Impact of historic translocations of European larch (*Larix decidua* Mill.) in naturally regenerated populations

Master thesis submitted by

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Summary

Past and present human-induced (intentional or unintentional) translocation of organisms is one of the greatest threats to the long-term viability of local populations due to detrimental evolutionary implications (e.g. hybridisation, genetic swamping). The protection and conservation of genetic diversity is a central part of biodiversity and has become an important issue in global environmental politics. This study considers 16 populations of two races of *Larix decidua* (N = 771) within their native distribution range of the Alps and Carpathians. Our research tests for the first time whether documented extensive historic larch plant transfer originating from the Alps (Tyrol) occurred, which has the potential to effect genetic pollution and intraspecific hybridisation in the scattered native populations of the Southern and Eastern Carpathians. Thirteen SSR markers revealed high genetic diversity (overall H_e = 0.752; SE = 0.01; allelic richness R_S = 9.4; SE = 0.28) and a strong differentiation (F_{ST} = 13%; G'_{ST} = 28-33%) among populations of the two regions and within the regions, especially in the scattered populations of the Carpathians. As expected, we were able to ascertain the existence of Alpine (Tyrolean) material in Romania. However, their impact on native stands was found to be rather low, as the highest proportion of intraspecific hybrids was 6.3% in a juvenile stand and a relatively low amount (N = 26) of first-generation migrants in all the Romanian samples were detected. The findings indicate that, despite extensive historic translocation, the native genetically structures in the Carpathians have not been significantly influenced, which has positive consequences for conservation of biodiversity.

Kurzfassung

Historische und rezente anthropogene (gewollte oder ungewollte) Translokationen von Organismen stellen durch ihre möglichen evolutionären Auswirkungen (z.B. Hybridisierung, Veränderung des Genpools) eine der größten Gefahren für das langfristige Bestehen von lokalen Populationen dar. Der Schutz und die Erhaltung der genetischen Diversität ist ein zentraler Bestandteil der Biodiversität, welche in den letzten Jahren eine zunehmend wichtigere Rolle in der globalen Umweltpolitik einnimmt. Diese Studie behandelt 16 Populationen der Art *Larix decidua* (N = 771) innerhalb des natürlichen Verbreitungsareals in den Alpen und Karpaten. Unsere Untersuchung prüft zum ersten Mal den Einfluss des dokumentierten historischen Transfer von Lärchenmaterial aus den Alpen (Tirol), welcher zur Vermischung des Genpools und intraspezifischen Hybridisation in den stark verstreuten natürlichen Populationen in den Süd- und Ostkarpaten geführt haben kann. Dreizehn Mikrosatelliten-Marker offenbaren eine hohe genetische Diversität (gesamt H_e = 0.752; SE = 0.01; *allelic richness* R_S = 9.4; SE = 0.28) und eine starke Differenzierung (F_{ST} = 13%; G'_{ST} = 28-33%) zwischen den Populationen der beiden Regionen und innerhalb der Regionen, vor allem zwischen den verstreuten Populationen in den Karpaten. Wie erwartet, konnten wir das Vorkommen von alpinen (Tiroler) Material in Rumänien beweisen. Trotzdem wurde deren Einfluss in die natürlichen Bestände, aufgrund des gefundenen Anteils an intraspezifischen Hybriden von höchstens 6.3% in einem Jungwuchsbestand sowie der relativ geringen Anzahl an *first-generation migrants* in allen rumänischen Proben, als gering eingestuft. Die Ergebnisse zeigen, dass trotz dieses starken historischen Transfers, die natürlich genetischen Strukturen in den Karpaten nicht signifikant beeinflusst wurden, was sich positiv auf die Erhaltung der Biodiversität auswirkt.

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Introduction

European Larch (*Larix decidua* Mill.) is a monoecious, anemophilous, and endemic European pioneer tree (Pinaceae) with a highly disjunctive native distribution in Europe (e.g. Bauer 2012). The deciduous conifer naturally grows from the montane (collin-planar, exceptionally Polish lowland provenances) to the subalpine altitudinal belt; in addition to pure stands it occurs also in mixed stands associated with stone pine (*Pinus cembra*), Norway spruce (*Picea abies*), Swiss pine (*Pinus mugo*), Silver fir (*Abies alba*), and/or European beech (*Fagus sylvatica*). From the forelands of the Alps and Carpathians, which represented the main refugial areas of the species during the last glacial period, it has re-colonized the Alps as well as the Central European area (Mayer 1992; Wagner *et al*. 2015b). The Central European native area is split into four regions, which include the Eastern Sudetes, the Polish lowland and the Western Carpathians with major occurrences in the High and Low Tatra Mountains as well as in the Beskids, Fatra and Ore Mountains. Further, the fourth region includes strongly scattered occurrences in the Southern and Eastern Carpathians and in the Bihar Mountains (Wagner *et al*. 2015a). The ecotypes in these geographically varying regions are differentiated at a molecular, morphological and ecophysiological level and form – other than previously treated subspecies – varieties (races) of *L. decidua* (var. *decidua*, var. *carpathica*, and var. *polonica*; Farjon 2010). Wagner *et al*. (2015a) show a possible genetic distinction of the native range in these regions by using nuclear and mitochondrial DNA sampled from a provenance trial (*ex situ*). Morphological differences of growth traits, colour of female flowers (Geburek *et al*. 2007), cone size and stomata rows (Mayer 1992) exist between the races and provide an indication about origin.

European larch is a significant forest tree species mainly used for its timber while its turpentine as well as larch shingles are locally also of importance (Øyen 2006). Hence, it was one of the favoured planted tree species between the 17th and the early 20th century also outside of the native range. In the second half of the 19th century the rapid establishment of the railway system in Central and Northern Europe enhanced the trade with plant material and triggered larch cultivations outside and inside of the native range (Pardé 1957). Following this, due to forestry and the long history of afforestation (Jansen & Geburek 2016), the native area of *L. decidua* has more than doubled to 1.5 million hectares current distribution (Pâques *et al*. 2013), therefore the species can be found throughout the temperate zone of Europe (esp. Germany, France, Denmark, Great Britain, Sweden, and Norway) which indicates its high relevance in contemporary forestry.

In this study, we focused on the native range of larch in the Southern and Eastern Carpathians, which was affected by a strong plant material transfer originating from other areas of the native range, especially from Tyrolean (Alpine) ones. In particular forests in Transylvania and along the Prahova River were affected by these transfers starting in the middle of the 19th century (Rubţov 1965). Gava (1963) and Rubţov & Mocanu (1958) report about larch cultivations of uncertain provenances in Transylvania (Sighişoara), the Southern (Bucegi Mountains, region of Azuga) and Eastern Carpathians (Dofteana), as well as south of the Carpathian arc (Câmpina, Piteşti). However, usage of Alpine material is likely, because during that time Transylvania was under the power of the Austro-Hungarian Empire, which promoted cultivations of Alpine larch (Rubţov & Mocanu 1958). Also the Austrian seed trading companies Jenewein (Innsbruck) and Steiner (Wiener Neustadt) advertised the usage of allochthonous larch material (esp. from Tyrol and the Vienna Woods) for reforestations and cultivations in the Southern Carpathian arc (Rubţov 1965). Since 1890 the trade of Alpine plant material has been documented and shows Austria as the main source of seeds used (Gava 1963). However, information on the exact region of origin is not available. Different records show the usage of Alpine seeds, mainly from the Mieminger Plateau (North Tyrol, Austria) and the Etsch and Eisack valley (South Tyrol = Autonomous Province of Bolzano, Italy) (Gothe 1961), but also from other areas of South (e.g. St. Johann, the Fiemme valley) and North Tyrol (e.g. Götzens, Seefeld) seeds were translocated (Jansen & Geburek 2016).

Through the transfer of larch material within the native range of Southern and Eastern Carpathians and associated gene flow of maladapted alleles, the gene pool and mean fitness of the local *L. decidua* var. *carpathica* on the long term could have been affected (migration load, gene swamping) by possible consequences in the adaption to environmental changes (Lefèvre 2004). The extent of such genetic impact depends on the genetic composition of the resident populations and the environmental difference between the emigrated and immigrated sites (Kremer *et al*. 2012; Kopp & Matuszewski 2014) and has higher impact when local populations are small, as they occur in Romania. Here, the genetic introgression in Romanian populations based on nuclear microsatellite markers was investigated to test our main research questions: 1) Are the larch populations in our study area genetically differentiated? 2) Is a Tyrolean influence on the gene pool in Romania still detectable, both in adults and in the natural regeneration? The fact that no genetic inventory of European larch within the current distribution area exists underlines the high relevance of this study for protection and conservation of biodiversity.

Materials and methods

Population sampling

Needle or cambium samples were collected from 16 populations (*in situ*) of *Larix decidua* from the Alps and Carpathians. In the Alps sampled regions were located in North Tyrol (Austria) and South Tyrol (Autonomous Province of Bolzano) - Trentino - Belluno (Italy) (hereafter, the denotation 'Tyrol' stands for South and North Tyrol); Carpathian material were samples in Vâlcea, - Prahova, - Braşov County of Romania (Fig.1; Table 1). Plant tissue was mainly collected from old dominant trees evenly distributed across space in the forest stand considering at least 30 m of inter-tree distance to avoid sampling of closely related individuals. Furthermore we sampled seedlings from natural regeneration to determine a potential recent influence of the Tyrolean variety on the Carpathian gene pool. The sample sites were selected based on documented evidence (Rubţov & Mocanu 1958; Gothe 1961) and the help of local experts. One of the sampled Romanian mature stands (R3) originated presumably from a Tyrolean source. Additionally, we sampled three spot checks (SC) (overall *N* = 10; Table 1) in the vicinity of the sampled native stands due to their Tyrolean-like habitus (Rubner & Svoboda 1944; Geburek *et al*. 2007). Fifty individuals of each population were sampled and collected material was stored in zip lock plastic bags containing silica gel. In all Romanian populations additionally 50 individuals from the natural regeneration were sampled. Geographic coordinates were recorded with a GPS-apparatus (60CSx; Garmin International, Inc.) and diameter at breast height (DBH; 1.3 m) or at stem base (BD; for individuals with height <1.3 m) were measured with a sliding calliper. These diameter measurements were used as surrogate for age (we defined rejuvenation as trees <10 cm DBH). Approximately 3 cm² sized cambium samples at then stem base were collected by using a hollow punch whilst needle samples were mostly taken when young material was to be collected.

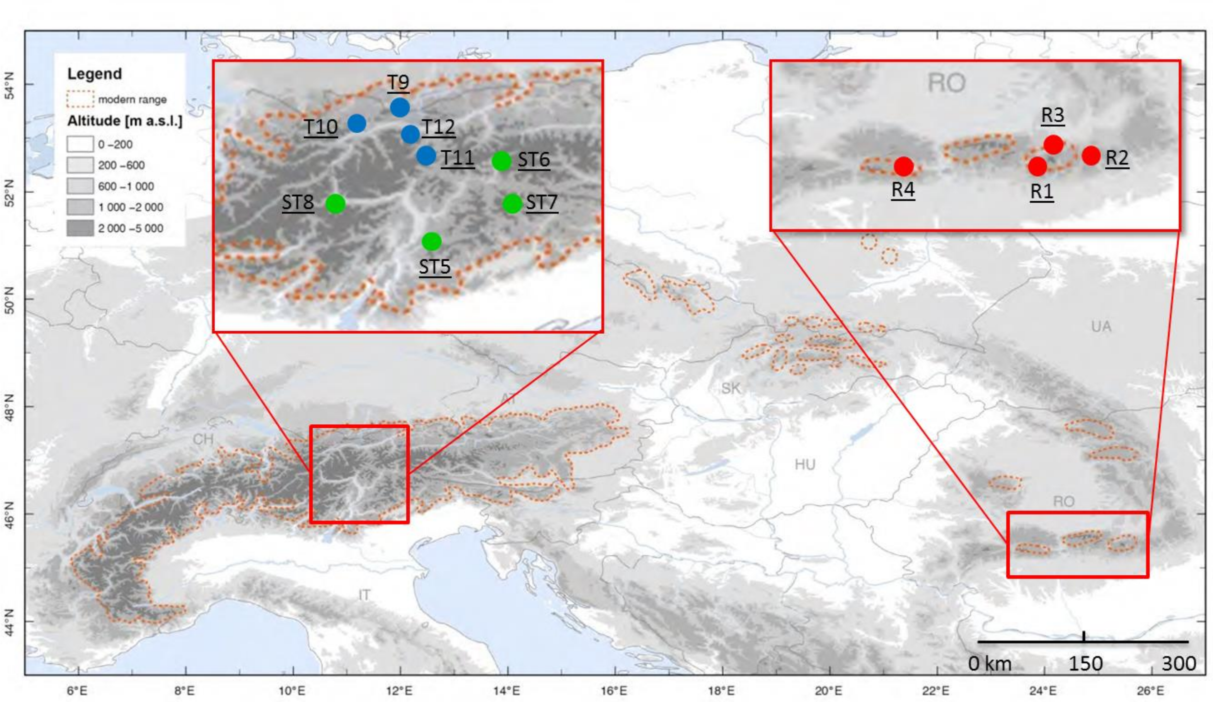


Fig.1 Sampling locations and group membership for all sampled populations of *Larix decidua* within the natural distribution range, which is indicated by the orange dashed line. Colours indicate geographical regions (blue - North Tyrol, green - South Tyrol, red - Romania). The map was modified from Wagner (2013) based on the distribution data of Meusel *et al*. (1965).

DNA extraction and microsatellite genotyping

Total DNA was extracted from approx. 100 mg of dried cambium or needle tissue, this material was frozen for 4 min in liquid nitrogen and crushed for 1 min at 20 Hz using a Qiagen TissueLyser device (Qiagen, Inc.). Genomic DNA was extracted by using the DNeasy 96 Plant Kit (Qiagen, Inc.) following the manufacturers' protocol. Quality and concentration of obtained DNA were measured using an ND-1000 spectrophotometer (NanoDrop, Inc.). DNA was stored at 4 °C. All samples were genotyped with 13 highly polymorphic nuclear microsatellite loci (Wagner *et al*. 2012). Multiplex PCR amplification was optimised to be performed in a 10 µl reaction volume containing 2-10 ng of genomic DNA, 5 µl HotStarTaq Master Mix (Qiagen, Inc.), double distilled water, and 0.3µM of forward and reverse primers each. We used the following cycling protocol on a TC-412 Programmable Thermal Controller (Techne): 35 cycles with 94°C for 30 s, 56°C for 90 s, and 72°C for 60 s. Before the first cycle, a prolonged denaturation step (95°C for 15 min) was included and the last cycle was followed by a 30 min extension at 72°C. Genotyping was outsourced to a commercial provider (ecogenics, Balgach, Switzerland) using Applied Biosystems (Foster City, CA, USA) chemistry and allele calling tools with manual checking of scores.

Table 1 Geographical origin of the 16 *Larix decidua* populations used in this study

Pop.Code	Location	*N* analysed	Latitude	Longitude	Altitude (m)
R1 (Adult)	Bucegi, Prahova County, Romania	47	45.3551	25.5085	1420-1770
R1 (Juvenile)	Bucegi, Prahova County, Romania	48	45.3551	25.5085	1420-1770
R2 (Adult)	Ciucos, Prahova County, Romania	43	45.4763	25.9826	1330-1830
R2 (Juvenile)	Ciucos, Prahova County, Romania	39	45.4763	25.9826	1330-1830
R3 (Adult)	Braşov, Braşov County, Romania	45	45.6259	25.5818	700-820
R3 (Juvenile)	Braşov, Braşov County, Romania	49	45.6259	25.5818	700-820
R4 (Adult)	Malaia,Vâlcea County, Romania	44	45.3748	23.9280	780-1650
R4 (Juvenile)	Malaia,Vâlcea County, Romania	49	45.3748	23.9280	780-1650
ST5	Altrei, South Tyrol/Trient, Italy	49	46.2775	11.3892	1200-1320
ST6	St. Johann, South Tyrol, Italy	48	46.9787	11.9823	1620-1850
ST7	Misurina, South Tyrol/Belluno, Italy	50	46.5725	12.2449	1760-1930
ST8	Prad am Stilfserjoch, South Tyrol, Italy	50	46.6371	10.5465	980-1550
T9	Seefeld in Tyrol, North Tyrol, Austria	51	47.3100	11.2187	1200-1740
T10	Mieminger Plateau, North Tyrol, Austria	50	47.2946	10.8913	1110-1660
T11	Steinach in Tyrol, North Tyrol, Austria	50	47.0317	11.4500	1390-1930
T12	Götzens, North Tyrol, Austria	49	47.2011	11.3379	1680-1830
	Total	**761**			
SC1	Bucegi, Prahova County, close to R1	2	45.3567	25.5181	1428
SC2	Sinaia, Prahova County, 7.4 km from R1	5	45.3094	25.5746	794-805
SC3	Cheia, Prahova County, 5.6 km from R2	3	45.4788	25.9053	1257
	Total	**771**			

N, number of samples.

Data analyses

Individuals with more than two failed loci in the genotyping process were excluded from the dataset. In the following analysis, only populations with more than ten individuals (*N* = 761) were used, except *Structure* and *GeneClass* for which all available individuals were considered (*N* = 771; Table 1).

Genetic diversity within populations. Microsatellite data were analysed for allele dropout, null alleles and slight changes in allele sizes during PCR amplification using *Micro-Checker* 2.2.3 (van Oosterhout *et al*. 2004). Furthermore, the Bayesian approach of individual inbreeding coefficient F_i implemented in *INEst* 2.2 (Chybicki & Burczyk 2009) was used to check row data for null allele frequencies and to estimate unbiased inbreeding coefficients F_i and unbiased observed and expected heterozygosity within populations (settings: 500.000 Markov chain Monte Carlo iterations, burn-in of 50.000, thinning parameter of 50). Deviations from Hardy-Weinberg equilibrium (HWE) expressed as heterozygote excess and deficiency, as well as genotypic disequilibrium among pairs of loci were assessed using in *Genepop* 4.7.0 (Raymond & Rousset 1995; Rousset 2008) implemented Monte

Carlo Markov chain simulation of Fischer's test with 10.000 dememorizations, 100 batches and 10.000 iterations.

Several population genetic diversity indices, including deviations from HWE, allele frequencies, effective number of alleles (N_e), observed (H_o) and expected heterozygosity (H_e), fixation index (F), number of private alleles (A_p), as well as percentage of polymorphic loci (*PPL*) were calculated per locus and as means over all loci with corresponding standard errors (SE) using *GenAlEx* 6.502 (Peakall & Smouse 2006; 2012). The number of alleles corrected for equal sample size (allelic richness R_S) with a rarefaction to 39 individuals was calculated using *Fstat* 2.9.3.2 (Goudet 1995). Descriptive summarised statistics (e.g. mean, standard error) were performed using *R* 3.3.2 (R Development Core Team 2016).

Additionally, we characterised spatial genetic structure within the populations using the Nason's estimator of multilocus kinship coefficient F_{ij} (Loiselle *et al*. 1995) available in *SPAGeDi* 1.5 (Hardy & Vekemans 2002). It was used to visualize associations between genetic and a set of ten predefined spatial distance intervals among individuals within a population, in order to estimate gene dispersal distance parameters, such as neighbourhood size. Individual sampling locations and gene copies were each permuted 10.000 times. Standard error (SE) of mean F_{ij} values per distance class was generated by jackknifing over loci. We assessed the significances of estimated values by comparing them with the confidence interval of the coefficients under the assumption of no spatial genetic structure. Natural and non-natural (e.g. afforestation) populations can be distinguished by the slope of regression, with natural populations showing a regressive decline in kinship-function, whereas planted stands do not show such patterns.

Evidence of recent bottlenecks within populations was assessed using the graphical test of Luikart *et al*. (1998) implemented in *Bottleneck* version 1.0.02 (Piry *et al*. 1999), which in most cases is not sensitive to deviations from Hardy-Weinberg proportions (Luikart *et al*. 1998). Specifically, the test works based on a mode shift away from an L-shaped distribution of allele frequencies, i.e. it is expected that under bottlenecks low frequency (<0.1) alleles are less abundant than alleles in intermediate frequency classes (e.g. 0.101-0.2).

Genetic diversity among populations. To determine population differentiation and the relationship among populations, we calculated first, a principle co-ordinate analysis (PCoA) for visualizing population clusters due to relationships among inter-individual genetic distances and to identify a set of reduced dimension traits (eigen vectors) according to the number of populations using *GenAlEx*. In order to take into account the unequal sample sizes, we used Nei's unbiased genetic distance as algorithm for the PCoA (Nei 1978). Secondly, we computed an unweighted pair group method arithmetic average dendrogram (UPGMA) based on Nei's standard genetic distance (Nei 1972) using 1.000 bootstrapped matrices created by *Microsatellite Analyser* (Dieringer & Schlötterer 2003). For consensus tree construction, we used the programs *Neighbour* and *Consense* implemented in the *Phylip* 3.63 package (Felsenstein 1989).

Furthermore, we used *Structure* 2.3.4 (Pritchard *et al*. 2000) to infer the most likely number of population clusters and attempt to assign individuals to populations by reference to their genotypes. The software uses a Bayesian clustering algorithm to pool individuals to a predefined number of clusters (*K*) by minimizing deviations from Hardy-Weinberg equilibrium and gametic-phase disequilibrium within the clusters. We used the admixture-model, where each individual does not have any information about population affiliation, with *K*-values ranging from 2 to 10 and a run length of 800.000 iterations with a burn-in period of 200.000. Four runs per *K* were performed for reasons of iteration. In these computations we included all available samples, also groups (spot checks) with a sample size <10 (cf. Table 1). In addition, we performed further runs with the Alpine and the Romanian populations separately. To predict the appropriate number of clusters, we used the four new supervised statistics (MedMeaK, MaxMeaK, MedMedK, MaxMedK) of Puechmaille (2016), which are based on the count of *K*-clusters that are contained in at least one subpopulations and outperform existing methods (Evanno *et al*. 2005) especially on unevenly sampled dataset, implemented in *StructureSelector* (Li & Liu 2017).

Information about population differentiation at various levels of population aggregations were obtained using an analysis of molecular variance (AMOVA) implemented in *Arlequin* 3.5 (Excoffier & Lischer 2010), with which global F_{ST} (Weir & Cockerham 1984) and R_{ST} (Slatkin 1995) values were calculated separately with 10.000 permutations. Thereby we defined the population aggregations according to the groups detected by PCoA, UPGMA dendrogram and individual-based population assignment, as well as to their geographical proximity and demographic grouping (adults/juveniles). To take allele size and stepwise mutations into account, we compared the observed differentiation F_{ST} with R_{ST}. If stepwise mutations have contributed to differentiation, R_{ST} is expected to be higher than F_{ST}. In order to take allelic identity into account, we calculated G'_{ST} (Hedrick 2005), which unlike the G_{ST} value (Nei 1972), also includes the restricted amount of genetic variation given by overlapping sets of alleles among subpopulations (Hedrick 1999) using *GenAlEx* each with 10.000 permutations and bootstraps. To assess the effect of geographical proximity (and perhaps population history) on genetic diversity of the two regions, we compared diversity indices (R_S, H_o, H_e, F_{is}) and differentiation (F_{ST}) among groups using *Fstat*. Populations were grouped according to the Structure analysis (Fig.4) and significance was assessed based on 10.000 permutations.

Finally, to examine whether populations or single individuals in the Southern and Eastern Carpathians are likely to be the result of a recent Tyrolean (Alpine) introduction, we tested for the existence of first-generation migrants in Romanian populations using *GeneClass* 2.0 (Piry *et al*. 2004). Thereby, we used the Bayesian criterion of Baudouin & Lebrun (2000) for computing the likelihood of occurrence of the individual genotype within the population where the individual has been sampled. *L_home* as the test statistic was used in order to prevent a potential bias in likelihood ratios caused by missing source populations (ghost populations) (Peatkau *et al*. 2004). For probability computation and better performance of calculation in case of ghost populations (Leblois 2011), we chose the Monte-Carlo resampling algorithm of Cornuet *et al*. (1999) with 10.000 simulated individuals and a type I error (probability of detecting a resident as immigrant) of <0.05. All available individuals (N = 771), including the three spot checks (SC) were used for this computation.

Results

Genetic diversity within populations

The *Micro-Checker* analysis of microsatellite data showed signs of occurrence of null alleles; the average null allele frequency across all loci per population ranged between 1.9% and 8.5% (mean of 0.045; SE= 0.004; data not shown) and therefore, as shown in a simulation study with frequencies between 5% and 8% null alleles (Chapuis & Estoup 2007), it should only have minor effects on classical estimates of population differentiation. All loci showed signs neither of large allele dropouts nor of scoring of stutter peaks.

We found no evidence for genotypic disequilibrium between loci within populations (P <0.05). However, all populations showed a significant deficit of heterozygotes, except population T9 and T12 in North Tyrol. Although in 11 populations highly significant (P <0.001) deviations from HWE were detected (Table 2), whereas none of the populations showed a significant heterozygote excess.

The 13 microsatellites scored a high level of polymorphism in *L. decidua* resulting in a total number of 113 alleles, ranging from six (locus Ld101_565) to a maximum of 38 (locus bcLK263_550) with an average of 18.46 (SD ±9.21) alleles per locus. Genetic diversity statistics varied significantly according to population location (Table 3), summarised data are shown in Table 2. The lowest mean number of observed alleles (N_a) was calculated in population R2 in Prahova County (6.77, SE= 1.04), whereas the largest value in ST5 in southern South Tyrol (11.23, SE= 1.32). The average number of effective alleles (N_e) showed similar results, with values ranging from 3.56 (SE= 0.587) in R2 to 5.66 (SE= 0.806) in ST5 and a maximum of 5.87 (SE= 0.844) in ST7 (eastern South Tyrol). The total mean over all loci and populations of N_a and N_e were 9.88 (SE= 0.305) and 4.99 (SE= 0.180), respectively. In all populations we found comparatively high values of the Shannon information index I with an averaged value of 1.71 (SE= 0.038). Observed heterozygosity H_o ranged from 0.623 (SE= 0.062) in R2 to 0.770 (SE= 0.046) in T12 (central North Tyrol) with a total mean over all loci and populations of 0.725 (SE= 0.01), whereas expected heterozygosity (H_e) showed similar results, ranging from 0.654 (SE= 0.064) in R2 to 0.789 (SE= 0.036) in R3 and ST5 with a total mean of 0.752 (SE= 0.01), resulting into a positive fixation index (F) of 0.038 (SE= 0.006).

