | | | | | | 0,01 | 0 | | | | | | |
| Allele Y | | | | | | | | | | | | | | | | 0,01 | 0 | 0 | | | | | |
| Allele Z | | | | | | | | | | | | | | | | | 0,02 | | | | | | |

G3: R. intermedium

G1: R. hirsutum

G2: R. ferrugineum



1.8 Populationsgenetische Analysen der Gewebekultur-Samenherkünfte

| | | | | |
|----|-------|-------------|-------|---|
| 12 | Locus | Sample Size | D01 | 6 |
| | | | D02 | 8 |
| | | | D06 | 8 |
| | | | AG13 | 8 |
| | | | AG218 | 8 |
| | | | AG230 | 8 |

| | | | | |
|----|-------|-------------|-------|---|
| 13 | Locus | Sample Size | D01 | 4 |
| | | | D02 | 8 |
| | | | D06 | 6 |
| | | | AG13 | 6 |
| | | | AG218 | 8 |
| | | | AG230 | 8 |

| | | | | |
|----|-------|-------------|-------|---|
| 14 | Locus | Sample Size | D01 | 4 |
| | | | D02 | 6 |
| | | | D06 | 6 |
| | | | AG13 | 0 |
| | | | AG218 | 6 |
| | | | AG230 | 6 |

| | | | | |
|----|-------|-------------|-------|----|
| 15 | Locus | Sample Size | D01 | 8 |
| | | | D02 | 8 |
| | | | D06 | 8 |
| | | | AG13 | 10 |
| | | | AG218 | 10 |
| | | | AG230 | 10 |

| | | | | |
|----|-------|-------------|-------|---|
| 17 | Locus | Sample Size | D01 | 6 |
| | | | D02 | 6 |
| | | | D06 | 6 |
| | | | AG13 | 6 |
| | | | AG218 | 6 |
| | | | AG230 | 6 |

| | | | | |
|----|-------|-------------|-------|----|
| 22 | Locus | Sample Size | D01 | 10 |
| | | | D02 | 10 |
| | | | D06 | 2 |
| | | | AG13 | 6 |
| | | | AG218 | 10 |
| | | | AG230 | 10 |

| | | | | |
|----|-------|-------------|-------|----|
| 16 | Locus | Sample Size | D01 | 10 |
| | | | D02 | 10 |
| | | | D06 | 10 |
| | | | AG13 | 10 |
| | | | AG218 | 10 |
| | | | AG230 | 10 |

| | | | | |
|----|-------|-------------|-------|----|
| 18 | Locus | Sample Size | D01 | 12 |
| | | | D02 | 14 |
| | | | D06 | 12 |
| | | | AG13 | 12 |
| | | | AG218 | 14 |
| | | | AG230 | 14 |

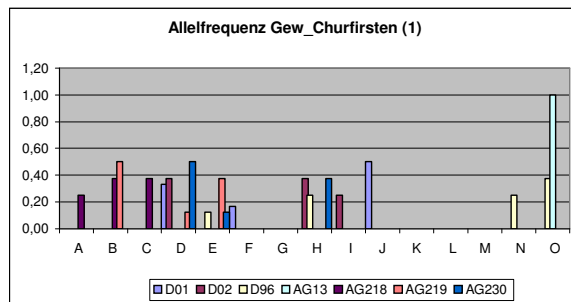
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|----|-------|-------------|-------|----|
| 19 | Locus | Sample Size | D01 | 14 |
| | | | D02 | 16 |
| | | | D06 | 14 |
| | | | AG13 | 16 |
| | | | AG218 | 12 |
| | | | AG230 | 16 |

| | | | | |
|----|-------|-------------|-------|----|
| 20 | Locus | Sample Size | D01 | 12 |
| | | | D02 | 12 |
| | | | D06 | 10 |
| | | | AG13 | 6 |
| | | | AG218 | 12 |
| | | | AG230 | 12 |