Table 2 Genetic diversity indices of all 16 *Larix decidua* populations based on 13 SSR markers

Pop.Code	N_a	(SE)	N_e	(SE)	I	(SE)	R_S	(SE)	H_o	(SE)	H_e	(SE)	F	(SE)		*Avg*(F_i)	A_p	*PPL*
R1 (Adult)	9.308	(1.278)	4.312	(0.581)	1.594	(0.168)	8.845	(1.183)	0.708	(0.052)	0.731	(0.049)	0.040	(0.018)	***	0.034	2	100.0
R1 (Juv.)	9.923	(1.416)	4.241	(0.571)	1.599	(0.167)	9.232	(1.257)	0.689	(0.052)	0.733	(0.053)	0.062	(0.013)	***	0.034	3	100.0
R2 (Adult)	7.154	(1.024)	3.564	(0.587)	1.343	(0.175)	6.938	(0.979)	0.623	(0.062)	0.654	(0.064)	0.051	(0.017)	***	0.030	0	100.0
R2 (Juv.)	6.769	(1.039)	3.953	(0.601)	1.399	(0.177)	6.693	(1.016)	0.658	(0.064)	0.666	(0.065)	0.014	(0.019)	**	0.027	2	100.0
R3 (Adult)	11.154	(1.181)	5.804	(0.890)	1.888	(0.138)	10.690	(1.124)	0.764	(0.043)	0.789	(0.036)	0.038	(0.017)	*	0.036	1	100.0
R3 (Juv.)	10.154	(1.131)	4.996	(0.687)	1.744	(0.140)	9.566	(1.019)	0.704	(0.045)	0.759	(0.042)	0.079	(0.017)	***	0.065	0	100.0
R4 (Adult)	9.462	(1.141)	5.004	(0.773)	1.688	(0.171)	9.145	(1.097)	0.724	(0.050)	0.746	(0.050)	0.026	(0.017)	***	0.027	3	100.0
R4 (Juv.)	10.077	(1.407)	5.216	(0.745)	1.756	(0.158)	9.578	(1.252)	0.763	(0.043)	0.766	(0.044)	0.002	(0.020)	***	0.013	2	100.0
ST5	11.231	(1.316)	5.657	(0.806)	1.871	(0.143)	10.595	(1.168)	0.757	(0.038)	0.789	(0.036)	0.043	(0.013)	***	0.042	2	100.0
ST6	10.769	(1.241)	5.337	(0.718)	1.810	(0.147)	10.160	(1.128)	0.747	(0.041)	0.778	(0.036)	0.043	(0.016)	***	0.024	2	100.0
ST7	11.077	(1.179)	5.869	(0.844)	1.849	(0.161)	10.410	(1.082)	0.725	(0.042)	0.781	(0.043)	0.071	(0.018)	***	0.068	5	100.0
ST8	10.308	(1.227)	5.407	(0.822)	1.799	(0.141)	9.699	(1.103)	0.737	(0.040)	0.777	(0.036)	0.055	(0.015)	***	0.034	3	100.0
T9	10.077	(1.129)	5.184	(0.665)	1.783	(0.115)	9.390	(0.976)	0.766	(0.035)	0.781	(0.029)	0.022	(0.012)	ns	0.011	3	100.0
T10	10.154	(1.250)	4.918	(0.659)	1.735	(0.147)	9.488	(1.148)	0.718	(0.042)	0.755	(0.042)	0.044	(0.025)	***	0.026	1	100.0
T11	10.692	(1.293)	5.140	(0.708)	1.793	(0.139)	10.079	(1.156)	0.751	(0.043)	0.772	(0.036)	0.031	(0.018)	**	0.016	3	100.0
T12	9.769	(1.105)	5.245	(0.846)	1.754	(0.149)	9.367	(1.041)	0.770	(0.046)	0.762	(0.041)	-0.007	(0.014)	ns	0.005	0	100.0

N_a, number of alleles; N_e, effective number of alleles; I, Shannon information index; R_S, allelic richness based on the smallest sample size of 39; H_o, unbiased observed heterozygosity; H_e, unbiased expected heterozygosity; F, fixation index; *,**,***, deviation from HWE significant at the P <0.05, <0.01 and <0.001 level, respectively, ns, not significant; *Avg*(*F*i), unbiased inbreeding coefficient; A_p, number of private alleles; *PPL*, percentage of polymorphic loci; SE, standard error.

Lower values tended to be found in Romanian stands, except R3 in Braşov County. We similarly detected trends in measures of average allelic richness (R_S) with slightly higher values in North and South Tyrol and lower ones in Romania ranging from 6.69 (SE= 1.02) in R2 to 10.69 (SE= 1.12) in R3 and 10.59 (SE= 1.17) in ST5. H_o, H_e and R_S varied significantly (P <0.001) among the two regions (Table 3). Within Romanian and of all sampled stands, R2 showed the lowest values of genetic diversity indices.

The mean inbreeding coefficient (*Avg(F*i*)*) varied among populations from 0.005 (T12) to 0.068 (ST7) and showed no tendencies according to the geographical origin. Anyway, significant (P <0.05) differences in inbreeding coefficients between Tyrolean (including R3) and Romanian stands were found (Table 3). We detected a total of 32 private alleles in 13 populations with a minimum of one private allele in R3 and T10 (in North Tyrol) and a maximum of five private alleles in ST7. ST7 showed also the highest frequency of private alleles (0.06); 26 out of the 32 private alleles showed a frequency <0.02 (data not shown). Larch stands in North Tyrol had the least number of private alleles (7) compared to stands in the other two regions South Tyrol (12) and Romania (13).

The kinship coefficient gives information about the level of relatedness between individuals, e.g. 0.5 of full sibs and 0 for no relatedness. Spatial structuring with ten predefined distance classes resulted in a mean value of distance intervals ranging from 50 (SE= 6.7) to 995 (SE= 132) m over all populations, from 37 (SE= 8.2) to 963 (SE= 188) m within Romanian (R1-R4) and from 62 (SE= 9.0) to 1028 (SE= 199) m within Tyrolean populations (ST5-ST8, T9-T12). The mean pairwise kinship coefficient F_{ij} (Loiselle *et al.* 1995) over all loci in Romanian populations was 0.015 (SE= 0.003) in the first distance class and estimated coefficients were not significant between 37 (SE= 8.2) and 99 (19.7) m based on the 95% confidence interval. F_{ij} was 0.010 (SE= 0.002) in Tyrolean populations within the first distance class and estimated coefficients lost significance between 62 (SE= 9.0) and 137 (SE= 24.2) for 95% confidence interval of randomly permuted data. The highest average value of F_{ij} (0.025) in the first distance class was found in R1 (juveniles) within Romanian and a F_{ij} of 0.020 in ST7 within Tyrolean samples. Five Romanian (R1 (both), R2 (juveniles), R3 (adults), R4 (juveniles)) as well as four Tyrolean populations (ST7, ST8, T1, T3) showed a significant deviation of Kinship coefficients from the permuted mean value in the first distance class. In contrast, seven populations did not show kinship relations (data not shown). We tested for recent bottlenecks on each population; thereby an L-shaped distribution of allele frequencies was obtained on each population, indicating that the populations have been near mutation drift equilibrium (data not shown).

Table 3 Differences in genetic diversity indices of 16 *Larix decidua* populations of the two biogeographic regions

	Tyrol	Romania	*P*-value
R_S	9.944	8.405	***
H_o	0.716	0.62	***
H_e	0.761	0.693	***
F_{is}	0.059	0.106	*
F_{ST}	0.016	0.05	ns

R_S, allelic richness; H_o, observed heterozygosity; H_e, expected heterozygosity; F_{is}, inbreeding coefficient; F_{ST}, ; F_{ST} value; *P*-value, *, **, ***, significance at the P <0.05, <0.01 and <0.001 level, respectively, ns, not significant.

Genetic diversity among populations

The PCoA based on Nei's unbiased genetic distance (Nei 1978) revealed strong affiliation of the Romanian population R3 to populations from North and South Tyrol. Within the Tyrolean pattern, populations from South Tyrol were also somewhat differentiated with some overlapping of the two regions. Population R1 clustered with R4; R2 was not assigned to the Romanian group and formed its own cluster (Fig.2). The first two axes of the PCoA explained 75.7 % and 11.2 % of the observed variation, respectively. Similar results of relationships among populations according to geographic proximity were provided by UPGMA dendrogram using Nei's standard genetic distance (Nei 1972), where each region, i.e. Romania, North and South Tyrol formed its own clade (Fig.3). Exceptions were the populations R3 as well as ST8, which were placed in the North Tyrolean cluster. The three Romanian populations formed a more diverged clade with potentially three single branches/clusters, whereas population R1 and R4 grouped together within one sub-branch.

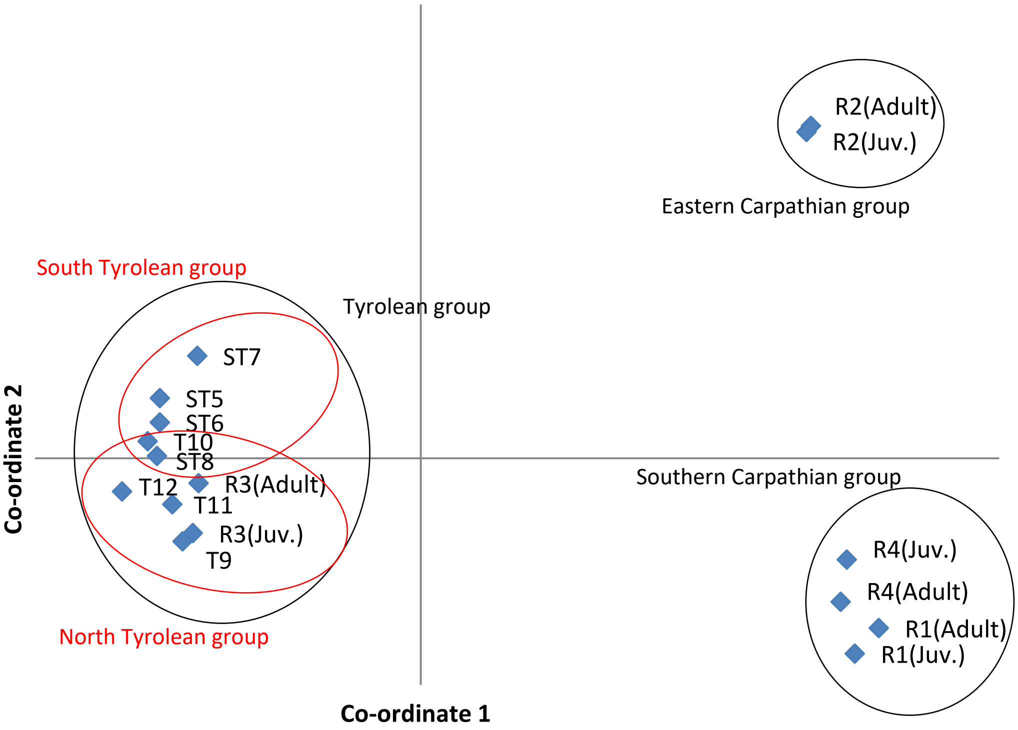


Fig. 2 Principal co-ordinate analysis (PCoA) on the basis of Nei's unbiased genetic distance (Nei 1978) showing the multivariate relationships of 16 *Larix decidua* populations. The first and second axes explain 75.7 % and 11.2 % (86.9 %) of the observed variation, respectively. Circles indicate possible clusters of related populations.

The Bayesian clustering conducted by Structure showed consistent high assignment coefficients for different clusters, resulting from strong population differentiation. Results interpreted using the method of Puechmaille (2016) revealed three clusters (*K* = 3) as the most likely group structure supporting the results from PCoA as well as from the UPGMA dendrogram. These highly distinct and biologically meaningful clusters corresponded to the two main regions of occurrence, Tyrol (two clusters corresponding to a north-south trend) and Romania. The population R3 in Braşov County as well as the three spot checks (SC) in the vicinity of populations R1 and R2 showed a strong affiliation to the Tyrolean cluster. Nearly all individuals were assigned to a predominant cluster (Fig. 4a). However, some populations contained admixture individuals (individuals that were assigned to different clusters), especially population R1 (juveniles), R3 (adults) and R4 (both) (Fig.4a). Separate runs of both, the Tyrolean (including R3) and the Romanian cluster, revealed a value of *K* = 2 within the Tyrolean's and a grouping into three clusters within the Romanian ones.

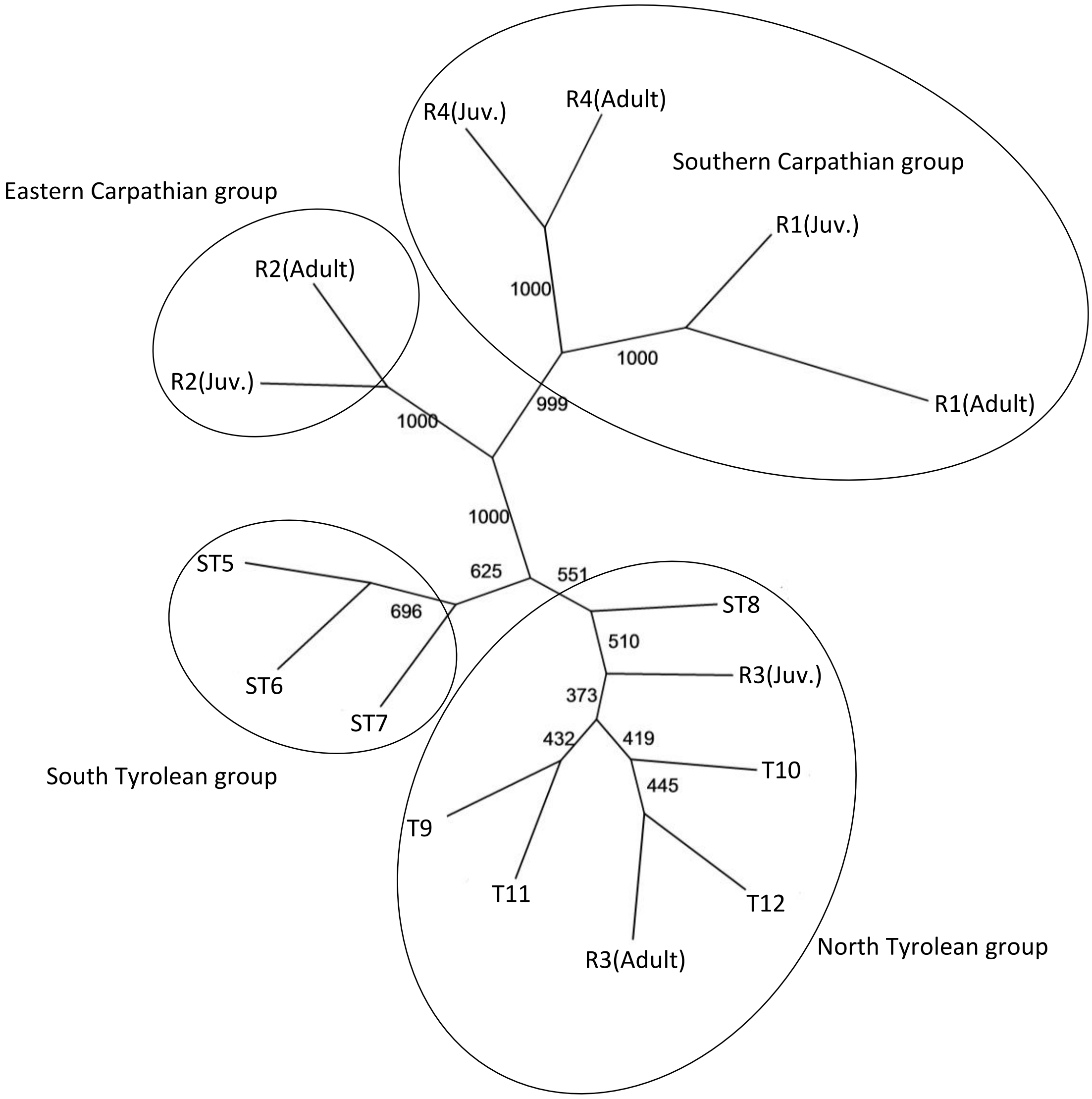


Fig. 3 UPGMA consensus tree showing relationships between 16 *Larix decidua* populations created out of 1000 bootstrapped matrices using Nei's standard genetic distance (Nei 1972). Numbers beside the branches indicate bootstrap support for nodes. Circles indicate possible grouping of related populations.

South Tyrolean populations (except ST8 in western South Tyrol) formed a separate cluster, whereas the other populations R3, ST8 and from North Tyrol (T) showed a similar colour pattern in the bar plot (Fig.4c). All native Romanian populations were separated from each other and formed three different clusters (Fig.4b).

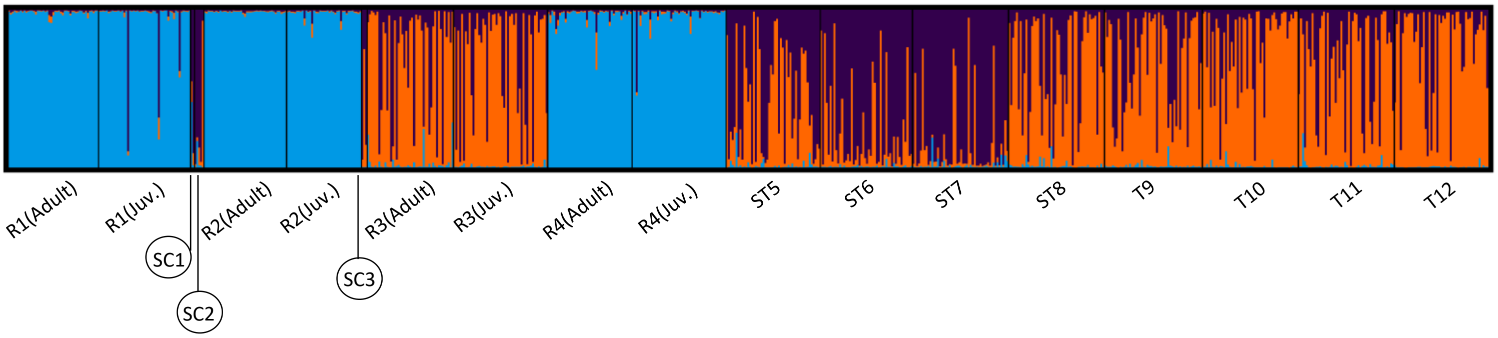
The AMOVA revealed an F_{ST} value of 13.3% and an R_{ST} value of 8.01% within the adults when groups were defined according to the Structure analysis (Fig.4). Within the juveniles an F_{ST} value of 13.6% and a R_{ST} value of 9.22% were calculated (Table 4). When adult and juvenile groups were defined according to the PCoA and UPGMA, F_{ST} and R_{ST} (values given in brackets) partitioned molecular variance to 12.0% (5.9%) among groups, 1.6% (2.0%) within populations among groups and 86.4% (92.1%) within populations [F_{ST} 13.6% (7.9%)] for adults and to 4.9% (-0.5%) among groups, 2.6% (2.7%) within populations among groups and 92.6% (97.8%) within populations [F_{ST} 7.5% (2.2%)] for juveniles. Grouping according to geographical proximity, variation pattern among and within groups decreased slightly, however, R_{ST} never exceeded F_{ST}. By contrast we observed a G'_{ST} value within adults of 27.7 % and 32.6 % for juveniles (Table 4).

Table 4 Results of analysis of molecular variance (AMOVA) based on F_{ST} and R_{ST}, respectively, and of computation of G'_{ST} (Hedrick 2005) values from data of 13 SSR markers of *16 Larix decidua* populations computed for both, adults and juveniles separately

	F_{ST}			R_{ST}			G'_{ST}
Source of variation	Sum of squares	Variance components	Percentage variation	Sum of squares	Variance components	Percentage variation	
Adults							
Among groups	267.25	0.61	11.03	18983.31	41.24	5.83	
Among populations within groups	169.20	0.13	2.26	21290.10	15.41	2.18	
Within populations	5481.93	4.83	86.71	737926.39	650.40	91.99	
Total	**5918.37**	**5.57**		**778199.80**	**707.05**		**0.277 (SE= 0.061)**
Juveniles							
Among groups	96.03	0.46	8.51	10457.85	54.41	6.71	
Among populations within groups	58.28	0.27	5.10	5146.09	20.39	2.51	
Within populations	1683.45	4.64	86.38	268234.77	736.57	90.78	
Total	**1837.76**	**5.37**		**283838.71**	**811.37**		**0.326 (SE= 0.072)**

Groups correspond to the two biogeographic regions (Tyrol, Romania) detected by the individual-based population assignment.

a) All sampled individuals



b) Within native Romanian populations

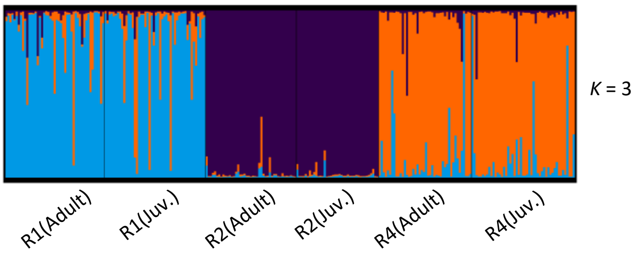
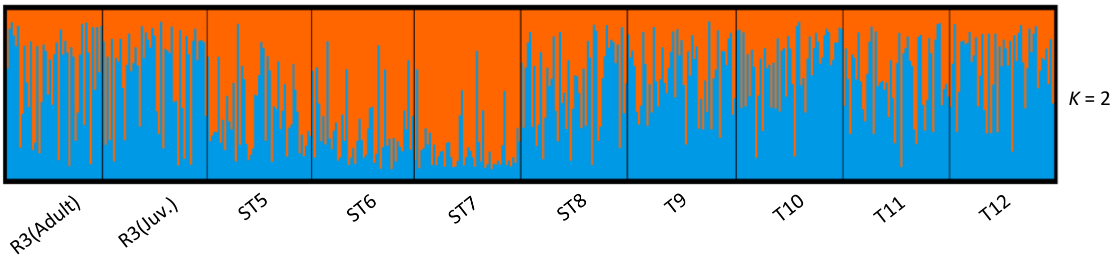


Fig.4 Bar plots of individual population assignment performed with *Structure* for (a) all sampled *Larix decidua* individuals for three assumed ancestral clusters (*K* = 3), (b) for the native Romanian populations with *K*-value of 3 and (c) for the Tyrolean populations with *K* = 2.

c) Within Tyrolean populations including population R3



Assignment analysis detected 30 individuals of the Romanian populations as first-generation migrants (*P* <0.05), 16 of them even with <0.001 significance, as they were not assigned to the population of origin. Thereby, nearly all individuals of the three spot checks (SC) (9 assignments) and those of population R3 (both) (14 assignments) were assigned to Tyrolean (Alpine) populations. Additionally, we found two individuals of R1 (juveniles) to be linked with population T15 and R3 (juveniles), respectively, and one individual of R4 (juveniles) with ST7 (Table 5).

Discussion

Genetic diversity within populations

Our results of nuclear microsatellite diversity are similar to other studies in *Larix decidua* (Pluess 2011; Wagner *et al*. 2012; King *et al*. 2013) or to other conifer species with similar habitat demands in boreal or temperate forest associations such as *Picea abies* (Tollefsrud *et al*. 2009; King *et al*. 2013), *Pinus cembra* (Dzialuk *et al*. 2014; Lendvay *et al*. 2014) or *Pinus sylvestris* (Pazouki *et al*. 2016). In general, high levels of genetic diversity within populations in such long-lived, outcrossing and late successional coniferous taxa were obtained. However, such comparisons are always limited as samples sizes and markers differ between studies. Nevertheless, comparisons with the results of Wagner (2013) obtained by the same marker-set showed similar results of F_{ST} values, but slightly higher inbreeding coefficients than ours, which might be the effect of the presence of null alleles. Moreover the marker bcLK263 and bcLK211 had the highest and Ld42 the lowest number of alleles in both studies. Comparisons with species within the genus *Larix* reveal higher genetic diversity for *L. decidua* (H_e = 0.75) than for *L. lyallii* and *L. occidentalis* (0.42 and 0.58; Khasa *et al*. 2006) as well as for *L. gmelinii* (0.41-0.60; Zhang *et al*. 2015), *L. sibirica* and *L. cajanderi* (0.63 and 0.56; Oreshkova *et al*. 2013), but similar results for *L. kaempferi* (0.72-0.76; Nishimura & Setoguchi 2011). Such differences – among already mentioned methodical limitations - could be due to a lack of historical bottlenecks affecting during re-colonisation events after the last glacial period or to the different size and distribution of refugial areas allowing survival of populations with relatively high or low genetic diversity. Combinations of paleontological and genetic data indicate seven distinct refugia *Larix decidua* located in four locations south of the Alps, in the Sudetes and in the western and southern Carpathians (Wagner *et al*. 2015b). These large and different refugial areas and their fusion to one population during re-colonisation might be the reason for the high genetic diversity, especially in the Alps.

Table 5 Detection of first-generation migrants based on the simulation algorithm of Cornuet *et al*. (1999) from data of 13 nuclear microsatellite loci of all sampled *Larix decidua* individuals

Sampled population	Source population	*P*-value
R1(Adult)	R4(Adult)	***
R1(Adult)	R4(Juv.)	*
R1(Juv.)	T11	***
R1(Juv.)	R4(Juv.)	***
R1(Juv.)	R3(Juv.)	***
SC1	R3(Adult)	***
SC1	ST5	***
SC2	ST6	***
SC2	ST5	***
SC2	ST8	**
SC2	R3(Adult)	***
SC3	ST5	***
SC3	ST5	***
SC3	T12	***
R3(Adult)	T10	*
R3(Adult)	ST7	*
R3(Adult)	T11	*
R3(Adult)	T10	**
R3(Adult)	ST6	**
R3(Adult)	ST5	*
R3(Adult)	ST7	**
R3(Adult)	ST7	***
R3(Adult)	T10	*
R3(Juv.)	ST5	***
R3(Juv.)	ST7	***
R3(Juv.)	T10	**
R3(Juv.)	ST8	*
R3(Juv.)	ST7	*
R4(Adult)	R1(Juv.)	***
R4(Juv.)	ST7	**

Sampled population, population from which the individual was sampled; source population, potential source population for the migrant (population code Table1); *P*-value, *, **, ***, significance at the *P* <0.05, <0.01 and <0.001 level, respectively, the probability that an individual is a resident and not a first-generation migrant.

Although almost all populations showed evidence of inbreeding, as we found that fixation indices (*F*) and unbiased inbreeding coefficients (*Avg(F*i*)*) were slightly positive and deviated significantly from Hardy-Weinberg equilibrium in 14 of 16 populations (Table 2). Similar signs of inbreeding are also reported in other studies of *Larix* spp. (Larionova *et al*. 2004; Nishimura & Setoguchi 2011; Oreshkova *et al*. 2013). This pattern might be explained by the monoecious character of larch and the accompanying lack of a self-incompatibility system (Stern & Roche 1974) and higher frequency of self-pollination in combination with high pollen sinking speed (absence of air bags on pollen grains) and thus restricted gene flow (Sjögren *et al*. 2010). This also implies mating among relatives within stands. The reduction in the number of effectively outcrossing males is a plausible explanation for higher inbreeding rates within populations (Burczyk *et al*. 2004). Alternatively, the long history of afforestation and cultivation of *Larix decidua* within and outside its native range (Rubţov 1965; Wagner *et al*. 2015a) could have contributed to the presence of Hardy-Weinberg disequilibrium within the populations, especially when larch stands have been derived from source material with low genetic diversity (e.g. seeds from only a few mother trees) and crossbreeding between a small number of closely related specimens is present.

Based on the microsatellite data, we found a comparatively low genetic diversity in R2 in the Eastern Carpathians (Romania) (Table 2) across all sampled populations. Within Tyrol (Alps), higher levels of genetic diversity were observed in South Tyrolean populations (ST), similar results showed R3 in Romania. A reason for lower diversity of Romanian populations (R1 and R2) might be by the isolated distribution of the populations in the Carpathians and therefore small population sizes with higher inbreeding coefficients (Table 3), particular in R2. These scattered populations could come, unlike the large Alpine refugia and their re-colonisation to a large population covering the Alps, from several small refugial areas in southern Carpathians (Wagner *et al*. 2015b) harbouring low genetic diversity. In the Alps, *Larix decidua* likely expanded out of the refugia using Alpine valleys as migration pathways, thereby for re-colonisation of the Central Alps the Adige-Inn valley (a connection of North and South Tyrol) should have contributed as major corridor of migration (Wagner *et al*. 2015b). Hence, slightly differences in genetic diversity in Tyrol supported by the decrease of the number of private alleles from South (12) to North Tyrol (7) and heterozygosity deficit in most populations, could be due to genetic bottlenecks influencing diversity during these migrations (also in Romania). Although we found no evidence of recent bottlenecks in any population, this does not mean that there were no past bottlenecks, as effects caused by bottlenecks are transient and likely to be detectable for only a few dozen generations (recent) until the population is adapted to the genetic and demographic problems (Luikart *et al*. 1998). Juveniles often differ genetically from adults, as diversity (e.g. loss of rare alleles; Kettle *et al*. 2007) or homozygote excess (Fujio & von Brand 1991; Stoeckel *et al*. 2006) might deplete during growth depending on the different selection rate between homozygotes (deleterious homozygote recessive alleles) and heterozygotes. However, we found no comparable reduction neither in essential differences of genetic diversity nor in rare allele pattern, as well as homozygote excess was present in both, adults and juveniles.

Spatial genetic structure was weak or absent as estimates did not deviate significantly from randomly permuted data, suggesting the weak relatedness within the neighbourhood and weak spatial genetic structure on the local scale, i.e. forest stand or few hundred meters. Our results of low kinship coefficients (<0.025) and significant deviations in mainly the first distance classes (40-140m) are reported also in other studies (e.g. Pluess 2011) and indicate low genetic differentiation among populations and even a spatial structuring on the landscape scale of outcrossing and wind-dispersed conifers (Androsiuk *et al*. 2013). The reason for the wide scaled genetic structure could be due to long distance seed dispersal of anemochorous conifers (e.g. Campbell *et al*. 1999; Nathan *et al*. 2002) and thus blurring of spatial structuring on a local scale. Such propagule dispersal over long distances is probably more common in *Larix decidua* than in other *Larix* sp., e.g. *L. laricina* where a main seed dispersal distance of two tree heights is reported (Duncan 1954; Brown *et al*. 1988). Unlike *L. decidua*, which occurs mainly from the upper montane to the sub-alpine altitudinal belt, where especially during winter falling seeds might get blown over large distances on the smooth snow surface by wind (Pluess 2011), such secondary seed dispersal might have an impact on the gene flow and mixing genes over long distances. On the other hand, mating within neighbourhood-trees could result in building up spatial genetic structure in juveniles, even though spatial structuring in adults is absent; this pattern would explain the higher values of kinship coefficients obtained in juveniles (F_{ij} = 0.023, SE= 0.0009) compared to adults (F_{ij} = 0.008, SE= 0.004) in native Romanian samples and their weak spatial genetic structures found in R2 and R4 juveniles (data not shown).

Genetic diversity among populations

Analyses of 16 populations of European larch from Tyrol (Alps) and Romania revealed high levels of genetic diversity and moderate differentiation among populations. Overall population differentiation was moderate in both, adults (F_{ST} = 0.133) and juveniles (F_{ST} = 0.136), reflecting the large, but disjunct distribution especially in the Central European area supported by the absent spatial genetic structure on the local scale. This partitioning of genetic variation is in accordance with the general pattern observed in outcrossing and wind pollinating conifers (Wang & Szmidt 2001; Porth & El-Kassaby 2014). However, within conifers *Larix decidua* showed comparatively high differentiation among populations as studies on *Picea abies* (e.g. Scotti *et al*. 2000; Androsiuk *et al*. 2013) or *Pinus sylvestris* (Belletti *et al*. 2012) revealed lower population differentiation and that could be explained by the more continuous distribution and extensive gene flow by pollen of these species than the larch shows, or the relatively small geographic scale of the surveys. Extensive gene flow of conifers leads to high levels of genetic diversity within populations, but low levels of population differentiation and decreases negative effects caused by genetic drift or directional selection (Burczyk *et al*. 2004). Alternatively, a G'_{ST} value of 28 % within adults and 33 % within juveniles indicates a strong population differentiation, which could be due to the big geographical distances between the populations in Tyrol and Romania and thus different genesis during the last glacial period.

Considering the allele size, R_{ST} could in no case explain more of the observed variance either by differences among groups or among populations within groups than F_{ST}, suggesting the absence of a phylogeographic pattern based on stepwise mutations. This pattern might be due to the long distance dispersal or the extensive gene flow ability of larch and generally of conifers (Nathan *et al*. 2002) or through translocations of plant material happened between the 17th and the early 20th century within and outside the regions of its natural distribution (Jansen & Geburek 2016). Further the fact that our whole Tyrolean sample set was differentiated into two clusters with strong detectable transition underlines the extensive gene flow of the species. Nevertheless, there exist criticisms about the comparatively application of F_{ST} and R_{ST} in questions of gene flow and mutation model estimations or sampling variance (Whitlock & McCauley 1999; Hardy *et al*. 2003), but it has been used successfully in many population genetic studies (e.g. Kadu *et al*. 2013; George *et al*. 2015) and gives a clue about phylogeographic pattern within a single species.

Assignment analysis resolved three clearly different groups of populations corresponding to the two main biogeographic regions: the Alps (Tyrol) and Carpathians (Romania), thereby all populations sampled in the respective region were also assigned there. Exceptions made R3 and the three spot checks (SC) in Romania, which shared clear genetic similarities with Tyrolean populations. This underlines the distinct genetically differentiation of the two biogeographic regions (supported by Table 3) and answers our first research question about the population differentiation. Our result confirmed the strong geographic structure on the basis of mitochondrial and nuclear markers reported by Wagner *et al*. (2015a) analysing material collected in a provenance trial covering a gradient over the native distribution range. Further insights into the population structure of the two regions revealed more detailed genetic differences, especially among autochthonous populations within the Southern and Eastern Carpathians. Where, each of the three populations might form obviously and biologically its own genetic cluster (Fig.4) supported by the result of K = 3 of the four statistics of Puechmaille (2016). Interestingly, results of the principle co-ordinate analysis as well as the UPGMA dendrogram revealed stronger genetically similarities of R1 with R4 in the Southern than R1 with R2 in the Eastern Carpathians even though there is larger aerial distance between them (ca. 125 vs. 40 km; Fig.1). Moreover, larger values of K would be consistent with the observed relatively high values of population differentiation revealed by AMOVA. Within Tyrol, the method of Puechmaille (2016) would suggest two genetic clusters (K = 2) as the most likely group structure. Therefore we focused on K = 2, where an interdependent assignment pattern is recognized with one cluster in South and another cluster in North Tyrol that contains beside the ST8 also the Tyrolean population R3 in Romania. This grouping of two assumed ancestral clusters (K = 2) was also supported by the PCoA and the UPGMA consensus tree. The three SC were assigned to the South Tyrolean cluster and are most likely, together with R3, afforestations or results of an afforestation (due to gene flow) from allochthones plant material of Tyrolean origin. Our study area, the Southern and Eastern Carpathians were in particular affected by these transfers originating especially from Alpine (Tyrolean) provenances and starting in the middle of the 19th century (Rubţov & Mocanu 1958; Gava 1963; Rubţov 1965). The strong genetic differentiation of the two regions and of populations within the regions could be explained by the different locations, quantity and size of refugial areas serving as a basis for re-colonization in the Alps and Carpathians. Small but numerous refugia might lead to small populations with a strong genetically divergence between them (as found in Romania), in contrast to large refugia expanding into populations with high diversity and low genetically differentiation (Central Alps).

Despite the extensive historic translocations of larch material in the Southern and Eastern Carpathians (Rubţov 1965), our study showed relatively low genetic impact on native Romanian stands. *Structure* analysis revealed that some populations containing admixed individuals, e.g. population R1 (juveniles), R3 (adults) and R4 (both); but the admixture frequencies ranged only from 6.3% in juveniles of R1, 2.3% in adults and 2.0% in juveniles of R4, respectively. Thus genetic introgression by the introduced individuals seemed to be low; compared, e.g. to Dietrichson (1991) who showed that a proportion of 5-10% of intraspecific hybrids in *Picea abies* can be detected in the offspring although the initial stand contained only 4% of allochthonous trees; or to Unger et al. (2014) who found a low to moderate male gametic gene flow of 6-8% from exotic plantations into two Iberian relict stands of *Pinus pinaster* and *Pinus sylvestris*. In the population R3 which is derived from Tyrolean material, 4.4% of admixed individuals were detected, which may suggest the initial but slow genetic introgression of the Tyrolean stand by native populations. Weak genetic pollution as demonstrated by *Structure* with Tyrolean material is confirmed by the low number of first-generation migrants detected in Romania using *GeneClass*, as we found only 26 individuals of total number analysed (N = 771) in stands in the Southern Carpathians to be backcrossed with individuals of Tyrolean origin. This non-invasive character of Tyrolean provenances in our study might be explained by the possible poor adaptation to climate conditions and hence stronger exposure to natural selection or a lack of overlap in flowering phenology between the two larch forms. Environmental factors are crucial for the successful establishment of translocated individuals into native populations as shown in the few existing studies (e.g. Deguilloux *et al*. 2003; Gum *et al*. 2006). To minimize genetic pollution and to accelerate the process of natural replacement of Tyrolean by autochthonous populations, we recommend to decrease rotation time and to afforest with appropriate material.

Conclusions

Our study showed high levels of molecular diversity and strong genetic differentiation of populations in two regions (Alps and Carpathians) within the natural distribution of European larch (*Larix decidua*). Such strong genetic differentiation was found not only among the regions, but also among populations, especially in the scattered populations occurring in the Southern and Eastern Carpathians. The extensive historic transfers of larch to these regions could be clearly demonstrated, although genetic pollution in the sampled Romanian populations was found to be low and the genetic effects cannot be generalized. Further sampling in the other areas of the native distribution range (Sudetes, Polish lowland and Western Carpathians) as well as more populations in other regions of the Alps are needed. Such information would be essential for future conservation of genetic resources and biodiversity in the Carpathians.

Appendix

Sample site description

In the summer of 2015 we sampled needle and cambium material from four larch sites in Transylvania, Romania (Fig.5; Table 1). Each site was divided into two parts of populations – the adult one and its rejuvenation, the latter was used to determine the gene flow of allochthonous larch on the next larch generation of the Carpathian population. The sites were selected with the help of Lucian Curtu, Professor of Dendrology and Forest Genetics at the Transylvania University of Braşov and the available literature.

The first site (R1, Fig.6) is a native stand of *Larix decidua* mixed with *Picea abies* in Cota on the Bucegi-Mountain, Prahova County. The sampled trees are located on an altitude between 1420 and 1770 m above sea level with eastern exposure. Additionally ten tree samples (spot check 1, 2 and 3) of putative Tyrolean origin located in the near of the native stand in Valea Largā (10 km from Sinoia) were collected. The second sampling site (R2, Fig.7) is located on the mountain Zāganu in Ciucos, Prahova County: This south-western slope reaches between 1330 and 1830 m asl and consists of an autochthonous *Laricetum*-stand. The third site (R3, Fig.8) is an approximately 120 years old presumed afforestation with Alpine larch plant material near the city of Braşov in Braşov County. Originally, the stand should be used for biomass production, but today it has developed into an urban recreational area. The sample area reaches between 700 and 820 m above mean sea level with an exposure to north-west. The last Romanian sample site (R4, Fig.9) is located in Malaia, Vâlcea County and contains a large *L. decidua* population associated with *Picea abies* and *Fagus sylvatica* (780-1650 m asl, exposure north-east). The autochthonous stand is one of the biggest remaining native larch sites of the Southern Carpathians.

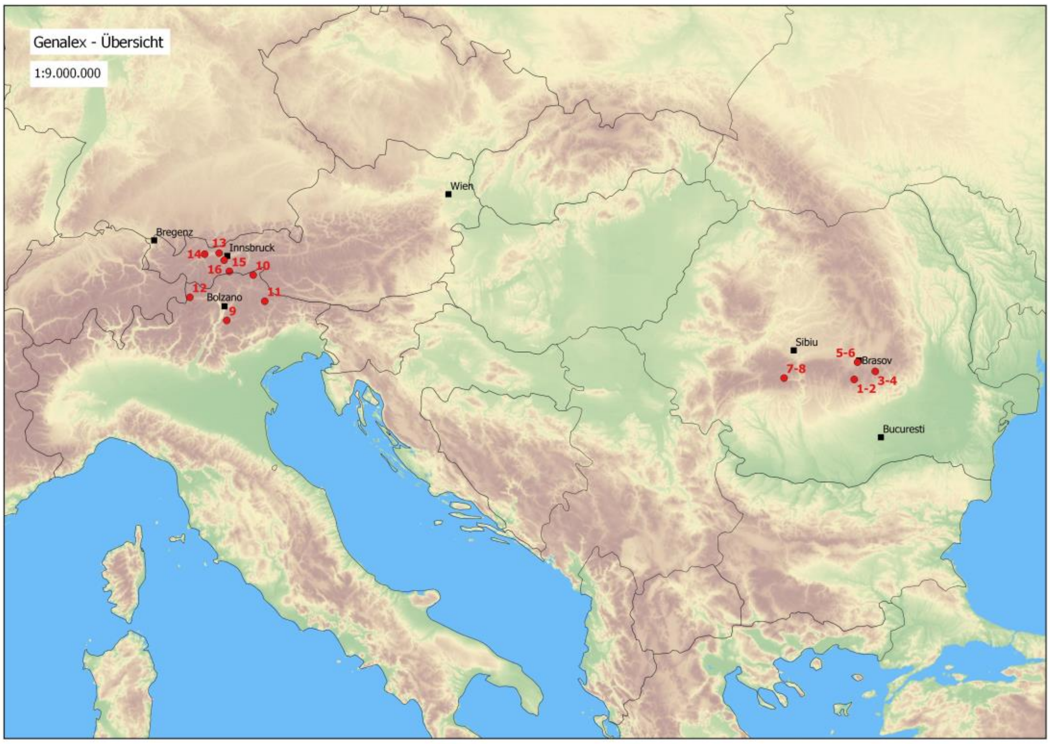


Fig.5 Sampling locations; 1-2=R1, 3-4=R2, 5-6=R3, 7-8=R4, 9=ST5, 10=ST6, 11=ST7, 12=ST8, 13=T9, 14=T10, 15=T11, 16=T12.

R1 in the Southern Carpathians

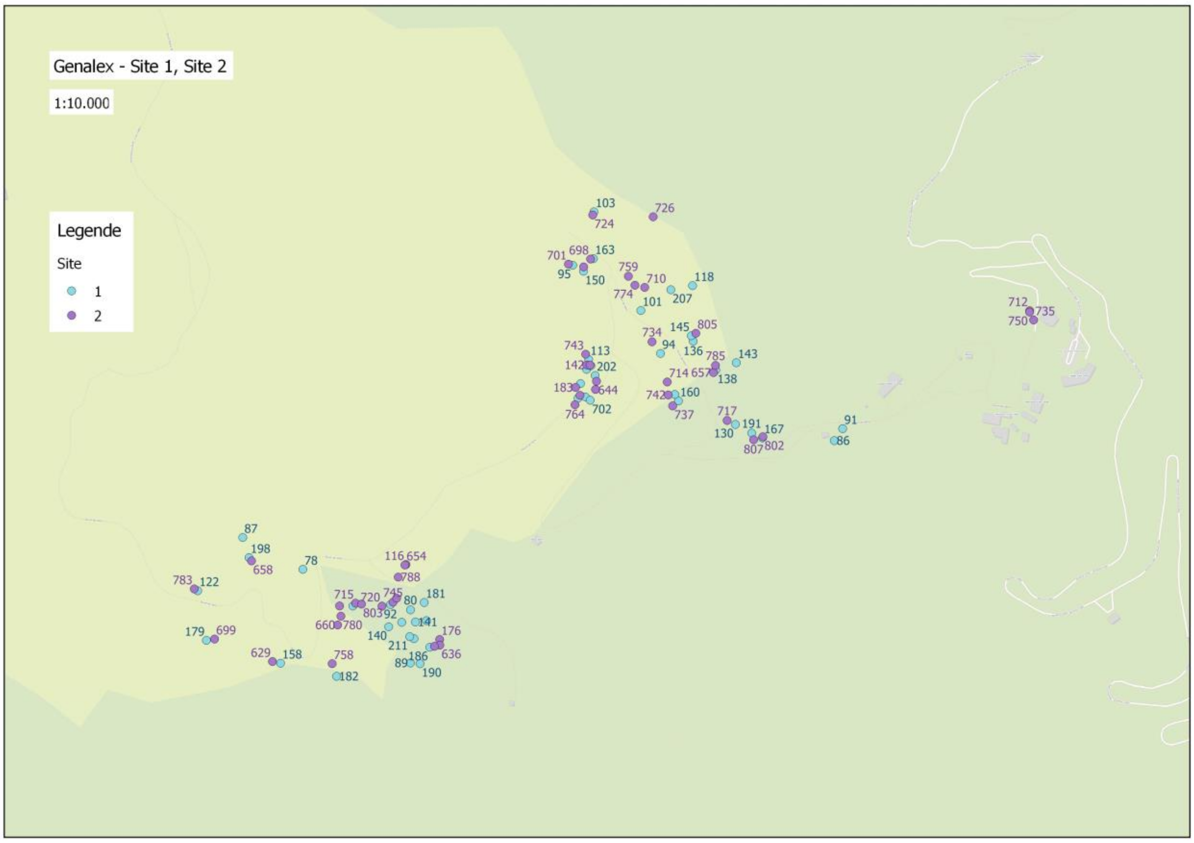


Fig.6 R1 sample number and position; 1=R1(Adult), 2=R1(Juv.).

R2 in the Eastern Carpathians

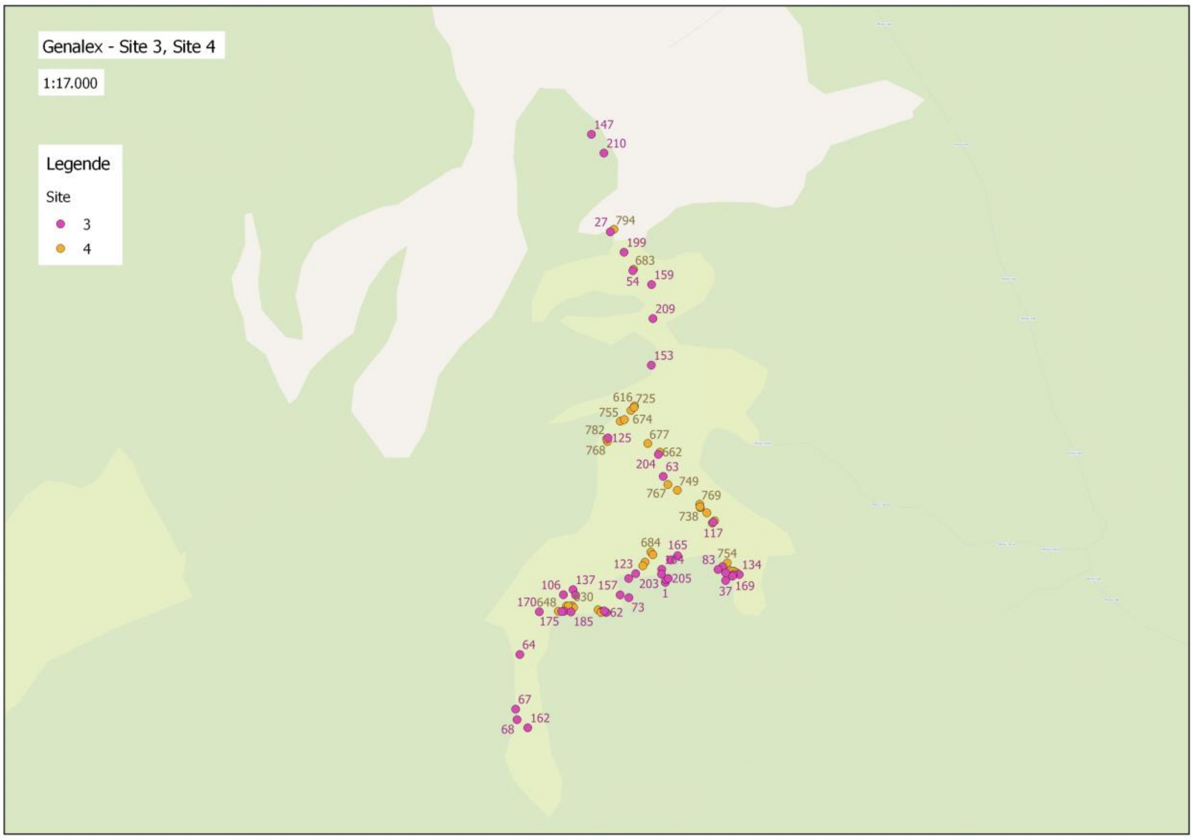


Fig.7 R2 sample number and position; 3=R2(Adult), 4=R2(Juv.).

R3 afforestation of Tyrolean origin

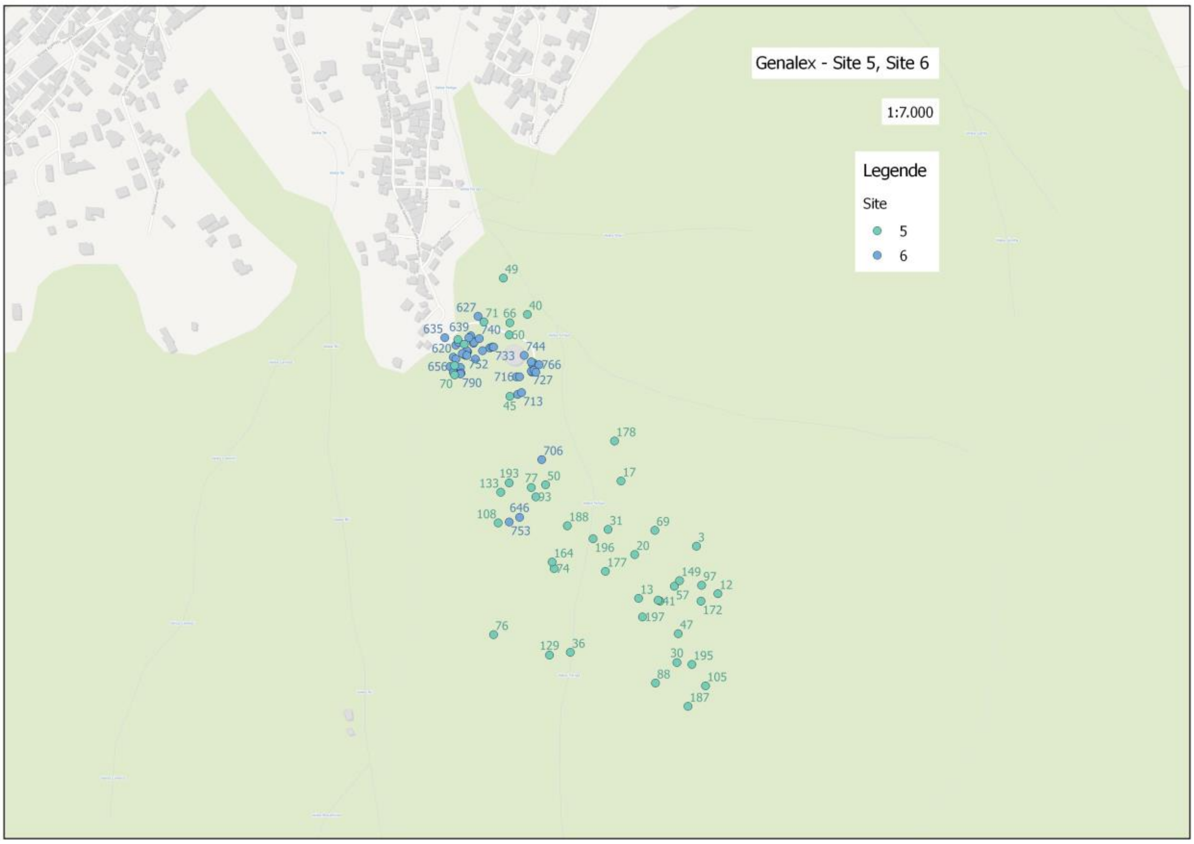


Fig.8 R3 sample number and position; 5=R3(Adult), 6=R3(Juv.).

R4 in the Southern Carpathians

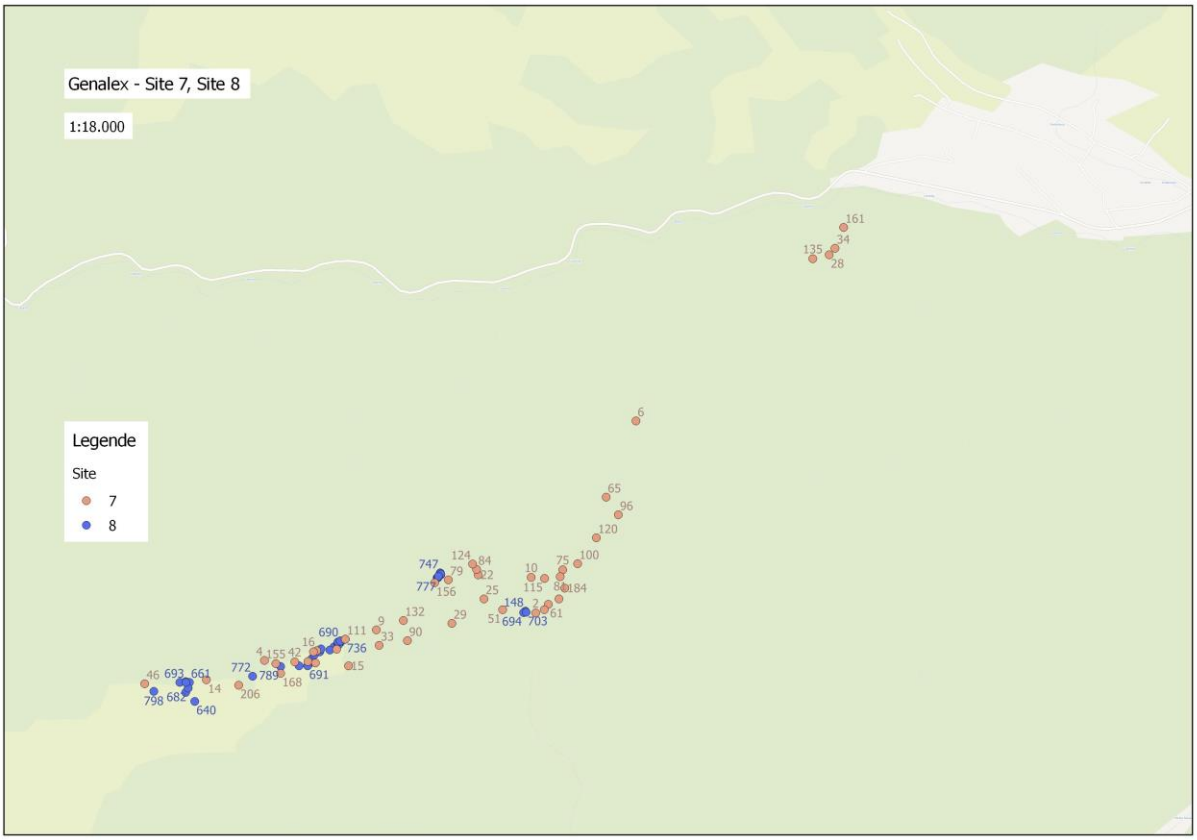


Fig.9 R4 sample number and position; 7=R4(Adult), 8=R4(Juv.).