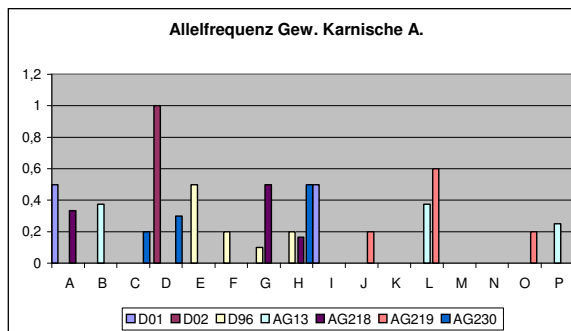
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|----|-------|-------------|-------|----|
| 21 | Locus | Sample Size | D01 | 10 |
| | | | D02 | 10 |
| | | | D06 | 10 |
| | | | AG13 | 8 |
| | | | AG218 | 6 |
| | | | AG230 | 10 |

Allelfrequenzen

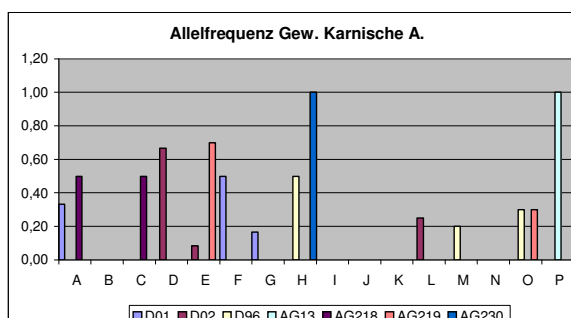
| Allele \ L | D01 | D02 | D96 | AG13 | AG218 | AG219 | AG230 |
|------------|------|------|------|------|-------|-------|-------|
| A | | | | | 0,25 | | |
| B | | | | | 0,38 | 0,50 | |
| C | | | | | 0,38 | | |
| D | 0,33 | 0,38 | | | | 0,13 | 0,50 |
| E | | | 0,13 | | | 0,38 | 0,13 |
| F | 0,17 | | | | | | |
| G | | | | | | | |
| H | | 0,38 | 0,25 | | | | 0,38 |
| I | | 0,25 | | | | | |
| J | 0,50 | | | | | | |
| K | | | | | | | |
| L | | | | | | | |
| M | | | | | | | |
| N | | | 0,25 | | | | |
| O | | | 0,38 | 1,00 | | | |



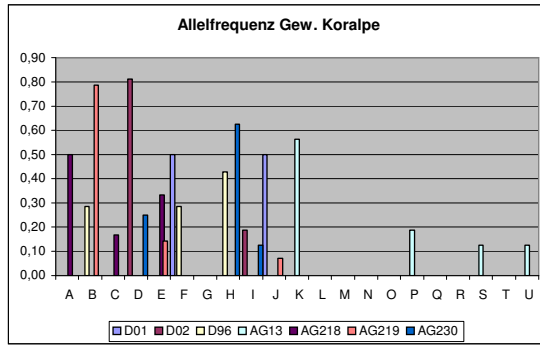
| Allele \ L | D01 | D02 | D96 | AG13 | AG218 | AG219 | AG230 |
|------------|-----|-----|-----|-------|--------|-------|-------|
| A | 0,5 | | | | 0,3333 | | |
| B | | | | 0,375 | | | |
| C | | | | | | | 0,2 |
| D | | 1 | | | | | 0,3 |
| E | | | 0,5 | | | | |
| F | | | 0,2 | | | | |
| G | | | 0,1 | | 0,5 | | |
| H | | | 0,2 | | 0,1667 | | 0,5 |
| I | 0,5 | | | | | | |
| J | | | | | | 0,2 | |
| K | | | | | | | |
| L | | | | 0,375 | | 0,6 | |
| M | | | | | | | |
| N | | | | | | | |
| O | | | | | | 0,2 | |
| P | | | | 0,25 | | | |