In Tyrol, we sampled cambium from eight larch sites distributed in North Tyrol (Austria) as well as in South Tyrol, Trento and Belluno (Italy) (Fig.5; Table 1). Only larch stands with an assumed or known usage as seed-harvesting purposes were taken. The sample sites were selected by means of documented evidence and expertise of the forestry authority.

The first stand (ST5, Fig.10), sampled in autumn 2015, is a typical human-influenced larch stand around an alp region in Altrei, Fiemme Valley, on the border to Trento. *L. decidua* was specifically promoted in the past by humans. The reasons were the simultaneously usage of a forest and a meadow or a pasture under the tree crown for grazing livestock (larch meadow). Only the larch sustained these challenges due to its high light demand and pioneer character, this has led to a wide-ranging distribution of such anthropogenic larch stands almost all over Tyrol. The sample site is a slightly sloped plateau located on an altitude between 1220 and 1330 m asl with a southern exposure. The second sampling site (ST6, Fig.11) is situated northwards of the city Bruneck in St. Johann in the Ahrntal Valley, South Tyrol. The mixed stand is a steep north-west slope, which comprises a *Larici Cembretum* - stand and reaches between 1670 and 1850 m asl. Remarkable was the conspicuous thin bark of the larch in this region in comparison to the remaining sample sites. The third South Tyrolean site (ST7, Fig.12) in Misurina, on the border to Belluno, is a subalpine larch forest mixed with *Pinus cembra* and *Pinus mugo*, which is used in combination with a mountain pasture (sampling range: 1730 and 1930 m asl, exposure to east). The last site sampled in South Tyrol (ST8, Fig.13) is a large population surrounding Prad on the Stilfserjoch in Vinschgau. The autochthonous mountain mixed forest consists of *Larix decidua* and *Picea abies* as main tree species and represents a typical seed-harvesting stand. In Prad on the Stilfserjoch was the only seed trade of South Tyrol (Klenge = facility to dry cones to make them lose their seed), therefore the most circumjacent larch trees were sampled and got their characteristically form (compact habitus with many thick branches, Fig.18b). The sample area is located on an altitude between 980 and 1550 m asl.

ST5 in southern South Tyrol/Trento

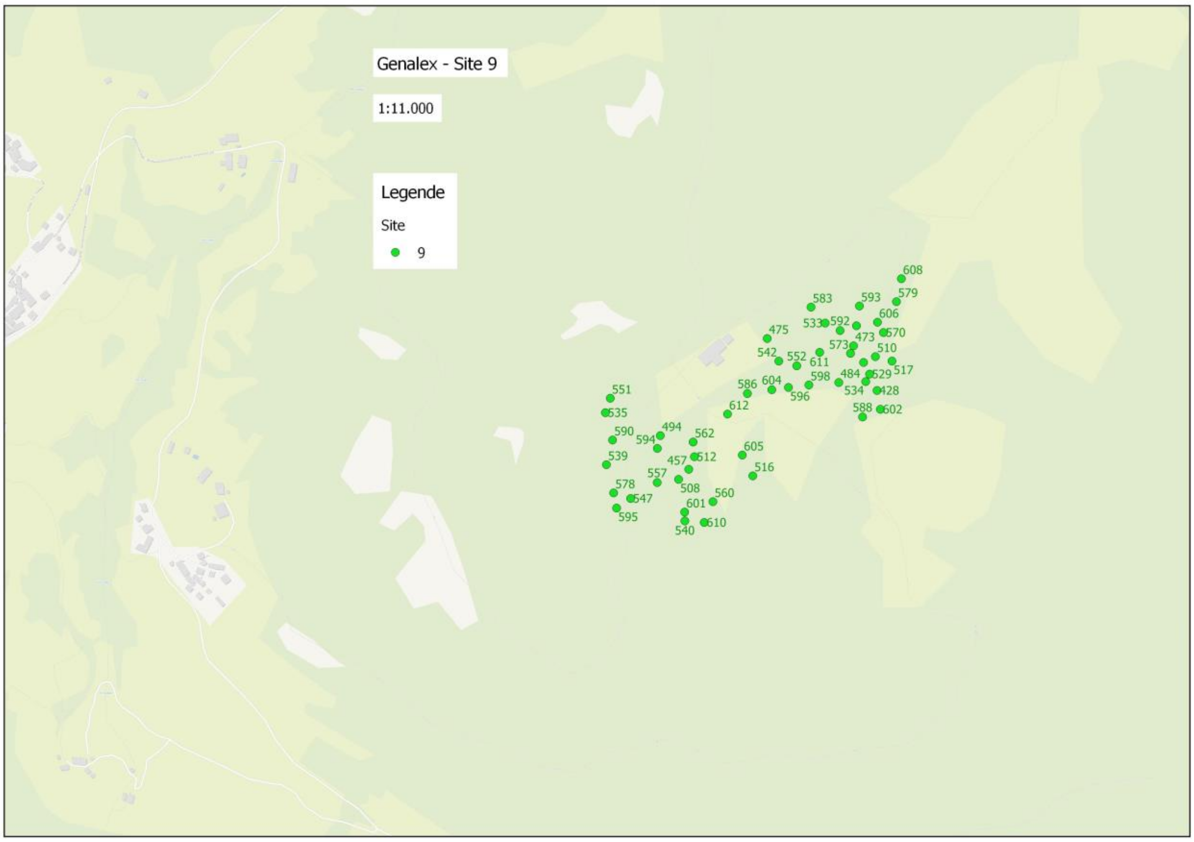


Fig.10 ST5 sample number and position; 9=ST5.

ST6 in northern South Tyrol

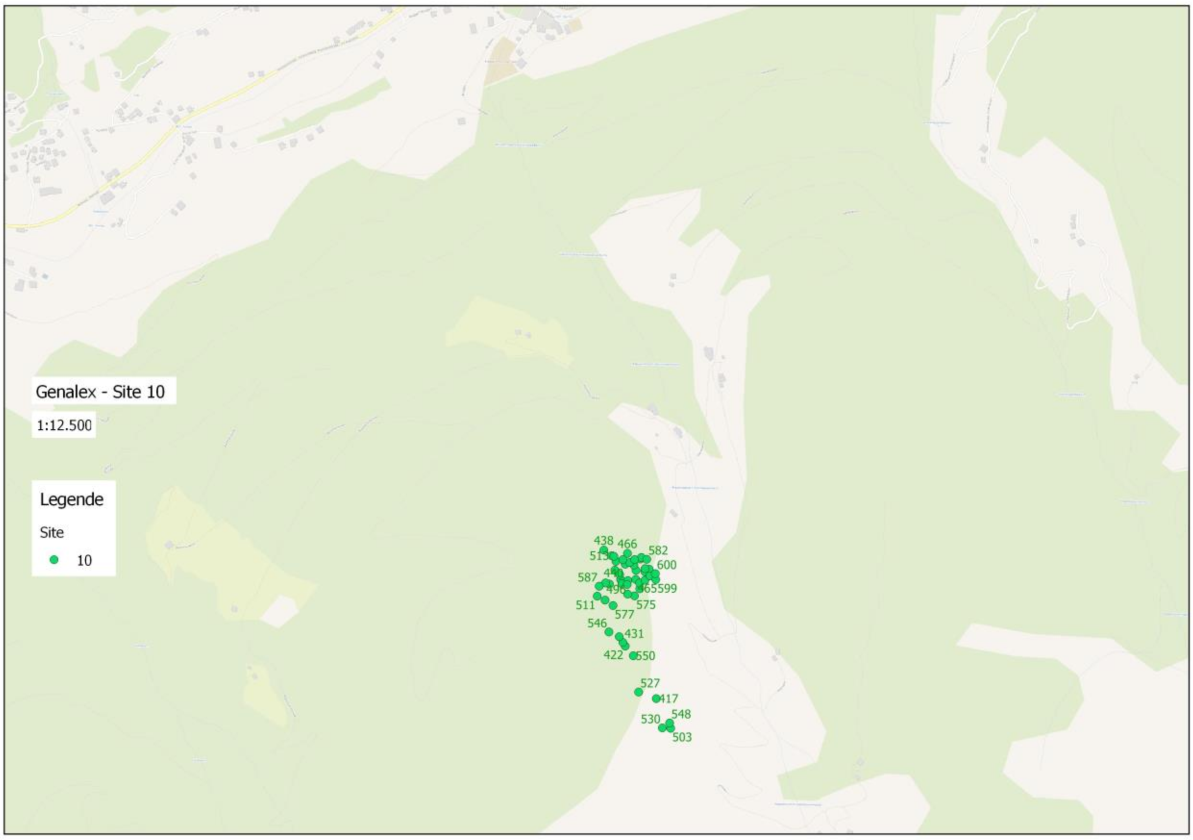


Fig.11 ST6 sample number and position; 10=ST6.

ST7 in eastern South Tyrol/Belluno

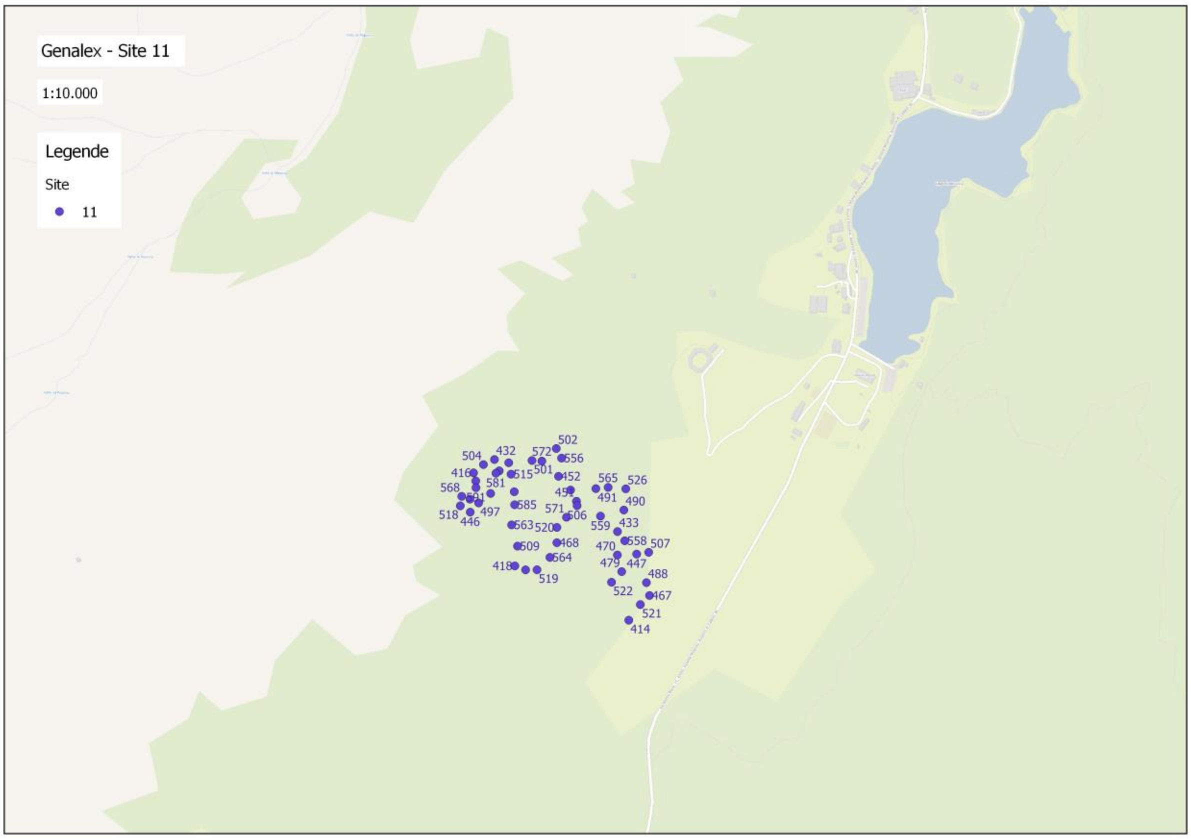


Fig.12 ST7 sample number and position; 11=ST7.

ST8 in western South Tyrol

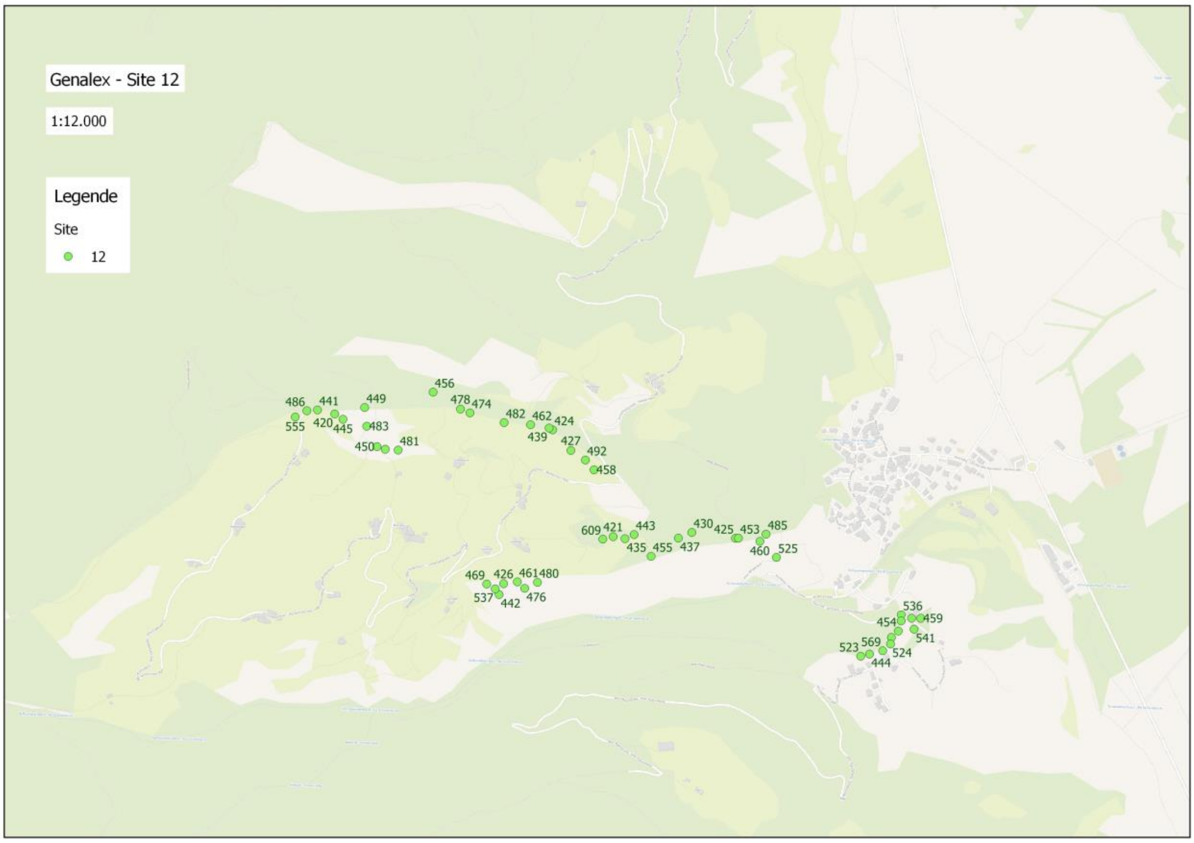


Fig.13 ST8 sample number and position; 12=ST8.

The four Austrian sample sites are located in North Tyrol (Fig.5; Table 1) and represented important seed-harvesting stands according to historic records. All stands are easily accessible from Innsbruck, which was a hot spot for seed trading companies in the 19th century (Rubţov, 1965). The sample site in Seefeld in Tyrol (T9, Fig.14) is characterized by an autochthonous subalpine *Larici Cembretum* forest with a gradual transition to a larch meadow at the lower part of the slope (sampling range: 1190 – 1740 m asl, south-west exposure). The second site (T10, Fig.15) is located in Obsteig at the Mieminger plateau, a large area variously covered with larch meadows and pastures. The larch on this plateau was favoured and planted by humans. It is assumed, that all plant material used originated from the native subalpine larch forest located on the lateral mountain slopes. On this slopes we sampled cambium material on a range between 1120 and 1660 m above sea level (north-east exposure). The larch occurs in combination with *Picea abies* and *Pinus mugo*. The sample site in Steinach in Tyrol, Vinaders (T11, Fig.16) is a large subalpine larch meadow with a south-east exposure. Sampled trees are located on an altitude between 1390 and 1930 m above sea level. The last sampled larch stand (T12, Fig.17) is located near a ski area in Götzens. The sample area is a north-eastern slope reaching between 1680 and 1830 m asl also is a mixed *Larix decidua*, *Picea abies* and *Pinus mugo* stand.

T9 in North Tyrol

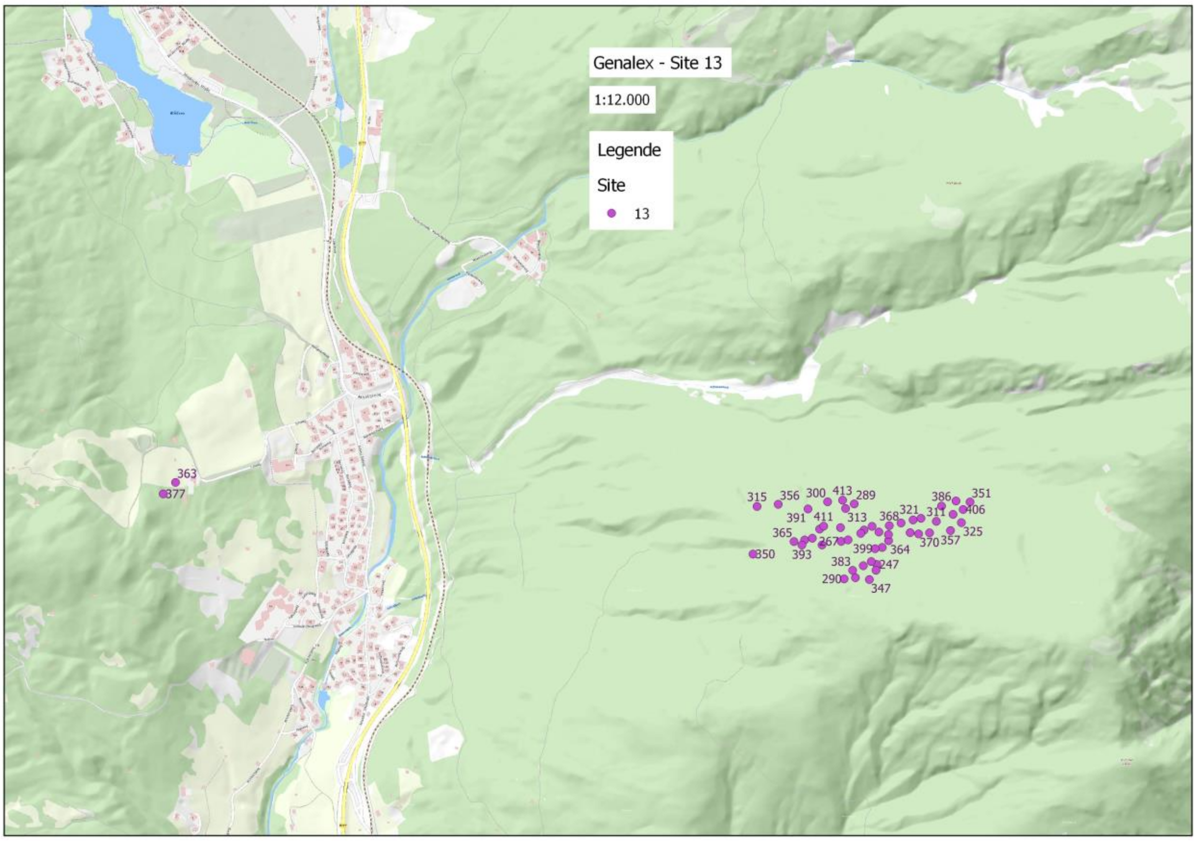


Fig.14 T9 sample number and position; 13=T9.

T10 in North Tyrol

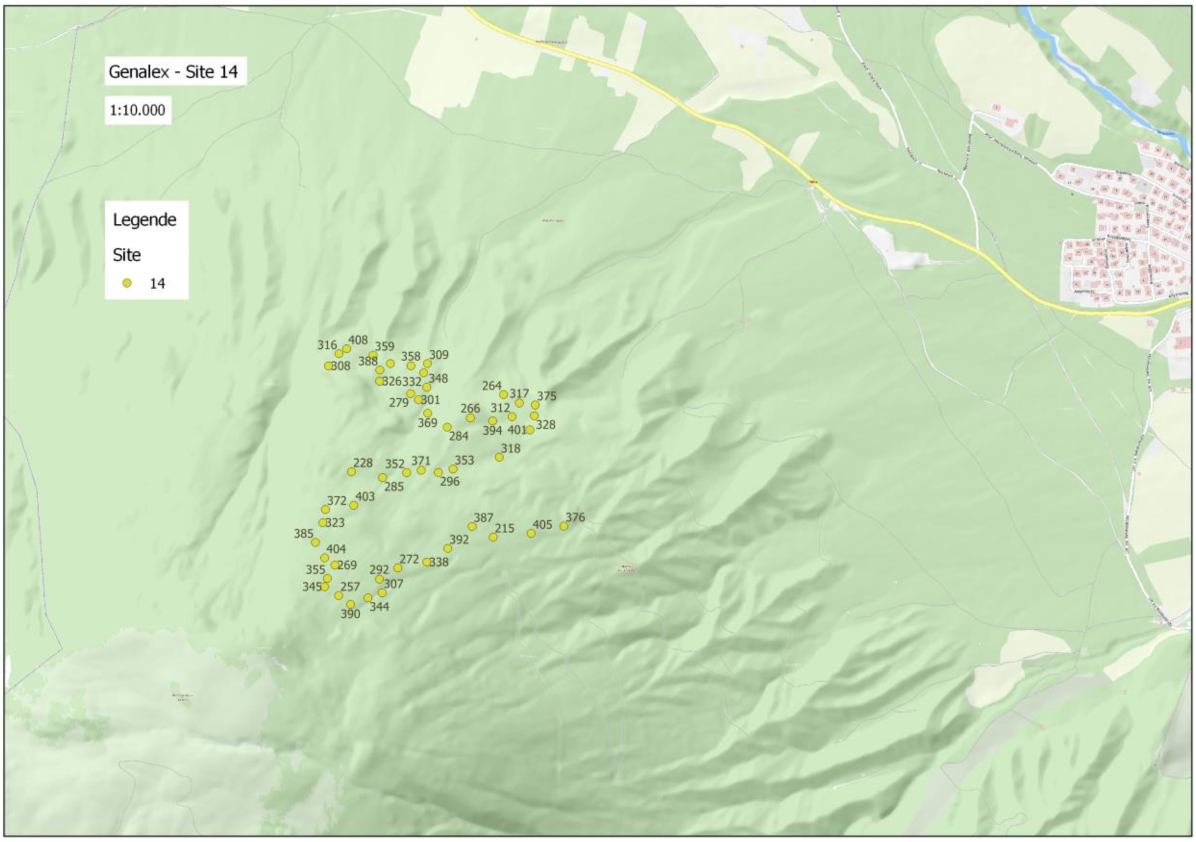


Fig.15 T10 sample number and position; 14=T10.

T11 in North Tyrol

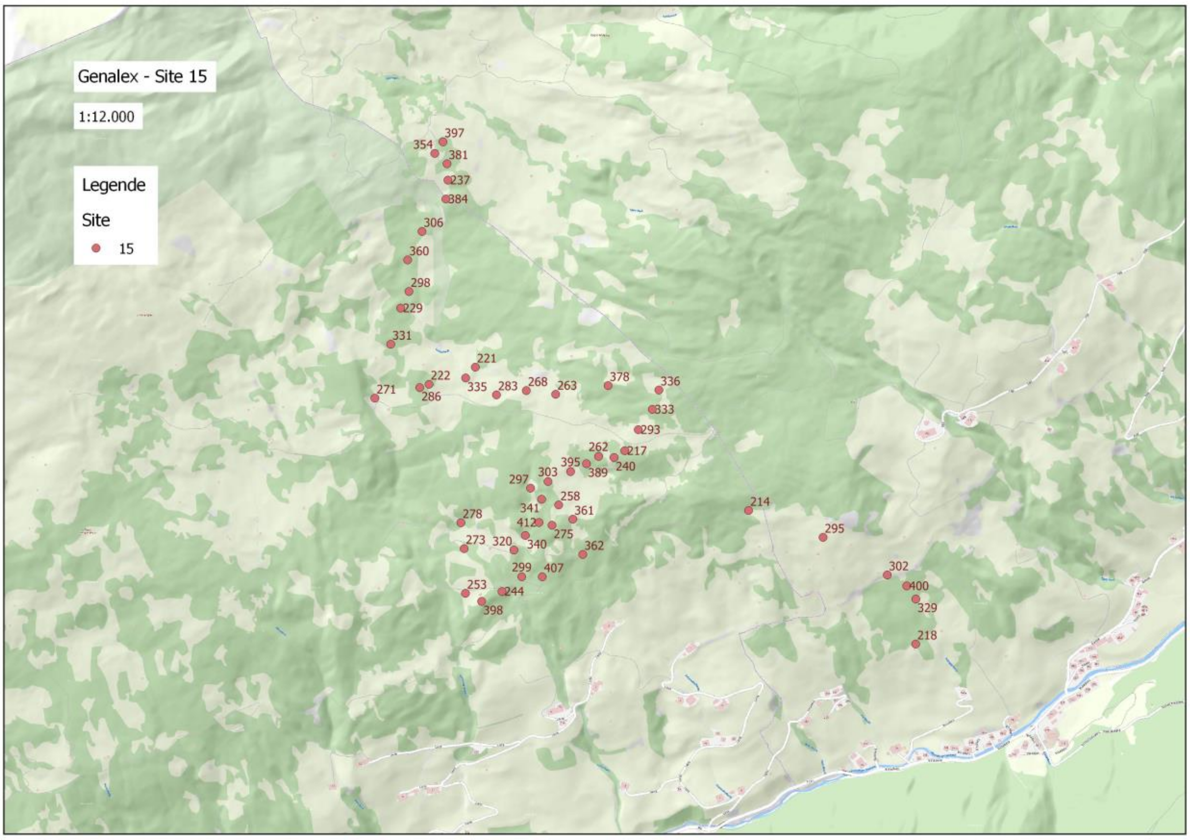


Fig.16 T11 sample number and position; 15=T11.

T12 in North Tyrol

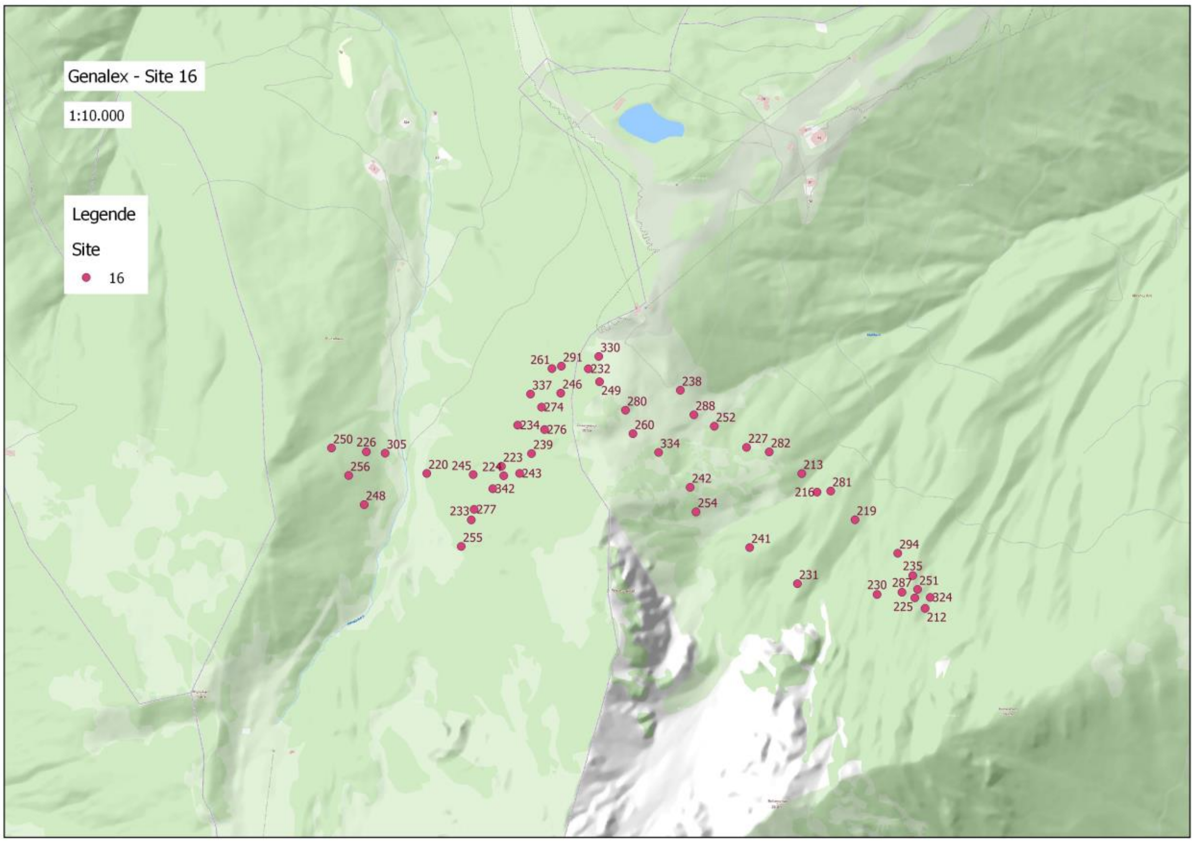


Fig.17 T12 sample number and position; 16=T12.

Sampling technique

The cambium samples were collected using an axe and hollow punch on the stem base. Thereby two sampling techniques were promising and depending on bark thickness, if the latter was thick, the hollow punch was positioned between the bark scales and with a few careful axe strokes the sample was obtained. The second technique on thin barked trees comprised of the removal of bark from the sampling area before the sampling was done, thereby a cleaner cambium sample in comparison to the first technique could be achieved. Fifty individuals of each population were sampled and collected material was stored in zip lock plastic bags containing silica gel.

Historic sampling of larch seeds was carried out at intervals with annual checking of the seed yield by cutting cones into halves and counting mature seeds (Fig.18a). Thereby when sampling, the outer part of branches was broken off starting on top and continuing to the button of the tree crown by using a long-handled hook. Through the repeat of this sampling technique, the sample trees have received their typically compact habitus with thick branches (Fig.18b)(Alois Alber, personal communication, 2015).

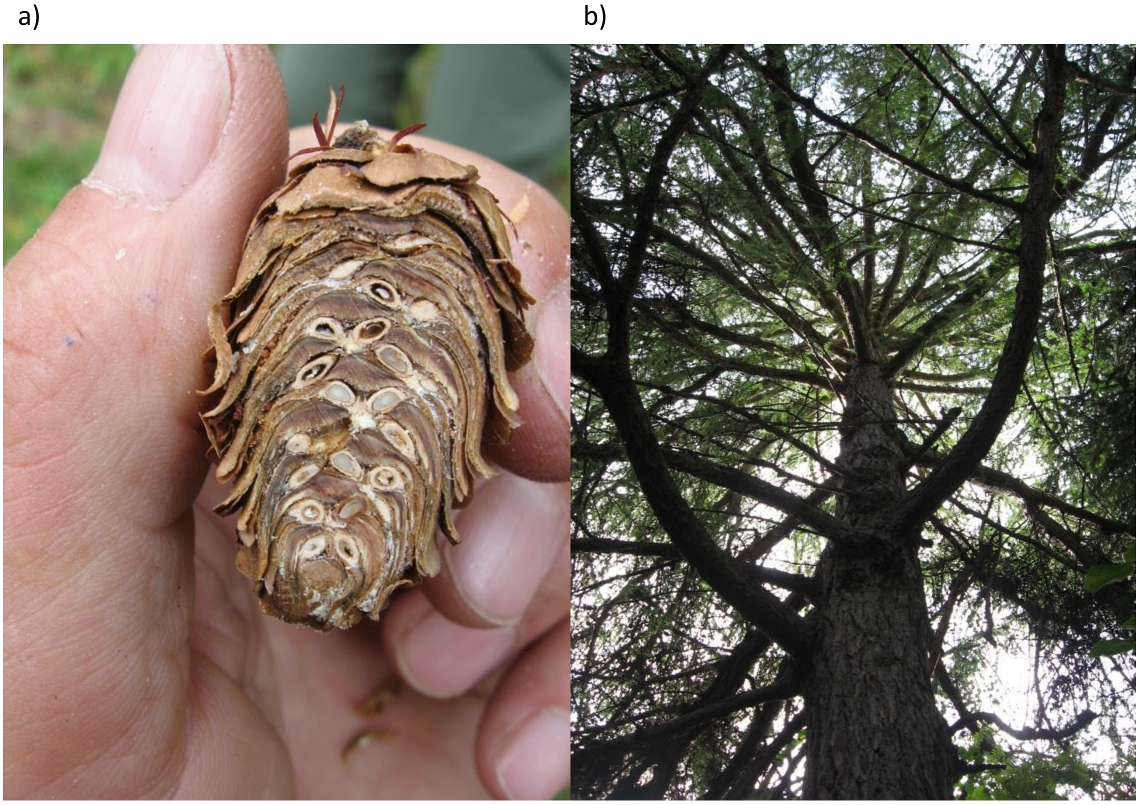


Fig.18 a) Cut cone of *Larix decidua* for estimating the seed yield, b) compact habitus of a larch individual as result of repetitive sampling.

DNA extraction and genotyping

Collected and dried cambium and needle samples were cut into small pieces with a scalpel (0.5 mm thin strips of cambium; 2 mm pieces of needles); approx. 100 mg of these were combined with one 4 mm glass bead and two 3 mm tungsten beads, which were added into a 2 ml tube. Following this, the filled tubes were frozen in liquid nitrogen for 4 min and crushed using a Qiagen TissueLyser device (Qiagen, Inc.) for 1 min at 20 Hz. These two actions (with rotating the racks) were repeated once more to get a finer consistency. Genomic DNA was extracted using modified CTAB method of Doyle and Doyle (1990) or the DNeasy 96 Plant Kit (Qiagen, Inc.) following the manufacturers' protocol.

Modified protocol of Doyle & Doyle (1990):

The used DNA extraction buffer for 1 litre is composed of 20 g CTAB that works like soap and cleans the material to be extracted, 10 g PVP 40000 a molecule with a large surface, which bonds big molecule like phenols, 40 ml EDTA 0,5 M pH=8 that inhibits enzyme activity, 100 ml Tris HCl 1 M pH=8, 280 ml NaCl 5 M that changes osmotic pressure inside the cells and breaks the cell wall to getting out the DNA, and distilled water to bring to volume.

1. Set the centrifuge to 4° C, heat extraction buffer to 65°C and put the 76% ethanol and isopropanol in freezer at -20°C.
2. Take care to use the right pipette with the right pipette tips (colours!). Add 800 µl of heated extraction buffer to tubes containing material to be extracted. After that mix the single tubes to a consistent suspension by using the Vortex.
3. Set the heated shaker to 55°C and incubate the tubes at 55°C for 1 h with manual shaking every 10 min.
4. Let tubes cool down for 5 min.
5. Add 800 µl of dichloromethane instead of chloroform, which was used by Doyle and Doyle (1990). Dichloromethane destroys proteins and enzymes definitely. After the adding shake the tubes gently for 8 min with your hands to get an emulsion. The whole step must be done under the fume hood!
6. Centrifuge the tubes for 10 min at 13000 rpm and 4°C. This step produces two phases, the supernatant fluid containing the DNA and a lower dichloromethane phase containing degraded lipids, proteins and other secondary compounds. Through the spinning of centrifuge the junk in the supernatant fluid sinks down, hence the aqueous phase will be clear.
7. Pipet 600 µl of the supernatant into a new 2 ml tube without disturbing the opaque layer.
8. Repeat step 5-7 and pipet 400 µl of the supernatant instead of 600 µl into a new 0.5 ml tube.

9. Add 0.5 volumes of ice-cold isopropanol into the tubes, thereby DNA precipitates. Following this put the tubes in freezer for 1 h at -20°C. Use a wide bore pipette to improve the length and quality of DNA, because DNA in solution is a skinny, long molecule, which can easily break. If no DNA precipitation can be observed, left the sample at room temperature for several hours (overnight).
10. After the cooling centrifuge for 5 min at 13000 rpm at 4°C.
11. Pour supernatant out of tubes and put them on paper towel upside down for 5 min to dry off.
12. Add 1 ml ice-cold 76% ethanol to the DNA-pellet to wash them, afterwards tap the tubes with a strong manual movement until pellet floats.
13. Centrifuge the tubes for 1 min at 13000 rpm and 4°C.
14. Carefully pour supernatant out of tubes and let pellets dry overnight.
15. The next day add 100 µl of TE buffer (Tris HCL, EDTA) or distilled water to the pellets and let them stay overnight in the fridge (4°C) for dissolving. If necessary, centrifuge the pellets with a small centrifuge for a better wetting. TE buffer inhibits molecules and randomly present DNase (deoxyribonuclease), usually is not used because it interferes with the PCR.
16. The next day pipet 1 µl (white pipette tips) of RNase to tubes with briefly manual shaking. After that put tubes on the heated shaker for 30 min at 37°C without shaking. RNase destroys the RNA and makes the DNA purer. Finally store tubes at 4°C in fridge.

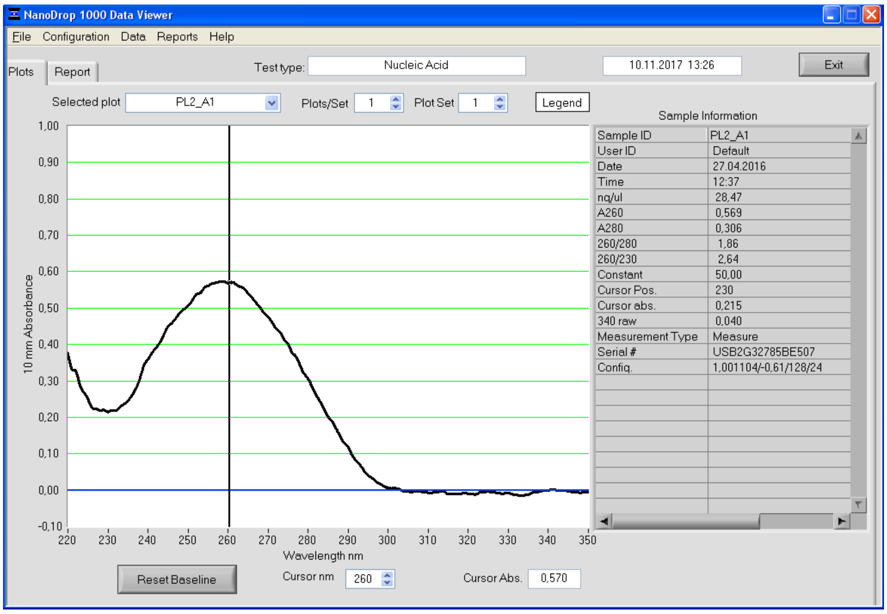
DNeasy 96 Plant Kit protocol of Qiagen:

Take care of the Buffer AW2 and Buffer AW1. These Buffers are concentrates and must be added with the appropriate amount of ethanol (96-100%) before the first using. If necessary, heat the Buffer AW1 to 65°C to re-dissolve possible precipitates developed during storage.

1. Set water bath to 65°C and the centrifuge to 40°C, heat Buffer AP1 to 80°C and Reagent DX (viscous) to 37°C. For the following steps use a multichannel pipet.
2. Make a working lysis solution by combining 90 ml Buffer AP1 (400 µl/sample), 225 µl RNase A (1 µl/sample) and 225 µl Reagent DX (1 µl/sample).
3. Knock the rack against a bench to remove any tissue from the caps.
4. After the preparing pipet 400 µl solution into each collection microtube, seal the rack of collection microtubes with the caps, shake it vigorously for 15 sec by hand and put it in the water bath for 10 min at 65°C with ballasting to prevent the caps from coming off.
5. Centrifuge until the centrifuge reaches 3000 rpm to collect any tissue from the caps.
6. Remove the caps and pipet 130 µl Buffer P3 into each collection microtube.

7. Close the collection microtubes with new caps, shake the rack vigorously for 15 sec by hand and centrifuge it until the centrifuge reaches 3000 rpm.
8. Put the rack in freezer for 10 min at -20°C. This step provides the precipitation of inhibitors and proteins.
9. Centrifuge the rack for 5 min at 6000 rpm, so compact pellets will form.
10. Remove the caps and carefully pipet 400 µl of the supernatant to a new rack without transferring any of floating particles. If less than 400 µl is obtained, adjust the amount of Buffer AW1 in step 11. Take care of the correct orientation of the new rack!
11. Add 1.5 volumes (600 µl) of Buffer AW1 to each collection microtube and close the rack with new caps.
12. Shake the rack vigorously for 15 sec by hand and centrifuge it until the centrifuge reaches 3000 rpm.
13. First, put a DNeasy 96 plate on top of an S-Block and be careful to mark the plates for sample identification. Further remove the caps from the rack and transfer 1 ml of each sample into the DNeasy 96 plate above the S-Block. To avoid cross-contamination remove only one set of caps each time. Take care not to low the pipet tips to the bottom, this may cause overflow of samples.
14. Seal DNeasy 96 plate with an AirPore Tape to prevent a cross-contamination and centrifuge it for 4 min at 6000 rpm. After centrifugation check the wells of the plate, if lysate remains in a single well, centrifuge for another 4 min. All the lysate should pass the membrane.
15. Discard AirPore Tape and add 800 µl Buffer AW2 to each sample.
16. Centrifuge the plate fitted without AirPore Tape for 15 min at 6000 rpm that provides a faster drying of the membranes. Remaining ethanol from the Buffer AW2 can be removed by centrifugation, otherwise it may inhibit PCR. A usage of too much starting material could lead to a dark coloration of the membrane, in this case a second wash step with 800 µl 96-100% ethanol to improve DNA quality is recommended.
17. First, put the DNeasy 96 plate on top of a rack of Elution Microtubes RS in the correct orientation, after that add 50 µl Buffer AE to each sample.
18. Seal the DNeasy 96 plate with an AirPore Tape and incubate the rack for 1 min at room temperature (15-25°C). After incubating centrifuge for 2 min at 6000 rpm.
19. For sufficient elution of DNA repeat step 17-18. Elution twice with 50 µl increases DNA concentration, but total DNA yield is decreasing. Finally use new caps and store the Elution Microtubes RS containing DNA at 4°C in fridge.

DNA-quality was measured using a ND-1000 spectrophotometer (NanoDrop, Inc.). In the process we identified concentration and light-absorbance that stands for purity of obtained DNA, this was done by pipetting 2 µl DNA-suspension onto the end of a fibre optic cable (measuring range) of spectrophotometer. When using the software we chose the button 'nucleo acit' and gauged the spectrophotometer twice with distilled water (or TE buffer, depending on the choice at step 15 of the modified protocol of Doyle and Doyle (1990)). Furthermore, after each measurement the measuring range was cleaned with a dust-free cloth. The software generates a plot (Fig.19), where the quality of DNA can be interpreted; thereby the ratio of the absorbance at a wavelength of 260 nm to the absorbance at 280 nm should be greater than 1.8 to indicate high DNA-quality.



Test type: Nucleic Acid

10.11.2017 13:26

Selected plot: PL2_A1

Plots/Set: 1

Plot Set: 1

Cursor nm: 260

Cursor Abs.: 0,570

Sample Information

Sample ID	PL2_A1
User ID	Default
Date	27.04.2016
Time	12:37
nq/ul	28,47
A260	0,569
A280	0,306
260/280	1,86
260/230	2,64
Constant	50,00
Cursor Pos.	230
Cursor abs.	0,215
340 raw	0,040
Measurement Type	Measure
Serial #	USB2G32785BE507
Config.	1,001104/-0,61/128/24

Fig.19 Plot showing the course of absorbance as a function of wavelength in a DNA solution.

All samples were genotyped with 13 highly polymorphic nuclear microsatellite loci, which combine microsatellites originally developed for the sister species *L. kaempferi* and newly designed one for *L. decidua*, namely Ld31, bcLK211, Ld30, bcLK228, Ld50, bcLK189, bcLK253, Ld58, Ld45, Ld42, bcLK263, Ld101 and Ld56 (Wagner *et al*. 2012).

Table6 Overview of the 13 nuclear markers used in this study

Locus	Repeat-motif	Primer sequence (F)	Primer sequence (R)	Size (bp)	Reference
Ld31	$(AC)_{18}$	TTGAACTAGGGAGATCCGGC	AATAAAATAGCATTCCATGTGTAGC	104–147	Wagner et al. (2012)
bcLK211	$(CT)_{16}$	CCATTCTCCATAGGTTCATTG	ATGCTCCTTACTAAGTCAGATACAC	174–242	Isoda & Watanabe (2006)
Ld30	$(AC)_{18}$	TTGTAGGTGTGTATGAAAGTTCTG	TGCCACTCTATTTCCTTAATGCC	100–138	Wagner et al. (2012)
bcLK228	$(AG)_{18}$	CCCTAACCCTAGAATCCAATAA	GAGGAAGGCGACAAGTCATT	165–215	Isoda & Watanabe (2006)
Ld50	$(CA)_{18}$	GAAGGCGACTTTACATGCCC	TCCATCTTTATGTCTCTTCCATGC	157–205	Wagner et al. (2012)
bcLK189	$(AG)_{17}AT(AG)_6$	ACCATACGCATACCCAATAGA	AGTTTTCCTTTCCCACACAAT	142–172	Isoda & Watanabe (2006)
bcLK253	$(AG)_{17}$	AACACCATAGTGCAATGTGC	TCCTCTTGTTGATGCCACTT	195–227	Isoda & Watanabe (2006)
Ld58	$(AC)_{15}$	AATGGCAAGAGCAGCAATCC	TCCAGGAATGATTTATCGAGAGC	131–183	Wagner et al. (2012)
Ld45	$(CA)_{13}$	TGTGGGAGGTATAGCTTGGC	AGTAGGATGGAATGATGGAAACAC	198–216	Wagner et al. (2012)
Ld42	$(TG)_{14}$	TCGTATGCATTGTCCAAATTTCC	TCCAAGTGAGGTCACACGAG	167–191	Wagner et al. (2012)
bcLK263	$(TC)_{20}$	CGATTGGTATAGTGGTCATTGT	CGATTGGTATAGTGGTCATTGT	185–259	Isoda & Watanabe (2006)
Ld101	$(AC)_{12}$	ACACCAAGGACTCTCTGACTAC	GGTGATTCCAGAAGCAGGTG	179–215	Wagner et al. (2012)
Ld56	$(AC)_{16}$	AGCCATCGTGGTTCTTCTTTG	CTTGTAACTGTGCACCCACC	219–247	Wagner *et al.* (2012)

Software description

Micro-Checker 2.2.3 (van Oosterhout *et al.* 2004)

Micro-Checker is a software to check microsatellite data for genotyping errors, such as null alleles, large allele dropouts and slight changes in allele sizes during PCR-amplification (stuttering) (Shinde *et al.* 2003) as well as typographic errors. Due to mutations within the primer can lead to fail correct amplification of one or more alleles (null alleles) during PCR, resulting in false homozygotes (Shaw *et al.* 1999). The amplification of large alleles is not as efficient as of small ones, preferring small allele amplification and short allele dominance (Wattier *et al.* 1998). These genotyping errors yield their own allelic signature (certain presence of particular genotypes), therefore a discrimination of deviations caused by non-panmixia is possible. The Windows-based software uses a Monte Carlo simulation (bootstrap) and estimates homozygote and heterozygote allele size difference frequencies taking account of minimizing deviations from Hardy-Weinberg equilibrium (HWE). Furthermore, under this assumption the software calculates expected allele frequencies and null allele frequencies. If null alleles are present, the software can adjust the observed allele and genotype frequencies, which can be used for further population genetic statistics.

The software accepts input-files in the Genepop (Raymond & Rousset 1995) (.txt or .dat) or Microsoft Excel (.xls) format. Alternatively the user can open a blank DataGrid, after setting the number of loci in the new population, the data can be entered by Copied and Pasted from correctly formatted files. We selected the repeat motif dinucleotide for all loci in the populations by clicking the ‘All’ button. Following a check of the data for possible typographic errors, the data can be analysed and the program generates graphs for every locus in every population. All of our settings are displayed in the Fig.20.

```
Locus: Locus 11

More than 50% of the alleles at this locus are of one allele size class.
Binomial analysis could not be performed.
```

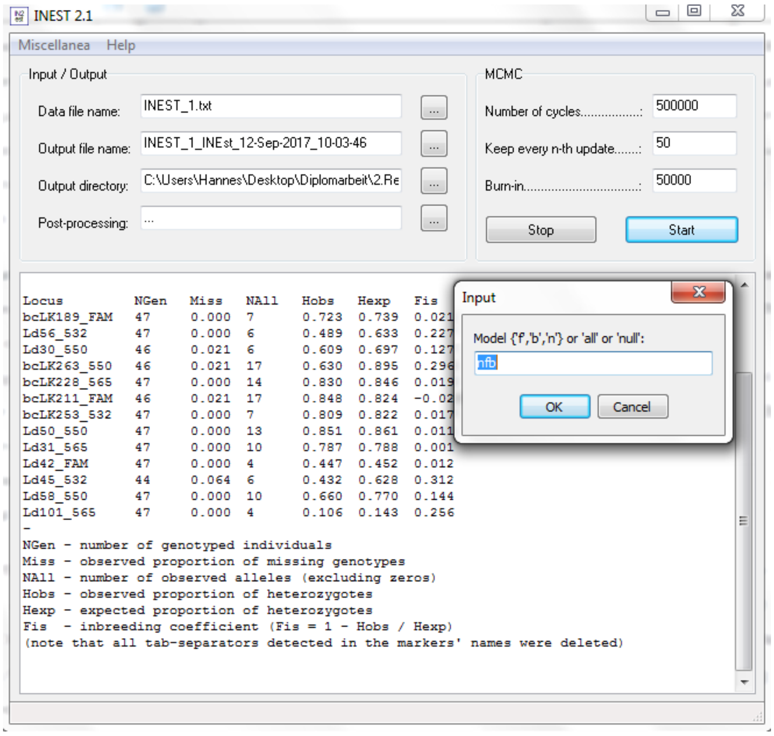
```
Locus: Locus 11
Total expected homozygotes: 16,795
Total observed homozygotes: 25

Analysis indicates homozygote excess at this locus.

No evidence for scoring error due to stuttering.

No evidence for large allele dropout.

Null alleles may be present at this locus, as is suggested by the general excess of
homozygotes for most allele size classes.
```

Fig.20 User interface of Micro-Checker.

INEst 2.2 (Chybicki & Burczyk 2009)

The main purpose of the software is to estimate unbiased multilocus inbreeding coefficients and observed and expected heterozygosity corrected for the occurrence of null alleles and genotyping errors. Null alleles usually arise from a point mutation in flanking regions of microsatellites (Holm *et al*. 2001). In high proportion, they may affect estimates of population parameters due to the large underestimation of observed heterozygosity. Commonly used null allele frequencies estimators can calculate biased estimates when inbreeding acts a part in a population. In such case, the Windows-based computer program can be applied for both, the estimation of null allele frequencies and inbreeding coefficients. Therefore, INEst offers two methods, the maximum likelihood approach of the population inbreeding model (PIM) and the Bayesian approach of the individual inbreeding model (IIM). The latter appeared to be better than PIM at estimating of both allele frequencies and average inbreeding coefficients. Moreover, the software enables additional calculations such as, permutation tests for heterozygosity excess, spatial genetic structure or bottleneck tests.

The program accepts only correctly formatted text files, which can be loaded in the standard open dialog pressing the button ‘Data file name’. We used the Bayesian approach of the individual inbreeding model (IIM). After entering the settings (see Fig.21) and pressing the ‘Start’ button, a model of choice must be specified based on three parameters (null alleles *n*, inbreeding coefficients *f*, genotyping failures *b*). Output-files can be loaded by pressing the button ‘Post-processing’, whereas the files .hyp, containing inbreeding level (Mean*F*) and average inbreeding coefficient (Avg(F_i)), .pjk, containing null allele frequencies (Mean), and .het, containing observed and expected heterozygosity, are important (Chybicki 2017).



Data file name: INEST_1.txt

Output file name: INEST_1_INEst_12-Sep-2017_10-03-46

Output directory: C:\Users\Hannes\Desktop\Diplomarbeit\2.Re

Post-processing: ...