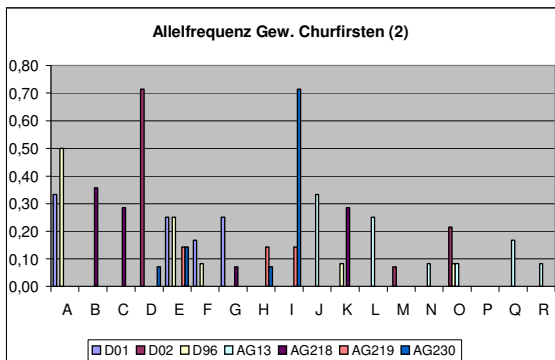
| Allele \ L | D01 | D02 | D96 | AG13 | AG218 | AG219 | AG230 |
|------------|------|------|------|------|-------|-------|-------|
| A | 0,33 | | | | 0,50 | | |
| B | | | | | | | |
| C | | | | | 0,50 | | |
| D | | 0,67 | | | | | |
| E | | 0,08 | | | | 0,70 | |
| F | 0,50 | | | | | | |
| G | 0,17 | | | | | | |
| H | | | 0,50 | | | | 1,00 |
| I | | | | | | | |
| J | | | | | | | |
| K | | | | | | | |
| L | | 0,25 | | | | | |
| M | | | 0,20 | | | | |
| N | | | | | | | |
| O | | | 0,30 | | | 0,30 | |
| P | | | | 1,00 | | | |



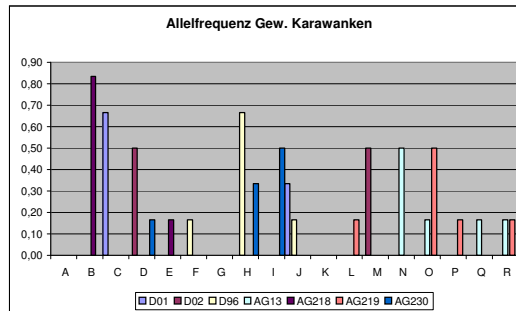
| Allele \ L | D01 | D02 | D96 | AG13 | AG218 | AG219 | AG230 |
|------------|------|------|------|------|-------|-------|-------|
| A | | | | | 0,50 | | |
| B | | | 0,29 | | | 0,79 | |
| C | | | | | 0,17 | | |
| D | | 0,81 | | | | | 0,25 |
| E | | | | | 0,33 | 0,14 | |
| F | 0,50 | | 0,29 | | | | |
| G | | | | | | | |
| H | | | 0,43 | | | | 0,63 |
| I | | 0,19 | | | | | 0,13 |
| J | 0,50 | | | | | 0,07 | |
| K | | | | 0,56 | | | |
| L | | | | | | | |
| M | | | | | | | |
| N | | | | | | | |
| O | | | | | | | |
| P | | | | 0,19 | | | |
| Q | | | | | | | |
| R | | | | | | | |
| S | | | | 0,13 | | | |
| T | | | | | | | |
| U | | | | 0,13 | | | |



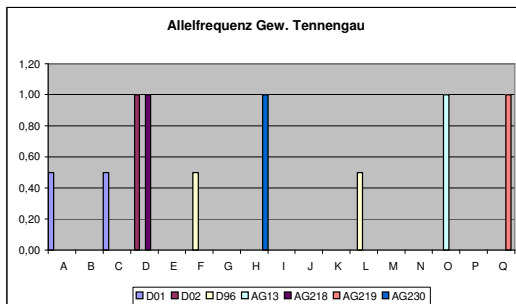
| Allele \ L | D01 | D02 | D96 | AG13 | AG218 | AG219 | AG230 |
|------------|------|------|------|------|-------|-------|-------|
| A | 0,33 | | 0,50 | | | | |
| B | | | | | 0,36 | | |
| C | | | | | 0,29 | | |
| D | | 0,71 | | | | | 0,07 |
| E | 0,25 | | 0,25 | | | 0,14 | 0,14 |
| F | 0,17 | | 0,08 | | | | |
| G | 0,25 | | | | 0,07 | | |
| H | | | | | | 0,14 | 0,07 |
| I | | | | | | 0,14 | 0,71 |
| J | | | | 0,33 | | | |
| K | | | 0,08 | | 0,29 | | |
| L | | | | 0,25 | | | |
| M | | 0,07 | | | | | |
| N | | | | 0,08 | | | |
| O | | 0,21 | 0,08 | 0,08 | | | |
| P | | | | | | | |
| Q | | | | 0,17 | | | |
| R | | | | 0,08 | | | |
| S | | | | | | | |
| T | | | | | | | |
| U | | | | | | 0,43 | |
| V | | | | | | | 0,14 |
| W | | | | | | | |