Number of cycles.................: 500000

Keep every n-th update.......: 50

Burn-in.................................: 50000

Model {'f','b','n'} or 'all' or 'null': nfb

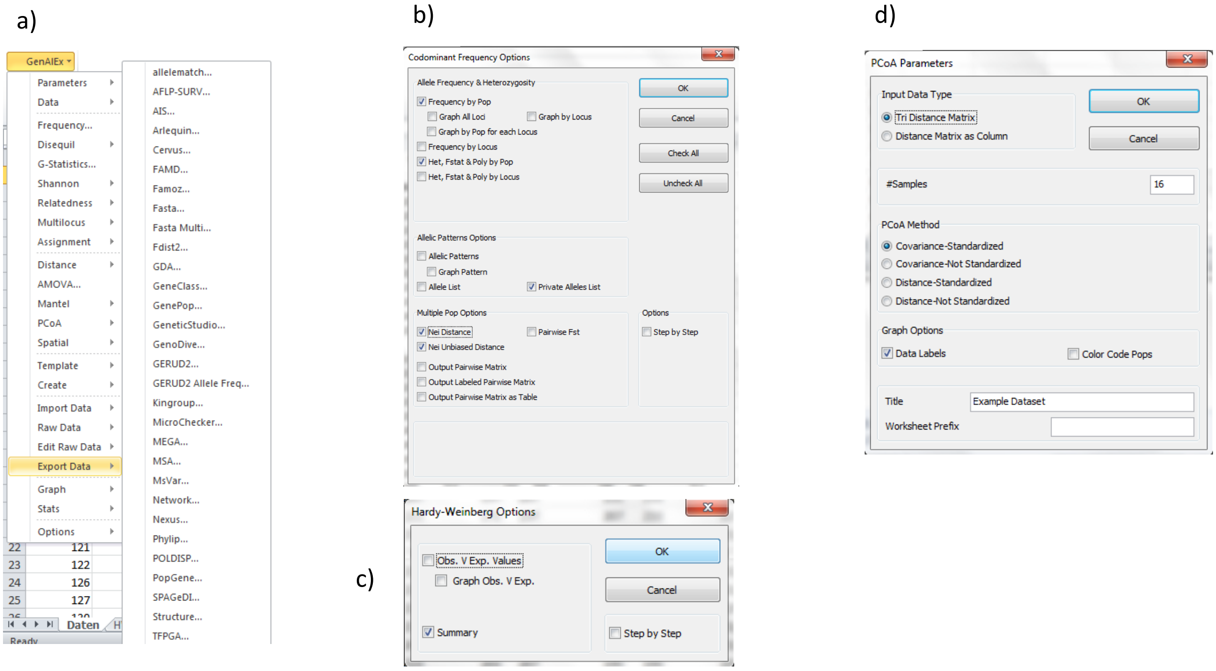
```
Locus          NGen   Miss   NAll   Hobs   Hexp   Fis
bcLK189_FAM    47     0.000  7      0.723  0.739  0.021
Ld56_532       47     0.000  6      0.489  0.633  0.227
Ld30_550       46     0.021  6      0.609  0.697  0.127
bcLK263_550    46     0.021  17     0.630  0.895  0.296
bcLK228_565    47     0.000  14     0.830  0.846  0.019
bcLK211_FAM    46     0.021  17     0.848  0.824  -0.02
bcLK253_532    47     0.000  7      0.809  0.822  0.017
Ld50_550       47     0.000  13     0.851  0.861  0.011
Ld31_565       47     0.000  10     0.787  0.788  0.001
Ld42_FAM       47     0.000  4      0.447  0.452  0.012
Ld45_532       44     0.064  6      0.432  0.628  0.312
Ld58_550       47     0.000  10     0.660  0.770  0.144
Ld101_565      47     0.000  4      0.106  0.143  0.256
-
NGen - number of genotyped individuals
Miss - observed proportion of missing genotypes
NAll - number of observed alleles (excluding zeros)
Hobs - observed proportion of heterozygotes
Hexp - expected proportion of heterozygotes
Fis  - inbreeding coefficient (Fis = 1 - Hobs / Hexp)
(note that all tab-separators detected in the markers' names were deleted)
```

Fig.21 User interface of INEst.

GenAlEx 6.5 (Peakall & Smouse 2006; 2012)

GenAlEx or Genetic Analysis in Excel is a software approach for population genetic analyses that operates within Microsoft Excel, a part of the cross-platform Microsoft Office. The program was originally developed as a teaching tool and represents an ideal launching pad for students, teachers and researchers. The user-friendly interface of the package results in a quick understanding and effective analysing of a wide range of population genetic data, taking advantage of the whole set of graphical options implemented in Excel. GenAlEx also offers analysis of nearly all kind of genetic data (diploid codominant, haploid and binary) and genetic markers, including SSRs, SNPs, amplified fragment length polymorphisms and DNA sequences. It provides both frequency-based (observed and expected heterozygosity, HWE, *F*-statistics, Nei´s distance etc.) and distance-based (AMOVA, Principle Coordinates Analysis PCoA, Mantel tests etc.) analysis as well as standard summary statistics (allele-frequencies, private alleles etc.). The updated version 6.5 contains new features to calculate population genetic structure (G'_{ST}, G''_{ST}, F'_{ST} etc.), diversity indices (Shannon information indices), fine scale genetic process analysis (heterogeneity tests) and Linkage disequilibrium (LD) tests for biallelic markers. Data export and correct formatting to the respective input-files of more than 30 other software packages is provided.

As input-file, a correctly formatted excel-sheet is needed. After choosing 'Enable Macros' of the security notice and loading the file in Excel, the whole GenAlEx menu is available via the Add-Ins tab. H_o, H_e, F_{is}, Nei's distance etc. can be calculated selecting 'Frequency' in the drop down list of GenAlEx. The settings we used with diploid codominant data are shown in Fig.22b. For HWE, the option 'Disequil' and 'HWE' in the drop down list of the menu must be selected; used settings are shown in Fig.22c. Data export to other software packages is provided by selecting 'Export Data' in the list (Fig.22a). Principle co-ordinate analysis (PCoA) is available with 'Analysis' in the menu point 'PCoA' (used settings are shown in Fig.22d). Consider that the worksheet of the distance matrix (eg. Nei's standard genetic distance; Nei 1972) is activated to perform the calculation. The menu item 'G-Statistics' enables different measurements of population differentiation (e.g. G'_{ST}, F_{ST}).



b) Codominant Frequency Options

Allele Frequency & Heterozygosity
☑ Frequency by Pop
☐ Graph All Loci ☐ Graph by Locus
☐ Graph by Pop for each Locus
☐ Frequency by Locus
☑ Het, Fstat & Poly by Pop
☐ Het, Fstat & Poly by Locus

Allelic Patterns Options
☐ Allelic Patterns
☐ Graph Pattern
☐ Allele List ☑ Private Alleles List

Multiple Pop Options
☑ Nei Distance ☐ Pairwise Fst
☑ Nei Unbiased Distance
☐ Output Pairwise Matrix
☐ Output Labeled Pairwise Matrix
☐ Output Pairwise Matrix as Table

Options
☐ Step by Step

c) Hardy-Weinberg Options

☐ Obs. V Exp. Values
☐ Graph Obs. V Exp.
☑ Summary
☐ Step by Step

d) PCoA Parameters

Input Data Type
● Tri Distance Matrix
○ Distance Matrix as Column

#Samples 16

PCoA Method
● Covariance-Standardized
○ Covariance-Not Standardized
○ Distance-Standardized
○ Distance-Not Standardized

Graph Options
☑ Data Labels ☐ Color Code Pops

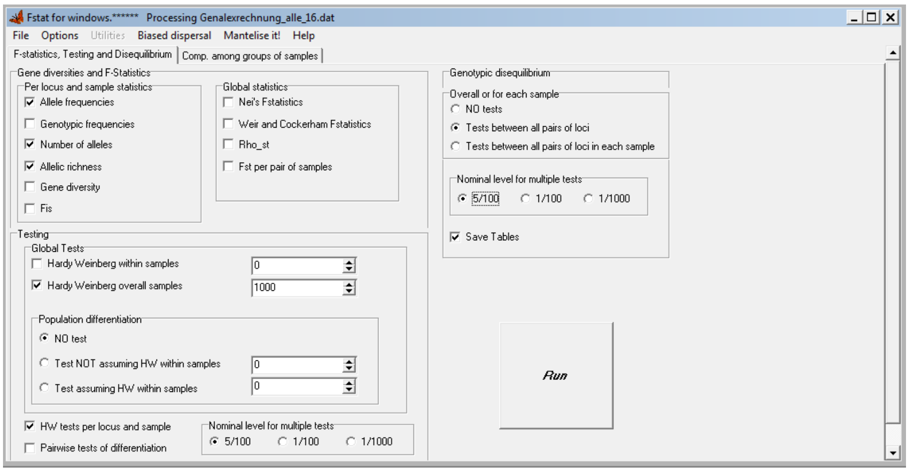
Title Example Dataset
Worksheet Prefix

Fig.22 a) GenAlEx menu options; b) settings we used for frequency based calculations, for (c) HWE and (d) the principle co-ordinate analysis.

Fstat 2.9.3.2 (Goudet 1995)

The computer package calculates different descriptive population genetic diversity-indices and statistics, as allele frequencies, observed/expected genotype frequencies, allelic richness etc. and tests potential deviations from Hardy-Weinberg equilibrium or the occurrence of linkage disequilibrium from codominant and haploid data. Moreover, Fstat computes gene diversities and differentiation statistics (F-statistics) of both Nei (1986) and Weir & Cockerham (1984), including F_{is}, F_{ST} and F_{it}. F_{is} is a measure of the within, F_{ST} of the among (Wahlund effect) and F_{it} of the global heterozygote deficit. The user can choose different options concerning tests for Hardy-Weinberg equilibrium or linkage disequilibrium such as the number of bootstraps and the level of significance. Additionally, a definition of groups within samples is also provided and the maximum processible number of individuals amounts to 200.000.

First, the user has to define the seeds of the random number generator, thereby prime numbers are found to be suitable. The input-file is created by the button ‘File conversion’ in the menu point ‘Utilities’ converting Genepop file (.gen) to Fstat format (.dat). The file is loaded by clicking ‘Open’ in the menu item ‘File’. Used settings are displayed below (Fig.23).



Gene diversities and F-Statistics

Per locus and sample statistics
☑ Allele frequencies
☐ Genotypic frequencies
☑ Number of alleles
☑ Allelic richness
☐ Gene diversity
☐ Fis

Global statistics
☐ Nei's Fstatistics
☐ Weir and Cockerham Fstatistics
☐ Rho_st
☐ Fst per pair of samples

Testing

Global Tests
☐ Hardy Weinberg within samples 0
☑ Hardy Weinberg overall samples 1000

Population differentiation
● NO test
○ Test NOT assuming HW within samples 0
○ Test assuming HW within samples 0

☑ HW tests per locus and sample
☐ Pairwise tests of differentiation

Nominal level for multiple tests
● 5/100 ○ 1/100 ○ 1/1000

Genotypic disequilibrium

Overall or for each sample
○ NO tests
● Tests between all pairs of loci
○ Tests between all pairs of loci in each sample

Nominal level for multiple tests
● 5/100 ○ 1/100 ○ 1/1000

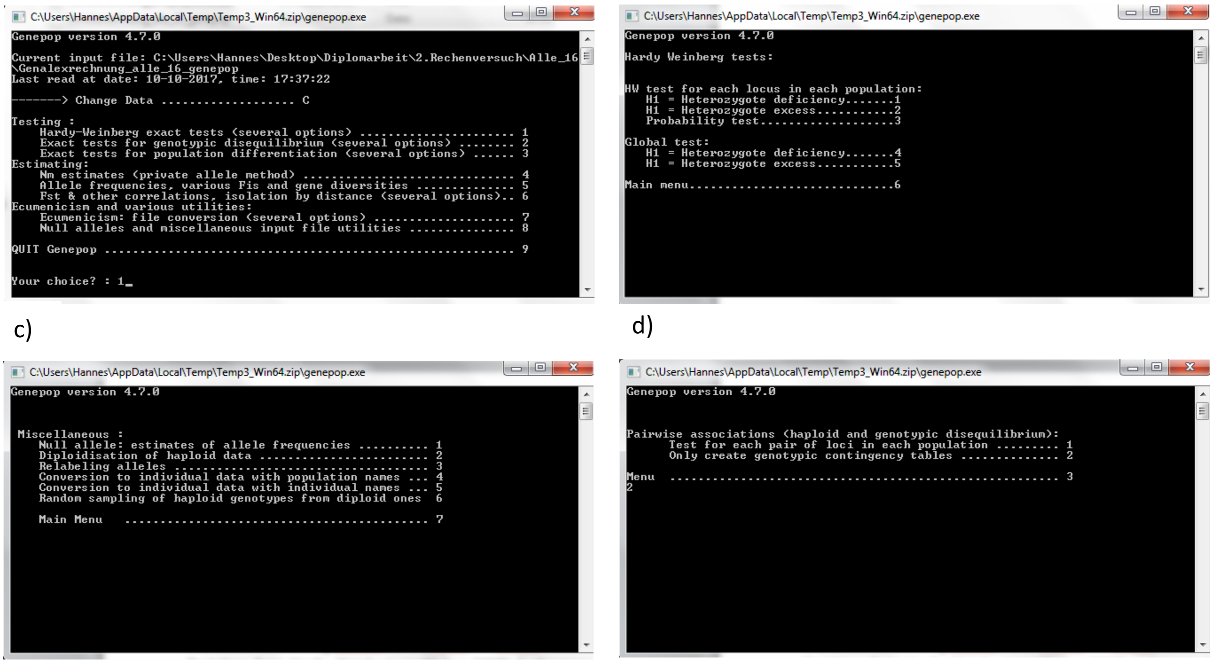
☑ Save Tables

Fig.23 User interface of Fstat.

Genepop 4.7.0 (Raymond & Rousset 1995; Rousset 2008)

Genepop is a program that implements a mixture of traditional genetic analyses, such as exact tests of Hardy-Weinberg equilibrium and genotypic disequilibrium or estimations of F-statistics and null allele frequencies etc., but also performs some additional analyses, including calculations of isolation-by-distance patterns. Additionally, the software converts the input-file to formats used by other genetic programs (Biosys, Diploidl, Linkdos). The new version is distributed both as R package and stand-alone software, the latter works from a command line and accepts only correctly formatted text files. For all exact tests the user has to define the Markov Chain parameters, which consist of the dememorisation number (minimum 100), the number of batches (minimum 10) and the number of iterations per batch (minimum 400).

The input-file, which we have created using the data export-option of GenAlEx, can be loaded by dragging it into the window of the command line by mouse. Tests of Hardy-Weinberg equilibrium as heterozygote excess or deficiency are available with the number one of the menu (Fig.24a) and either number four and five in the submenu (Fig.24b). To compute null allele frequencies, the number eight from the menu and number one of the submenu must be selected (fig.24c), respectively. Genotypic disequilibrium for each pair of loci can be calculated selecting the number one of the submenu (Fig.24d) in the menu point two. We used the Monte Carlo Markov chain simulation with 10.000 dememorisations, 100 batches and 10.000 iterations.



a)

```
Genepop version 4.7.0

Current input file: C:\Users\Hannes\Desktop\Diplomarbeit\2.Rechenversuch\Alle_16
\Genalexrechnung_alle_16_genepop
Last read at date: 10-10-2017, time: 17:37:22

-------> Change Data .................... C

Testing :
    Hardy-Weinberg exact tests (several options) ...................... 1
    Exact tests for genotypic disequilibrium (several options) ........ 2
    Exact tests for population differentiation (several options) ...... 3
Estimating:
    Nm estimates (private allele method) .............................. 4
    Allele frequencies, various Fis and gene diversities .............. 5
    Fst & other correlations, isolation by distance (several options).. 6
Ecumenicism and various utilities:
    Ecumenicism: file conversion (several options) .................... 7
    Null alleles and miscellaneous input file utilities ............... 8

QUIT Genepop .......................................................... 9


Your choice? : 1_
```

b)

```
Genepop version 4.7.0

Hardy Weinberg tests:


HW test for each locus in each population:
   H1 = Heterozygote deficiency.......1
   H1 = Heterozygote excess...........2
   Probability test...................3

Global test:
   H1 = Heterozygote deficiency.......4
   H1 = Heterozygote excess...........5

Main menu.............................6
```

c)

```
Genepop version 4.7.0



 Miscellaneous :
    Null allele: estimates of allele frequencies .......... 1
    Diploidisation of haploid data ........................ 2
    Relabeling alleles .................................... 3
    Conversion to individual data with population names ... 4
    Conversion to individual data with individual names ... 5
    Random sampling of haploid genotypes from diploid ones  6

    Main Menu   ........................................... 7
```

d)

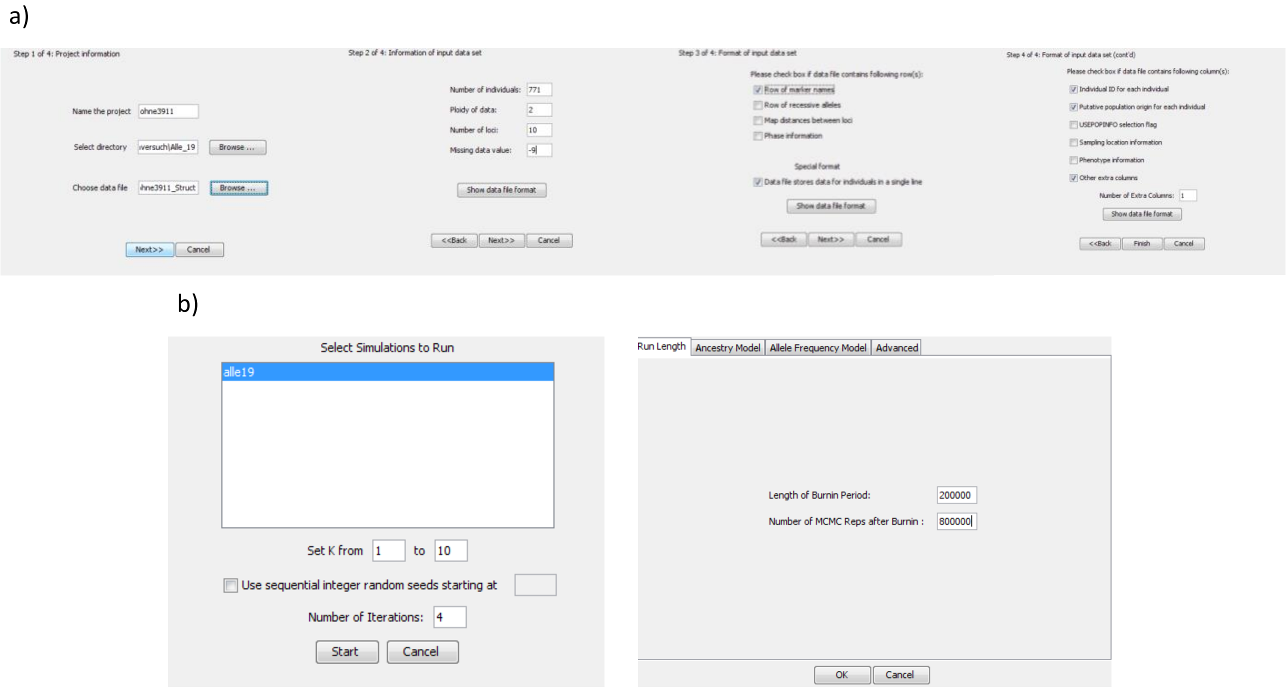
```
Genepop version 4.7.0



Pairwise associations (haploid and genotypic disequilibrium):
       Test for each pair of loci in each population ......... 1
       Only create genotypic contingency tables .............. 2

Menu  ........................................................ 3
2
```

Fig.24 a) Genpop menu options; b) computations of HWE, c) null allele frequencies and d) genotypic disequilibrium.

Structure 2.3.4 (Pritchard *et al*. 2000)

Structure uses multilocus genotype data to infer the most likely population structure and attempt to assign individuals to populations. The software uses a Bayesian clustering algorithm to pool individuals to a predefined number of clusters (named as *K* and may be unknown) taking account of minimizing deviations from Hardy-Weinberg equilibrium and gametic-phase disequilibrium within the clusters. The model does not consider a particular mutation process and it can be supplied with the most of the common genetic markers e.g. microsatellites, RFLPs (restriction fragment length polymorphisms) or SNPs (single nucleotide polymorphisms), but all loci should be unlinked and at linkage equilibrium (HWE). The Ancestry Model of the program is subdivided in four models: a) the model without admixture where each individual has its own population-information, b) the model with admixture where each individual does not have any information about population affiliation, c) the Linkage-model, which is able to deal with linked loci and d) a model that is able to take into account relevant prior information (e.g. geographic information).

The software accepts only correctly formatted text files, which we have created using the data export-option of GenAlEx. To load the text file, the option ‘New project’ from the menu item ‘File’ must be selected, thereafter the correct project and input-file information in the four steps of the project wizard notice is accessible (Fig.25a). Missing data are indicated by the value ‘-9’. Before starting the calculation, the parameter set must be defined selecting ‘New’ from the menu item ‘Parameter set’. After that the project can be started using the option ‘Start a Job’ in the menu item ‘Project’ and defining the *K*-set. The settings we used (Fig.25b) were *K*-values ranging from 2 to 10 and a run length of 800.000 iterations with a burn-in period of 200.000. Each run was repeated for four times for reasons of iteration. The bar plot is the main output of the software and can be shown with the option ‘Bar plot’ after selecting a specific run with the corresponding *K*-value. The set of different colours corresponds to the detected clusters and shows the influence of each cluster in each individual.



Step 1 of 4: Project information

Name the project: ohne3911
Select directory: ıversuch\Alle_19
Choose data file: ıhne3911_Struct

Step 2 of 4: Information of input data set

Number of individuals: 771
Ploidy of data: 2
Number of loci: 10
Missing data value: -9

Step 3 of 4: Format of input data set

Please check box if data file contains following row(s):
☑ Row of marker names
☐ Row of recessive alleles
☐ Map distances between loci
☐ Phase information

Special format
☑ Data file stores data for individuals in a single line

Step 4 of 4: Format of input data set (cont'd)

Please check box if data file contains following column(s):
☑ Individual ID for each individual
☑ Putative population origin for each individual
☐ USEPOPINFO selection flag
☐ Sampling location information
☐ Phenotype information
☑ Other extra columns
Number of Extra Columns: 1

Select Simulations to Run
alle19
Set K from 1 to 10
☐ Use sequential integer random seeds starting at
Number of Iterations: 4

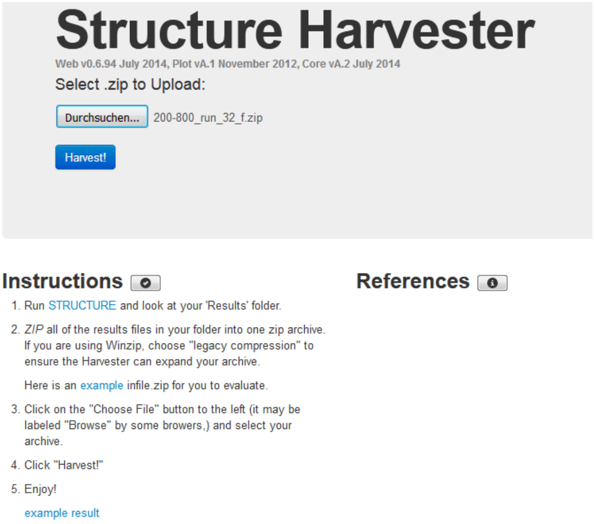
Length of Burnin Period: 200000
Number of MCMC Reps after Burnin : 800000

Fig.25 a) Four steps of the project wizard notice; b) settings we used for individual population assignment analysis.

Structure Harvester 0.6.94 (Earl & von Holdt 2012)

Structure Harvester is a web-based Python program for quickly collating, parsing and summarizing output data generated by the software Structure (Pritchard *et al*. 2000). The program visualizes likelihood values across a large set of *K*-values and iterations for easier delineation of the number of genetic groups and generates in-files for use in downstream programs (Clumpp, Distruct). In addition, Structure Harvester executes the Δ*K* method of Evanno *et al*. (2005) to detect the number of *K* groups that best fit the dataset. As results, plots of the mean likelihood values per *K* and for detecting the number of *K* groups (Fig.30), as well as a table of the Evanno output are generated.

Before starting the calculation, all the result files of the Structure 'Results' folder must be zipped into one zip archive, after that the user is recommended to upload the compressed file to start the analyses clicking the button 'Harvest!' (Fig.26). Above mentioned result-plots are shown below (Fig.30). The Evanno method can only be performed if at least three values of sequential *K* as well as three replicates are analysed and the sample standard deviation of the log likelihood values across all *K* values is non-zero.



1. Run STRUCTURE and look at your 'Results' folder.
2. *ZIP* all of the results files in your folder into one zip archive. If you are using Winzip, choose "legacy compression" to ensure the Harvester can expand your archive.

   Here is an example infile.zip for you to evaluate.
3. Click on the "Choose File" button to the left (it may be labeled "Browse" by some browers,) and select your archive.
4. Click "Harvest!"
5. Enjoy!

   example result

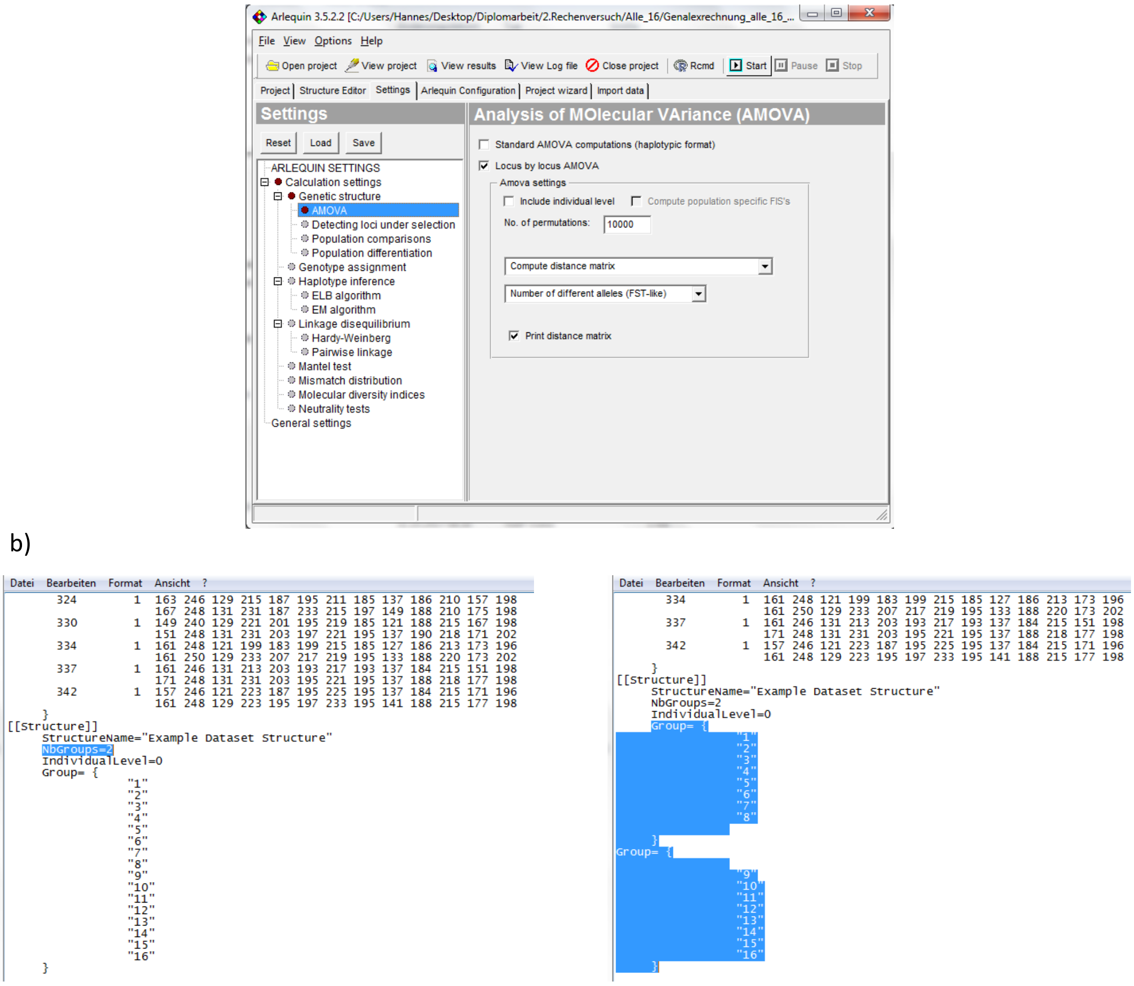
Fig.26 User interface of Structure Harvester.