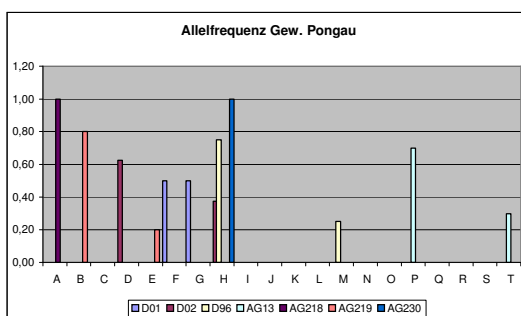
| Allele \ L | D01 | D02 | D96 | AG13 | AG218 | AG219 | AG230 |
|------------|------|------|------|------|-------|-------|-------|
| A | | | | | | | |
| B | | | | | 0,83 | | |
| C | 0,67 | | | | | | |
| D | | 0,50 | | | | | 0,17 |
| E | | | | | 0,17 | | |
| F | | | 0,17 | | | | |
| G | | | | | | | |
| H | | | 0,67 | | | | 0,33 |
| I | | | | | | | 0,50 |
| J | 0,33 | | 0,17 | | | | |
| K | | | | | | | |
| L | | | | | | | 0,17 |
| M | | 0,50 | | | | | |
| N | | | | 0,50 | | | |
| O | | | | 0,17 | | 0,50 | |
| P | | | | | | 0,17 | |
| Q | | | | 0,17 | | | |
| R | | | | 0,17 | | 0,17 | |



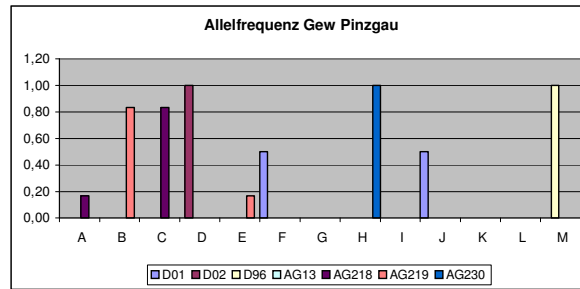
| Allele \ L | D01 | D02 | D96 | AG13 | AG218 | AG219 | AG230 |
|------------|------|------|------|------|-------|-------|-------|
| A | 0,50 | | | | | | |
| B | | | | | | | |
| C | 0,50 | | | | | | |
| D | | 1,00 | | | 1,00 | | |
| E | | | | | | | |
| F | | | 0,50 | | | | |
| G | | | | | | | |
| H | | | | | | | 1,00 |
| I | | | | | | | |
| J | | | | | | | |
| K | | | | | | | |
| L | | | 0,50 | | | | |
| M | | | | | | | |
| N | | | | | | | |
| O | | | | 1,00 | | | |
| P | | | | | | | |
| Q | | | | | | 1,00 | |



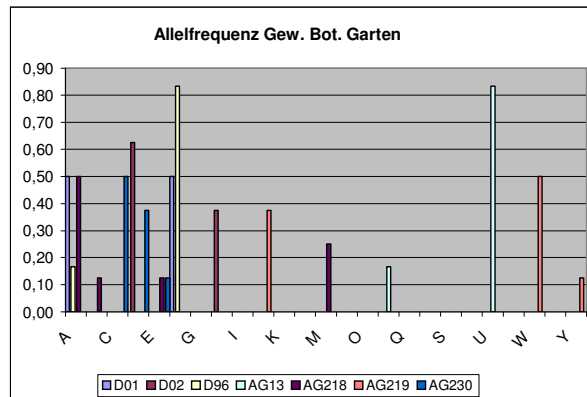
| Allele \ L | D01 | D02 | D96 | AG13 | AG218 | AG219 | AG230 |
|------------|------|------|------|------|-------|-------|-------|
| A | | | | | 1,00 | | |
| B | | | | | | 0,80 | |
| C | | | | | | | |
| D | | 0,63 | | | | | |
| E | | | | | | 0,20 | |
| F | 0,50 | | | | | | |
| G | 0,50 | | | | | | |
| H | | 0,38 | 0,75 | | | | 1,00 |
| I | | | | | | | |
| J | | | | | | | |
| K | | | | | | | |
| L | | | | | | | |
| M | | | 0,25 | | | | |
| N | | | | | | | |
| O | | | | | | | |
| P | | | | 0,70 | | | |
| Q | | | | | | | |
| R | | | | | | | |
| S | | | | | | | |
| T | | | | 0,30 | | | |



| Allele \ L | D01 | D02 | D96 | AG13 | AG218 | AG219 | AG230 |
|------------|------|------|------|------|-------|-------|-------|
| A | | | | | 0,17 | | |
| B | | | | | | 0,83 | |
| C | | | | | 0,83 | | |
| D | | 1,00 | | | | | |
| E | | | | | | 0,17 | |
| F | 0,50 | | | | | | |
| G | | | | | | | |
| H | | | | | | | 1,00 |
| I | | | | | | | |
| J | 0,50 | | | | | | |
| K | | | | | | | |
| L | | | | | | | |
| M | | | 1,00 | | | | |



| Allele \ L | D01 | D02 | D96 | AG13 | AG218 | AG219 | AG230 |
|------------|------|------|------|------|-------|-------|-------|
| A | 0,50 | | 0,17 | | 0,50 | | |
| B | | | | | 0,13 | | |
| C | | | | | | | 0,50 |
| D | | 0,63 | | | | | 0,38 |
| E | | | | | 0,13 | | 0,13 |
| F | 0,50 | | 0,83 | | | | |
| G | | | | | | | |
| H | | 0,38 | | | | | |
| I | | | | | | | |
| J | | | | | | 0,38 | |
| K | | | | | | | |
| L | | | | | | | |
| M | | | | | 0,25 | | |
| N | | | | | | | |
| O | | | | | | | |
| P | | | | 0,17 | | | |
| Q | | | | | | | |
| R | | | | | | | |
| S | | | | | | | |
| T | | | | 0,83 | | | |
| U | | | | | | | |
| V | | | | | | | |
| W | | | | | | 0,50 | |
| X | | | | | | | |
| Y | | | | | | | 0,13 |



| Allele \ L | D01 | D02 | D96 | AG13 | AG218 | AG219 | AG230 |
|------------|------|------|------|------|-------|-------|-------|
| A | | | | | | | |
| B | | | | | 0,20 | | |
| C | 0,70 | | | | 0,10 | | |
| D | | 1,00 | | | 0,20 | | 0,30 |
| E | 0,10 | | | | | | |
| F | | | 1,00 | | | | |
| G | | | | | | 0,25 | |
| H | | | | | | | 0,10 |
| I | | | | | | | 0,60 |
| J | | | | | 0,20 | 0,50 | |
| K | 0,20 | | | | | | |
| L | | | | 0,17 | | 0,13 | |
| M | | | | | | 0,13 | |
| N | | | | 0,17 | 0,30 | | |
| O | | | | 0,17 | | | |
| P | | | | | | | |
| Q | | | | | | | |
| R | | | | | | | |
| S | | | | 0,33 | | | |
| T | | | | | | | |
| U | | | | 0,17 | | | |