Arlequin 3.5.2 (Excoffier & Lischer 2010)

The software provides the user with quiet a large set of basic genetic methods and statistical tests. Furthermore, the user-friendly graphical interface allows a rapidly selection of the different options and enables analysing several times the same data set from different viewpoints. Arlequin performs both, intra-population (e.g. HWE, LD, standard genetic indices etc.) and inter-population methods, such as population differentiation measurements (F-statistics) and especially analysis of molecular variance (AMOVA) based on both, allele size dependent (R_{ST}) and allele size independent (F_{ST}) measurements. The computer package handles with several types of genetic data, either in haploid or diploid form, and genetic markers, including SSRs, RFLPs, DNA sequences and frequency data. The updated and enhanced version 3.5 includes a newly designed command-line (Arlecore) version to handle with a large series of files and generates XML output-files that can be processed in R. All calculations are performed on the R-surface.

Arlequin accepts only correctly formatted text files, which we have created using the data export-option of GenAlEx with the setting MICROSAT in the export parameters, or the 'import dat' option of

Arlequin converting a Genepop file. For AMOVA the user can predefine a certain number of groups to be computed in the text file by separating the groups in the Editor (Fig.27b). The name of the file must have an '.arp' extension. To load the input-file, 'Open Project' on the tool bar must be selected, thereafter different analyses can be chosen in the 'Settings' tab panel. Once the analysis is selected, their parameter can be tuned on the right panel. For AMOVA we used the settings below (Fig.27a) for R_{ST} and F_{ST}, respectively.



Analysis of MOlecular VAriance (AMOVA)

☐ Standard AMOVA computations (haplotypic format)
☑ Locus by locus AMOVA

Amova settings
☐ Include individual level ☐ Compute population specific FIS's
No. of permutations: 10000
Compute distance matrix
Number of different alleles (FST-like)
☑ Print distance matrix

b)

```
      324         1  163 246 129 215 187 195 211 185 137 186 210 157 198
                     167 248 131 231 187 233 215 197 149 188 210 175 198
      330         1  149 240 129 221 201 195 219 185 121 188 215 167 198
                     151 248 131 231 203 197 221 195 137 190 218 171 202
      334         1  161 248 121 199 183 199 215 185 127 186 213 173 196
                     161 250 129 233 207 217 219 195 133 188 220 173 202
      337         1  161 246 131 213 203 193 217 193 137 184 215 151 198
                     171 248 131 231 203 195 221 195 137 188 218 177 198
      342         1  157 246 121 223 187 195 225 195 137 184 215 171 196
                     161 248 129 223 195 197 233 195 141 188 215 177 198
     }
[[Structure]]
     StructureName="Example Dataset Structure"
     NbGroups=2
     IndividualLevel=0
     Group= {
                  "1"
                  "2"
                  "3"
                  "4"
                  "5"
                  "6"
                  "7"
                  "8"
                  "9"
                  "10"
                  "11"
                  "12"
                  "13"
                  "14"
                  "15"
                  "16"
     }
```

```
      334         1  161 248 121 199 183 199 215 185 127 186 213 173 196
                     161 250 129 233 207 217 219 195 133 188 220 173 202
      337         1  161 246 131 213 203 193 217 193 137 184 215 151 198
                     171 248 131 231 203 195 221 195 137 188 218 177 198
      342         1  157 246 121 223 187 195 225 195 137 184 215 171 196
                     161 248 129 223 195 197 233 195 141 188 215 177 198
     }
[[Structure]]
     StructureName="Example Dataset Structure"
     NbGroups=2
     IndividualLevel=0
     Group= {
                  "1"
                  "2"
                  "3"
                  "4"
                  "5"
                  "6"
                  "7"
                  "8"

     }
Group= {

                  "9"
                  "10"
                  "11"
                  "12"
                  "13"
                  "14"
                  "15"
                  "16"
     }
```

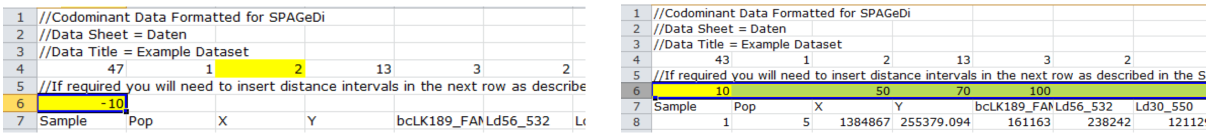
Fig.27 a) User interface of Arlequin with our settings and b) pre-definition of two groups in the text file for the AMOVA.

SPAGeDi 1.5 (Hardy & Vekemann 2002)

SPAGeDi or Spatial Pattern Analysis of Genetic Diversity is a software approach for characterising spatial genetic structure of mapped individuals or populations. The program computes various statistics ranging from genetic relatedness (e.g. kinship coefficient of Loiselle (1995)) to differentiation between individuals or populations (F_{ST}, G_{ST}, R_{ST} etc.) or estimation of inbreeding coefficients by pairwise comparison. Furthermore, it performs computations of isolation by distance and gene dispersal parameters within and among populations. The association between values computed from pairwise statistics describing genetic relatedness or differentiation and pairwise spatial distances is characterized by regressing and averaging the values for a set of predefined distance intervals. The slopes of the regression can be used to estimate the extent of gene dispersal parameters. Each statistic is computed for each locus and a multilocus weighted average. For multilocus data, the program provides a jackknife procedure over loci to generate approximate standard errors. Additionally, different permutation procedures enable to obtain relevant information about (spatial) genetic structure.

As input-file, an only correctly formatted text file is needed, which we have created using the data export-option of GenAlEx. The user has to define the number of distance classes, e.g. ‘-10’ for automatically searching of ten best fitting distance intervals, and the number of spatial coordinates, e.g. ‘2’ for using metrical coordinates (Fig.28a). Otherwise, it can be defined an optional number of distance classes and intervals (Fig.28b) or ‘-2’ as the number of spatial coordinates for longitude and latitude. The tab-delimited text file can be loaded by dragging it into the window of the command line by mouse. To calculate spatial genetic structure, we used a permutation test with the following setting series: First, we chose the number one twice for carrying out the kinship coefficient of Loiselle *et al*. (1995) at the individual level. In the next step we selected the number three for making a permutation test with the permutation options number two and three (Fig.28c) and permuted the individual sampling locations and gene copies each 10.000 times. Finally, we defined a prime number for the initial seeds of the random number generator and selected the number three of the output option to report all statistics of regression analyses. For interpreting the results, we opened the output-file with Excel and created a graph with the results of the ‘ALL LOCI’ section (Fig.28d).

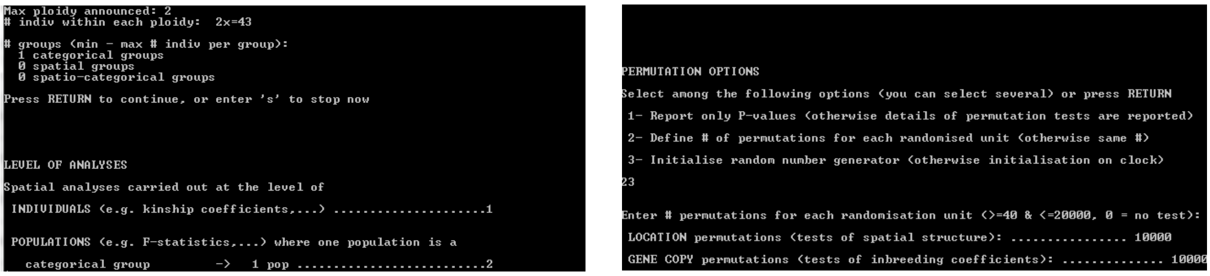
a)



1	//Codominant Data Formatted for SPAGeDi						
2	//Data Sheet = Daten						
3	//Data Title = Example Dataset						
4	47	1	2	13	3	2	
5	//If required you will need to insert distance intervals in the next row as describe						
6	-10						
7	Sample	Pop	X	Y	bcLK189_FA	Ld56_532	L

1	//Codominant Data Formatted for SPAGeDi						
2	//Data Sheet = Daten						
3	//Data Title = Example Dataset						
4	43	1	2	13	3	2	
5	//If required you will need to insert distance intervals in the next row as described in the S						
6	10		50	70	100		
7	Sample	Pop	X	Y	bcLK189_FA	Ld56_532	Ld30_550
8	1	5	1384867	255379.094	161163	238242	12112

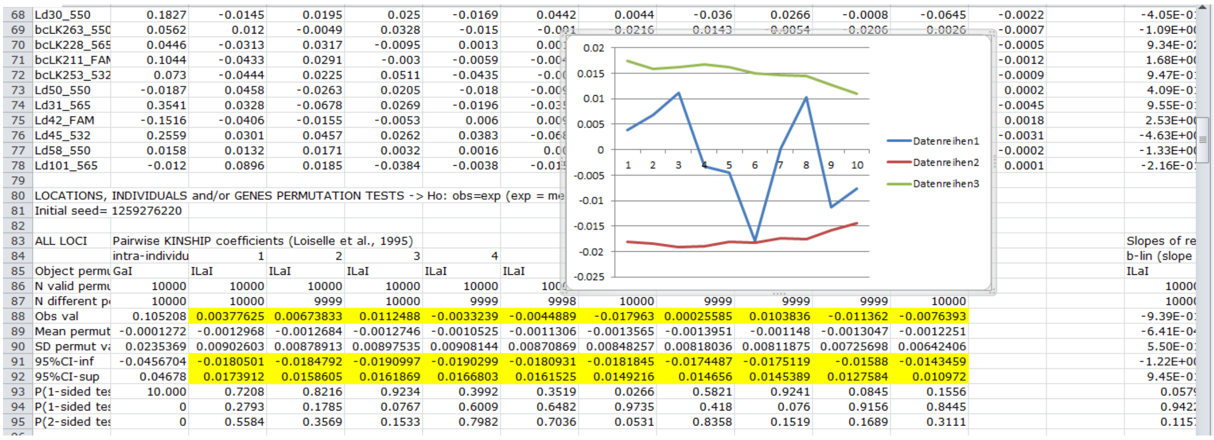
b)



```
Max ploidy announced: 2
# indiv within each ploidy:  2x=43

# groups (min - max # indiv per group):
  1 categorical groups
  0 spatial groups
  0 spatio-categorical groups

Press RETURN to continue, or enter 's' to stop now




LEVEL OF ANALYSES

Spatial analyses carried out at the level of

 INDIVIDUALS (e.g. kinship coefficients,...) .....................1


 POPULATIONS (e.g. F-statistics,...) where one population is a

   categorical group        ->   1 pop .........................2
```

```
PERMUTATION OPTIONS

Select among the following options (you can select several) or press RETURN

 1- Report only P-values (otherwise details of permutation tests are reported)

 2- Define # of permutations for each randomised unit (otherwise same #)

 3- Initialise random number generator (otherwise initialisation on clock)

23

Enter # permutations for each randomisation unit (>=40 & <=20000, 0 = no test):

 LOCATION permutations (tests of spatial structure): ................ 10000

 GENE COPY permutations (tests of inbreeding coefficients): .............. 10000
```

c)



68	Ld30_550	0.1827	-0.0145	0.0195	0.025	-0.0169	0.0442	0.0044	-0.036	0.0266	-0.0008	-0.0645	-0.0022		-4.05E-0
69	bcLK263_550	0.0562	0.012	-0.0049	0.0328	-0.015	-0.001	-0.0216	0.0143	-0.0054	-0.0206	0.0026	-0.0007		-1.09E+0
70	bcLK228_565	0.0446	-0.0313	0.0317	-0.0095	0.0013	0.00						-0.0005		9.34E-0
71	bcLK211_FAM	0.1044	-0.0433	0.0291	-0.003	-0.0059	-0.00						-0.0012		1.68E+0
72	bcLK253_532	0.073	-0.0444	0.0225	0.0511	-0.0435	-0.0						-0.0009		9.47E-0
73	Ld50_550	-0.0187	0.0458	-0.0263	0.0205	-0.018	-0.00						0.0002		4.09E-0
74	Ld31_565	0.3541	0.0328	-0.0678	0.0269	-0.0196	-0.03						-0.0045		9.55E-0
75	Ld42_FAM	-0.1516	-0.0406	-0.0155	-0.0053	0.006	0.00						0.0018		2.53E+0
76	Ld45_532	0.2559	0.0301	0.0457	0.0262	0.0383	-0.06						-0.0031		-4.63E+0
77	Ld58_550	0.0158	0.0132	0.0171	0.0032	0.0016	0.0						-0.0002		-1.33E+0
78	Ld101_565	-0.012	0.0896	0.0185	-0.0384	-0.0038	-0.01						0.0001		-2.16E-0
79															
80	LOCATIONS, INDIVIDUALS and/or GENES PERMUTATION TESTS -> Ho: obs=exp (exp = me														
81	Initial seed= 1259276220														
82															
83	ALL LOCI	Pairwise KINSHIP coefficients (Loiselle et al., 1995)													Slopes of re
84		intra-individu	1	2	3	4									b-lin (slope
85	Object permu	GaI	ILaI	ILaI	ILaI	ILaI	ILaI								ILaI
86	N valid permu	10000	10000	10000	10000	10000	100								1000
87	N different p	10000	10000	9999	10000	9999	9998	10000	9999	9999	9999	10000			1000
88	Obs val	0.105208	0.00377625	0.00673833	0.0112488	-0.0033239	-0.0044889	-0.017963	0.00025585	0.0103836	-0.011362	-0.0076393			-9.39E-0
89	Mean permut	-0.0001272	-0.0012968	-0.0012684	-0.0012746	-0.0010525	-0.0011306	-0.0013565	-0.0013951	-0.001148	-0.0013047	-0.0012251			-6.41E-0
90	SD permut va	0.0235369	0.00902603	0.00878913	0.00897535	0.00908144	0.00870869	0.00848257	0.00818036	0.00811875	0.00725698	0.00642406			5.50E-0
91	95%CI-inf	-0.0456704	-0.0180501	-0.0184792	-0.0190997	-0.0190299	-0.0180931	-0.0181845	-0.0174487	-0.0175119	-0.01588	-0.0143459			-1.22E+0
92	95%CI-sup	0.04678	0.0173912	0.0158605	0.0161869	0.0166803	0.0161525	0.0149216	0.014656	0.0145389	0.0127584	0.010972			9.45E-0
93	P(1-sided tes	10.000	0.7208	0.8216	0.9234	0.3992	0.3519	0.0266	0.5821	0.9241	0.0845	0.1556			0.057
94	P(1-sided tes	0	0.2793	0.1785	0.0767	0.6009	0.6482	0.9735	0.418	0.076	0.9156	0.8445			0.942
95	P(2-sided tes	0	0.5584	0.3569	0.1533	0.7982	0.7036	0.0531	0.8358	0.1519	0.1689	0.3111			0.115

Fig.28 a) Defining the number of distance classes (optional or automatically) and spatial coordinates; b) computation of spatial genetic structure with the kinship coefficient of Loiselle *et al*. (1995) and c) creating a graph with the yellow sections of 'ALL LOCI' results for interpreting significance of spatial structuring in Excel.

GeneClass 2.0 (Piry *et al*. 2004)

The main purpose of GeneClass is to assign or exclude populations as possible origins of individuals due to various genetic assignment criteria on the basis of multilocus genotype data. These genetic assignment and first-generation migrant detection addressing relationships, structure and classification at the individual level as well as estimates of real-time dispersal, are implemented in a user-friendly interface, which allows the treatment of large datasets. The simulation algorithms behind it are several Monte Carlo resampling methods computing which individuals are likely to be a resident or an immigrant from a given reference population.

The input-file must be in a recognised format, e.g. Genepop or Fstat files can be used and loaded via the 'Open' button. For detection of first-generation migrants the available option in the first tab with the appropriate likelihood computation (we selected *L_home*) must be chosen. For the computation we used the Bayesian method according to Baudouin & Lebrun (2000) and the Monte-Carlo resampling algorithm of Cornuet et al. (1999) with 10.000 simulated individuals and a *P*-value (type I error) threshold of 0.05.

Supplementary material

Hardy-Weinberg results by locus in all populations

Table 7 Hardy-Weinberg test for heterozygote deficit

Locus	*P*-value	SE	switches (ave.)
bcLK189_FAM	0.0002	0.0001	142131
Ld56_532	0.0001	0	213948.69
Ld30_550	0	0	106813.5
bcLK263_550	0	0	33936.06
bcLK228_565	0.0579	0.0041	74650.81
bcLK211_FAM	0.006	0.0022	21251.38
bcLK253_532	0.0776	0.0037	131097.19
Ld50_550	0	0	79796.12
Ld31_565	0	0	92517.88
Ld42_FAM	0.0033	0.0002	255687.75
Ld45_532	0	0	170127.38
Ld58_550	0	0	66346.06
Ld101_565	0.1926	0.0027	94105.06

Table 8 Hardy-Weinberg test for heterozygote excess

Locus	P-value	SE	switches (ave.)
bcLK189_FAM	0.9996	0.0001	142109.44
Ld56_532	1	0	213894.12
Ld30_550	1	0	106882.25
bcLK263_550	1	0	33955.25
bcLK228_565	0.94	0.0046	74581.69
bcLK211_FAM	0.9906	0.0017	21346.69
bcLK253_532	0.9224	0.0037	131103.75
Ld50_550	1	0	79712.38
Ld31_565	1	0	92467.44
Ld42_FAM	0.9963	0.0002	256021.12
Ld45_532	1	0	170076.94
Ld58_550	1	0	66527.94
Ld101_565	0.8116	0.0022	93994.94

Linkage-disequilibrium for all pairs of loci (Table 9)

P-value for genotypic disequilibrium
based on 1560 permutations.
Adjusted P-value for 5% nominal level is : 0.000641

	All
bcLK18 X Ld56_5	0.96282
bcLK18 X Ld30_5	0.20577
bcLK18 X bcLK26	0.03654
bcLK18 X bcLK22	0.51923
bcLK18 X bcLK21	0.53782
bcLK18 X bcLK25	0.61282
bcLK18 X Ld50_5	0.38333
bcLK18 X Ld31_5	0.14808
bcLK18 X Ld42_F	0.39295
bcLK18 X Ld45_5	0.33269
bcLK18 X Ld58_5	0.67949
bcLK18 X Ld101_	0.96282
Ld56_5 X Ld30_5	0.02308
Ld56_5 X bcLK26	0.06218
Ld56_5 X bcLK22	0.26538
Ld56_5 X bcLK21	0.06987
Ld56_5 X bcLK25	0.02756
Ld56_5 X Ld50_5	0.05064
Ld56_5 X Ld31_5	0.64231
Ld56_5 X Ld42_F	0.23013
Ld56_5 X Ld45_5	0.69167
Ld56_5 X Ld58_5	0.46923
Ld56_5 X Ld101_	0.60192
Ld30_5 X bcLK26	0.16026
Ld30_5 X bcLK22	0.75577
Ld30_5 X bcLK21	0.31026
Ld30_5 X bcLK25	0.35
Ld30_5 X Ld50_5	0.62308
Ld30_5 X Ld31_5	0.41859
Ld30_5 X Ld42_F	0.3859
Ld30_5 X Ld45_5	0.89038
Ld30_5 X Ld58_5	0.90192
Ld30_5 X Ld101_	0.475
bcLK26 X bcLK22	0.05128
bcLK26 X bcLK21	0.08333
bcLK26 X bcLK25	0.70064
bcLK26 X Ld50_5	0.32308
bcLK26 X Ld31_5	0.02179
bcLK26 X Ld42_F	0.11474
bcLK26 X Ld45_5	0.35769
bcLK26 X Ld58_5	0.00064

bcLK26 X Ld101_	0.16026
bcLK22 X bcLK21	0.01603
bcLK22 X bcLK25	0.68269
bcLK22 X Ld50_5	0.24423
bcLK22 X Ld31_5	0.19551
bcLK22 X Ld42_F	0.56538
bcLK22 X Ld45_5	0.58974
bcLK22 X Ld58_5	0.15192
bcLK22 X Ld101_	0.8609
bcLK21 X bcLK25	0.00641
bcLK21 X Ld50_5	0.48718
bcLK21 X Ld31_5	0.22436
bcLK21 X Ld42_F	0.22756
bcLK21 X Ld45_5	0.03269
bcLK21 X Ld58_5	0.57308
bcLK21 X Ld101_	0.39872
bcLK25 X Ld50_5	0.01603
bcLK25 X Ld31_5	0.91346
bcLK25 X Ld42_F	0.11923
bcLK25 X Ld45_5	0.61474
bcLK25 X Ld58_5	0.08526
bcLK25 X Ld101_	0.52179
Ld50_5 X Ld31_5	0.81795
Ld50_5 X Ld42_F	0.36923
Ld50_5 X Ld45_5	0.0109
Ld50_5 X Ld58_5	0.08846
Ld50_5 X Ld101_	0.45833
Ld31_5 X Ld42_F	0.10897
Ld31_5 X Ld45_5	0.30192
Ld31_5 X Ld58_5	0.00385
Ld31_5 X Ld101_	0.4109
Ld42_F X Ld45_5	0.4
Ld42_F X Ld58_5	0.72115
Ld42_F X Ld101_	0.62692
Ld45_5 X Ld58_5	0.01795
Ld45_5 X Ld101_	0.85321
Ld58_5 X Ld101_	0.36923

Allelic richness per locus and population for 13 nuclear microsatellites (Table 10)

Allelic Richness per locus and population based on min. sample size of 36 diploid individuals

	R1(Adult)	R1(Juv.)	R2(Adult)	R2(Juv.)	R3(Adult)	R3(Juv.)	R4(Adult)	R4(Juv.)	ST5	ST6	ST7	ST8	T9	T10	T11	T12
bcLK18	6.986	7.497	5.837	6.923	8.796	10.529	8.604	5.999	9.675	8.858	8.697	9.357	9.907	7.847	11.338	10.64
Ld56_5	5.946	8.147	3.837	3.000	7.000	7.000	6.963	5.982	8.649	6.939	7.921	7.720	7.412	6.719	6.719	7.862
Ld30_5	5.565	7.476	6.819	4.947	11.230	8.661	5.981	8.699	10.995	11.128	9.666	8.713	8.507	8.084	9.210	7.565
bcLK26	16.224	14.850	12.645	12.835	19.260	17.502	15.508	15.289	18.402	18.700	18.061	18.557	17.309	17.878	17.631	18.079
bcLK22	13.186	11.608	11.666	11.754	11.596	12.533	12.957	12.665	10.824	12.481	12.310	11.632	8.946	13.043	12.502	10.644
bcLK21	15.880	17.970	11.299	11.687	15.124	11.380	14.166	19.497	16.908	15.336	13.382	14.045	14.609	14.309	14.035	12.315
bcLK25	7.000	8.499	5.812	5.923	12.385	10.363	9.636	9.910	11.858	11.717	13.428	10.694	10.681	10.618	11.871	10.921
Ld50_5	11.905	14.318	10.479	8.995	10.322	8.182	12.448	12.326	9.166	7.436	8.598	9.082	7.159	7.399	7.847	7.400
Ld31_5	9.421	8.628	5.991	5.000	10.386	9.066	9.985	8.763	11.239	8.174	10.941	9.674	9.026	8.333	9.671	9.576
Ld42_F	3.988	3.999	2.837	2.000	5.962	4.996	3.636	3.734	4.000	4.922	5.618	4.000	4.992	4.995	4.000	4.996
Ld45_5	5.755	4.953	3.998	4.947	7.562	6.766	5.818	7.672	6.931	8.699	7.287	6.845	7.388	8.358	5.980	5.734
Ld58_5	9.415	10.068	6.996	7.000	14.587	13.453	10.209	9.994	14.227	12.935	14.981	12.062	11.219	13.038	15.311	12.118
Ld101_	3.711	1.999	1.975	2.000	4.762	3.927	2.969	3.979	4.859	4.754	4.435	3.700	4.915	2.720	4.917	3.927
overall	8.845	9.232	6.938	6.693	10.690	9.566	9.145	9.578	10.595	10.160	10.410	9.699	9.390	9.488	10.079	9.367

Spatial genetic structure of 16 populations (Fig.29)

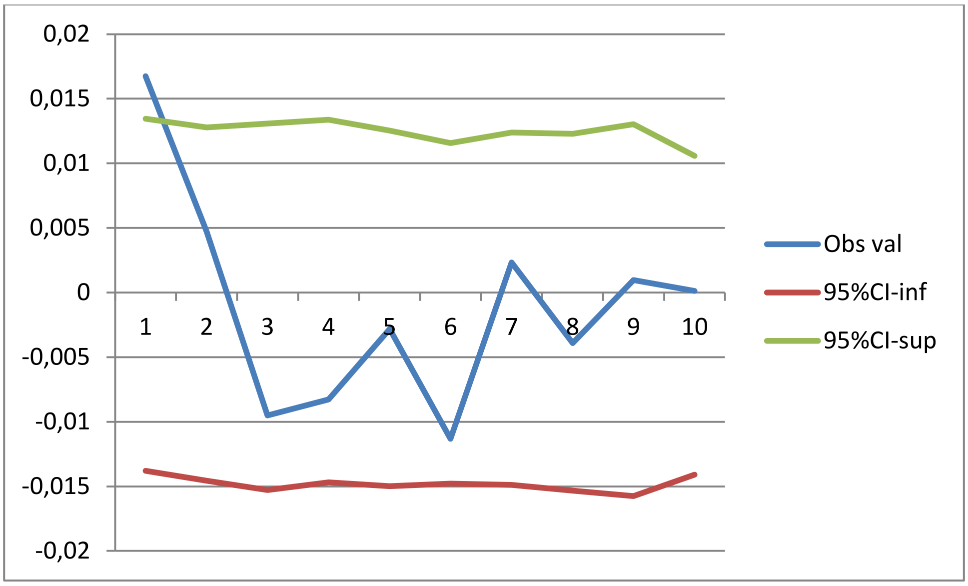


Fig.29a Spatial structuring of population R1(Adult).

Dist. classes	1	2	3	4	5	6	7	8	9	10
Max distance [m]	81	163	222	304	472	586	677	733	821	1155
Mean distance [m]	45	125	192	261	375	532	641	703	775	917

R1(Juv.)

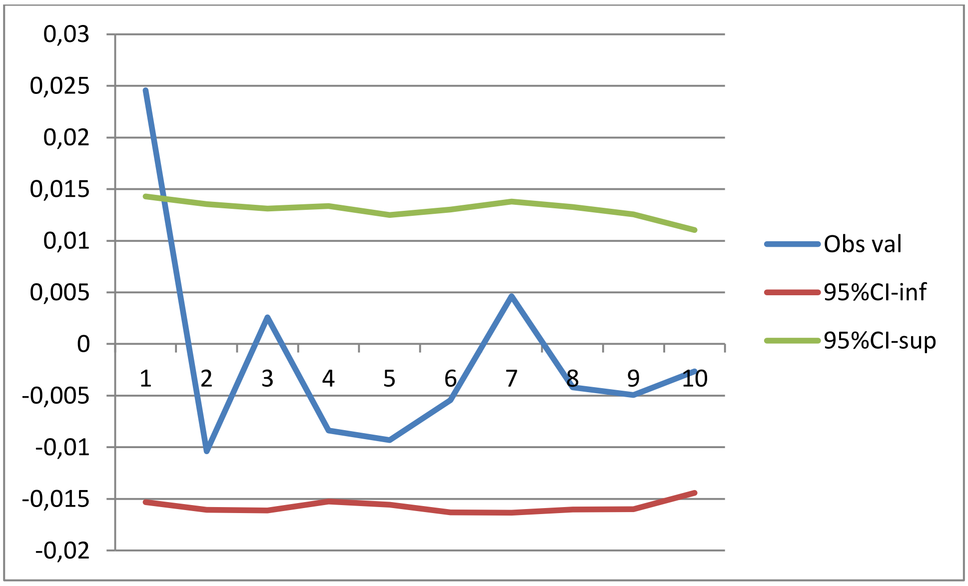


Fig.29b Spatial structuring of population R1(Juv.).

Dist. classes	1	2	3	4	5	6	7	8	9	10
Max distance [m]	100	159	222	326	526	625	685	760	859	1518
Mean distance[m]	52	131	191	270	437	575	657	720	795	1104

R2(Adult)

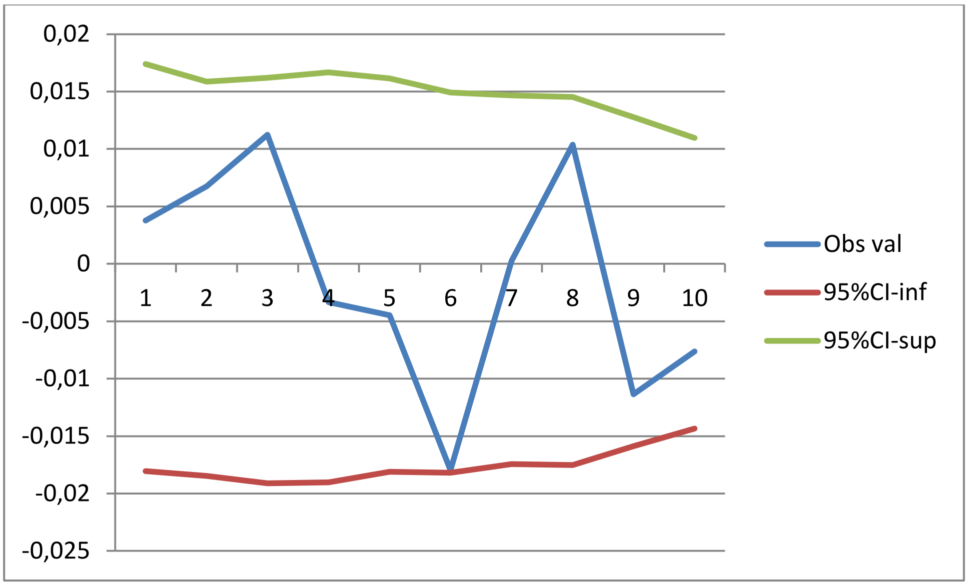


Fig.29c Spatial structuring of population R2(Adult).

Dist. classes	1	2	3	4	5	6	7	8	9	10
Max distance [m]	100	181	270	351	438	525	715	891	1077	1738
Mean distance [m]	50	147	218	307	389	481	609	801	983	1317

R2(Juv.)

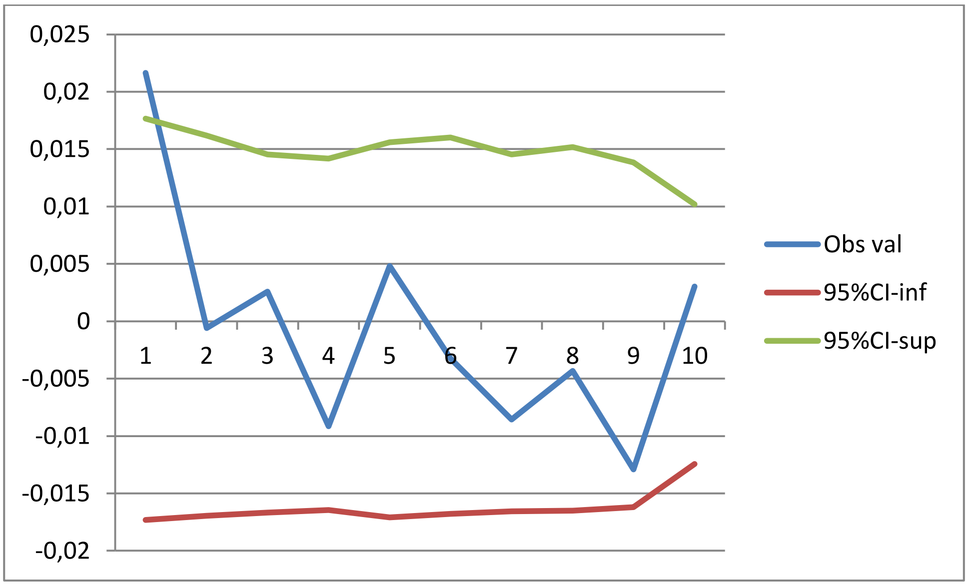


Fig.29d Spatial structuring of population R2(Juv.).

Dist. classes	1	2	3	4	5	6	7	8	9	10
Max distance [m]	72	161	236	298	401	452	492	529	606	1124
Mean distance [m]	27	116	207	261	360	420	477	509	565	861

R3(Adult)

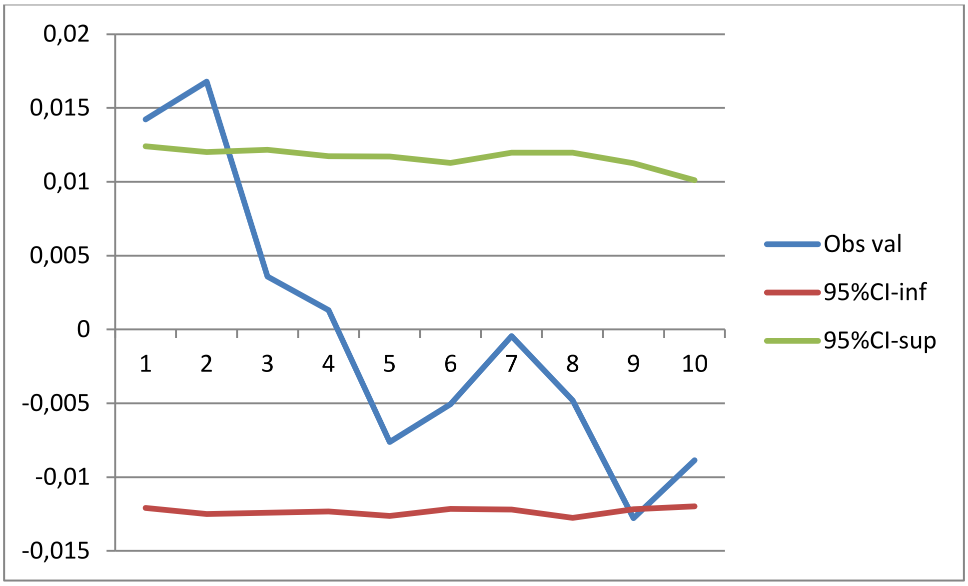


Fig.29e Spatial structuring of population R3(Adult).

Dist. classes	1	2	3	4	5	6	7	8	9	10
Max distance [m]	58	92	122	155	190	219	264	322	393	557
Mean distance [m]	39	77	107	140	175	202	241	292	364	447

R3(Juv.)

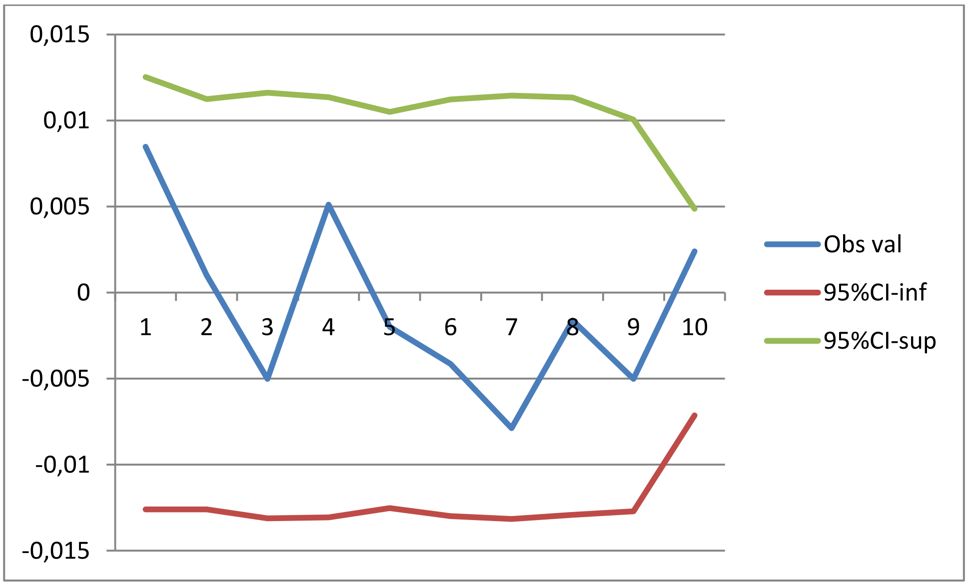


Fig.29f Spatial structuring of population R3(Juv.).

Dist. classes	1	2	3	4	5	6	7	8	9	10
Max distance [m]	12	20	28	41	56	74	83	92	147	249
Mean distance [m]	7	17	24	34	47	67	80	87	102	190

R4(Adult)

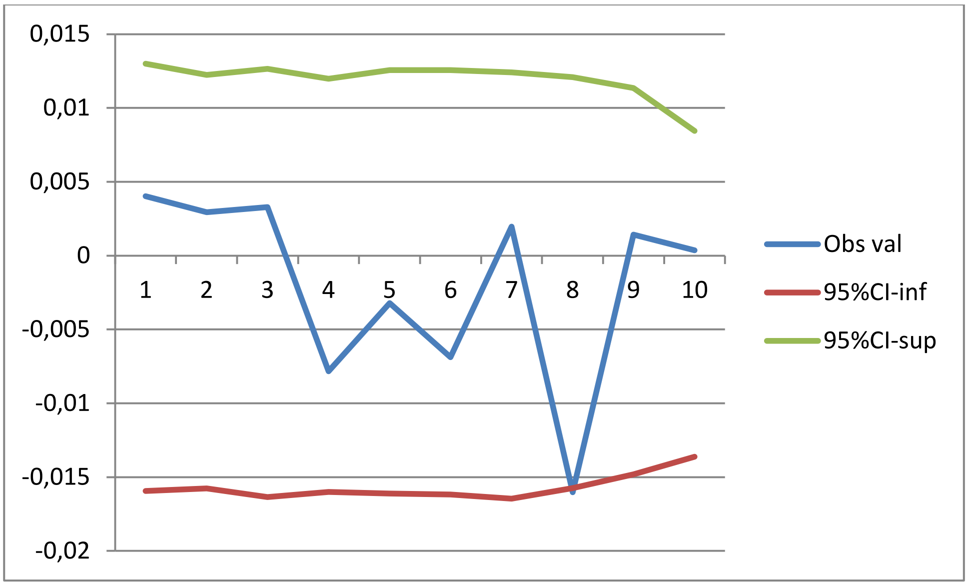


Fig.29g Spatial structuring of population R4(Adult).

Dist. classes	1	2	3	4	5	6	7	8	9	10
Max distance [m]	114	220	311	438	564	712	865	1130	1510	2587
Mean distance [m]	73	163	263	369	501	637	785	989	1328	1944

R4(Juv.)

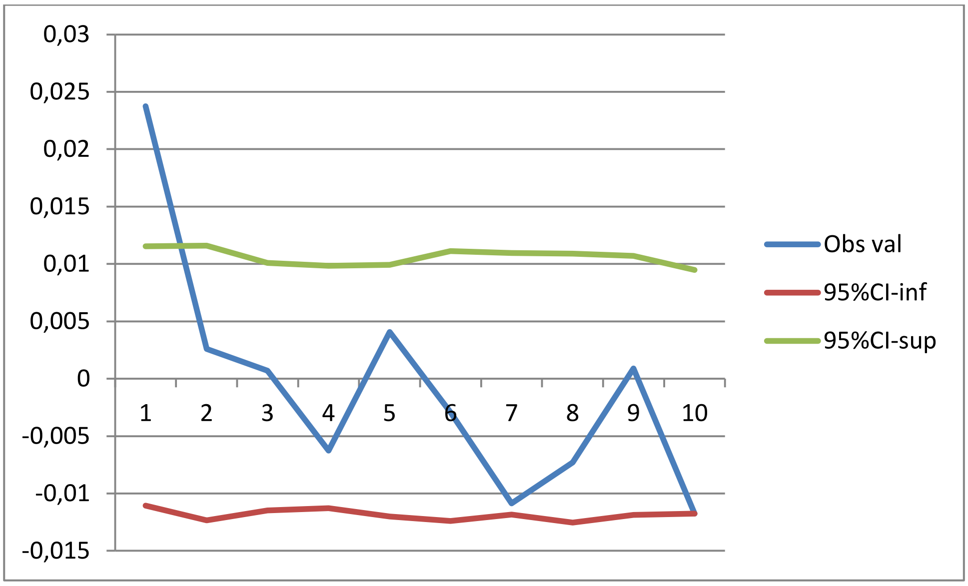


Fig.29h Spatial structuring of population R4(Juv.).

Dist. classes	1	2	3	4	5	6	7	8	9	10
Max distance [m]	11	43	191	360	377	432	488	582	849	1181
Mean distance [m]	5	20	98	292	370	400	466	523	722	923

ST5

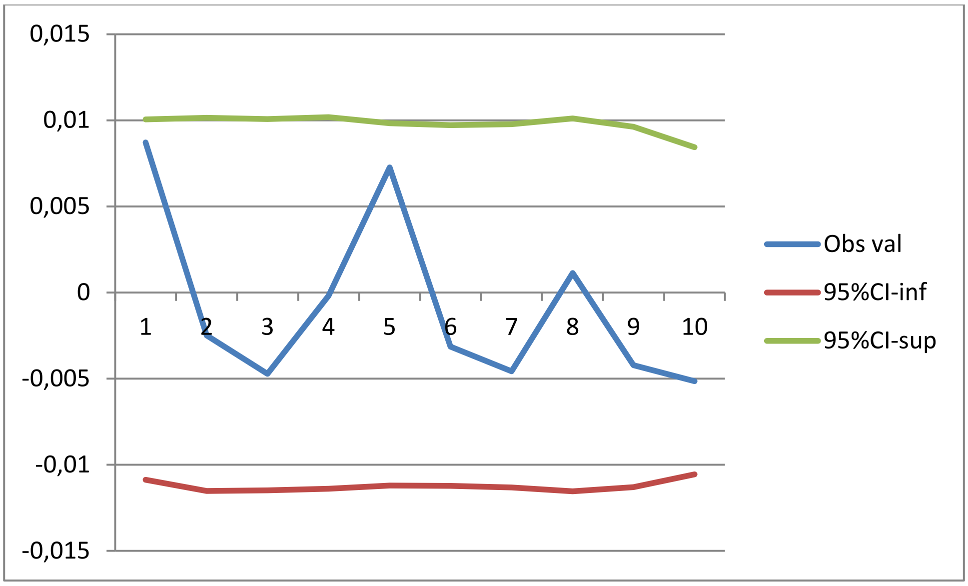


Fig.29i Spatial structuring of population ST5.

Dist. classes	1	2	3	4	5	6	7	8	9	10
Max distance [m]	73	111	144	179	239	302	374	430	497	680
Mean distance [m]	50	92	127	162	208	270	341	402	462	543

ST6

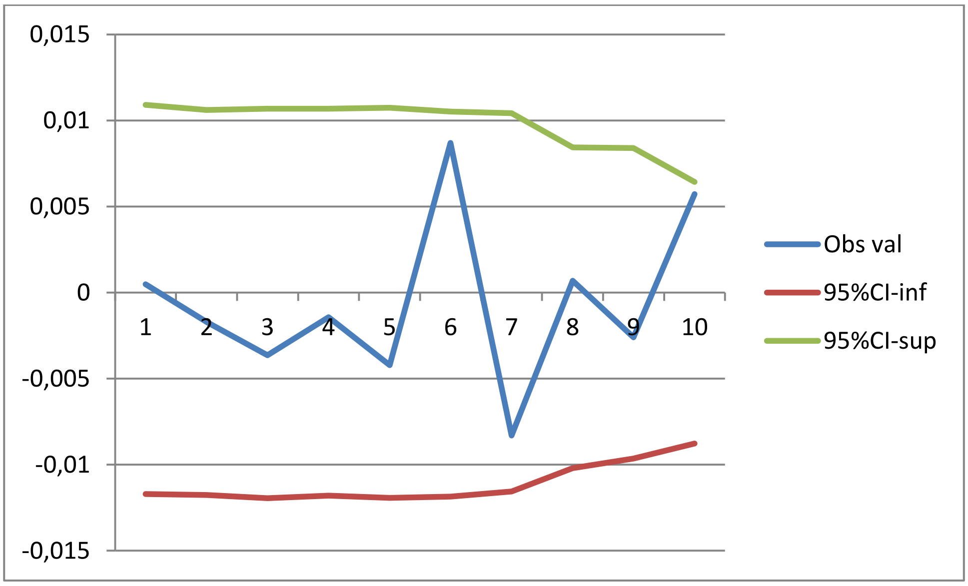


Fig.29j Spatial structuring of population ST6.

Dist. classes	1	2	3	4	5	6	7	8	9	10
Max distance [m]	38	57	75	92	113	144	192	269	428	582
Mean distance [m]	27	49	67	84	101	128	166	232	350	487

ST7

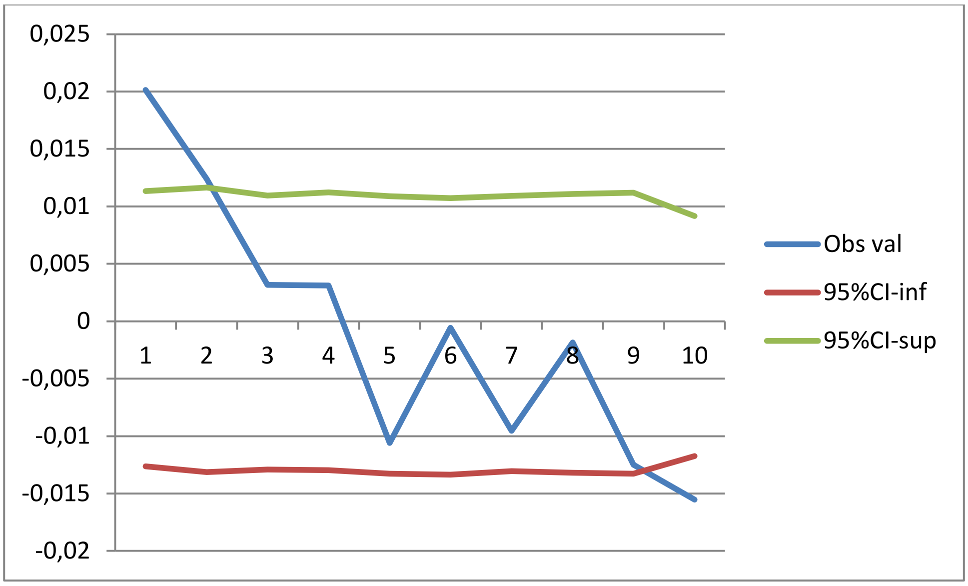


Fig.29k Spatial structuring of population ST7.

Dist. classes	1	2	3	4	5	6	7	8	9	10
Max distance [m]	70	113	148	185	217	247	277	329	401	526
Mean distance [m]	47	92	130	166	202	233	261	301	366	457

ST8

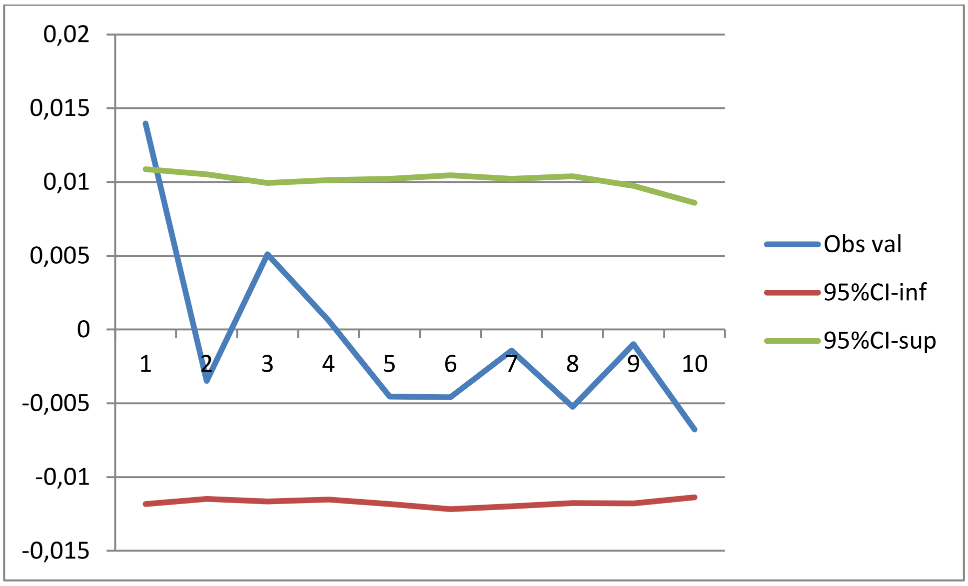


Fig.29l Spatial structuring of population ST8.

Dist. classes	1	2	3	4	5	6	7	8	9	10
Max distance [m]	133	328	461	542	676	796	997	1170	1471	1929
Mean distance [m]	70	227	404	499	605	732	879	1089	1277	1696

T9

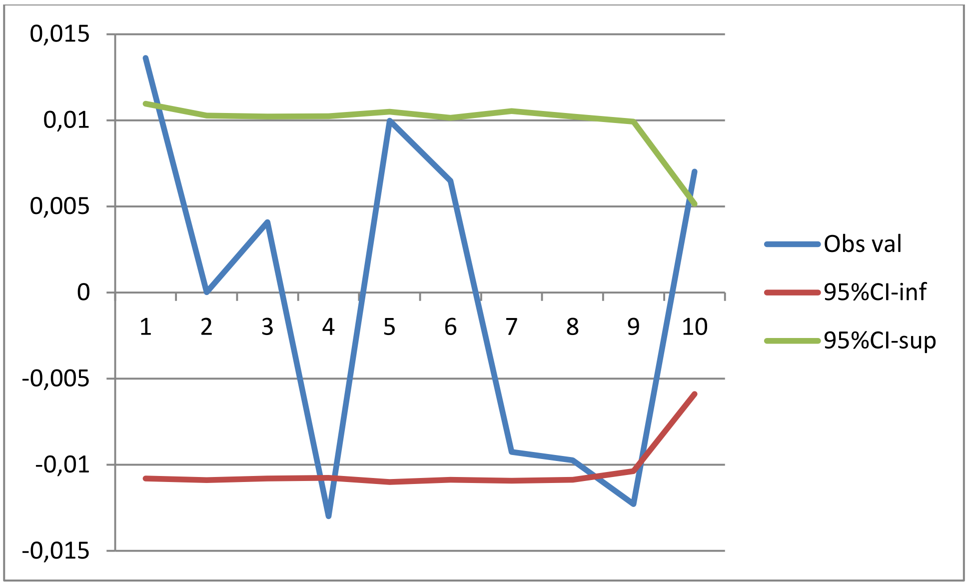


Fig.29m Spatial structuring of population T9.

Dist. classes	1	2	3	4	5	6	7	8	9	10
Max distance [m]	67	107	139	171	204	240	291	357	491	2372
Mean distance [m]	45	87	122	153	187	221	265	325	410	1711

T10

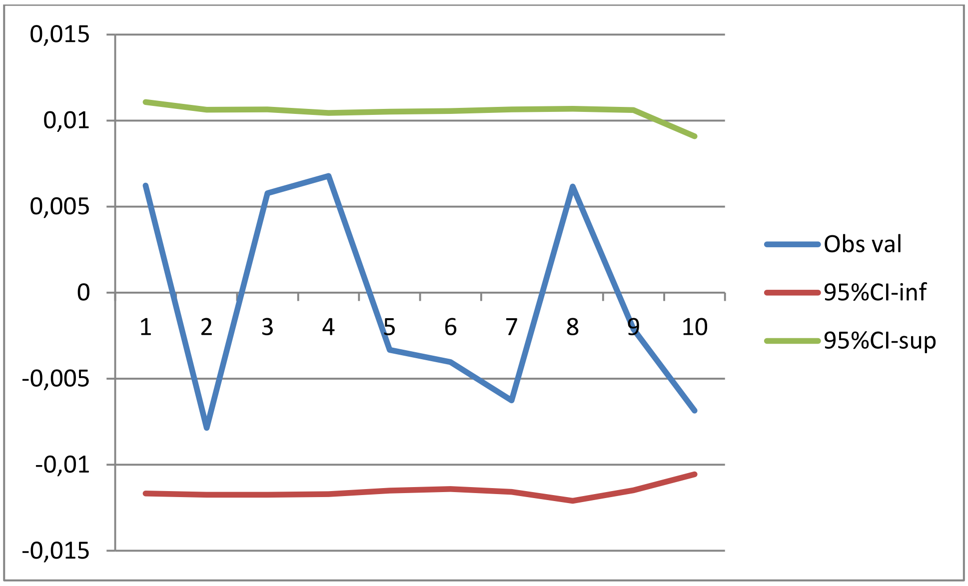


Fig.29n Spatial structuring of population T10.

Dist. classes	1	2	3	4	5	6	7	8	9	10
Max distance [m]	107	181	234	281	325	382	445	504	562	698
Mean distance [m]	67	141	209	258	303	354	413	476	531	603

T11

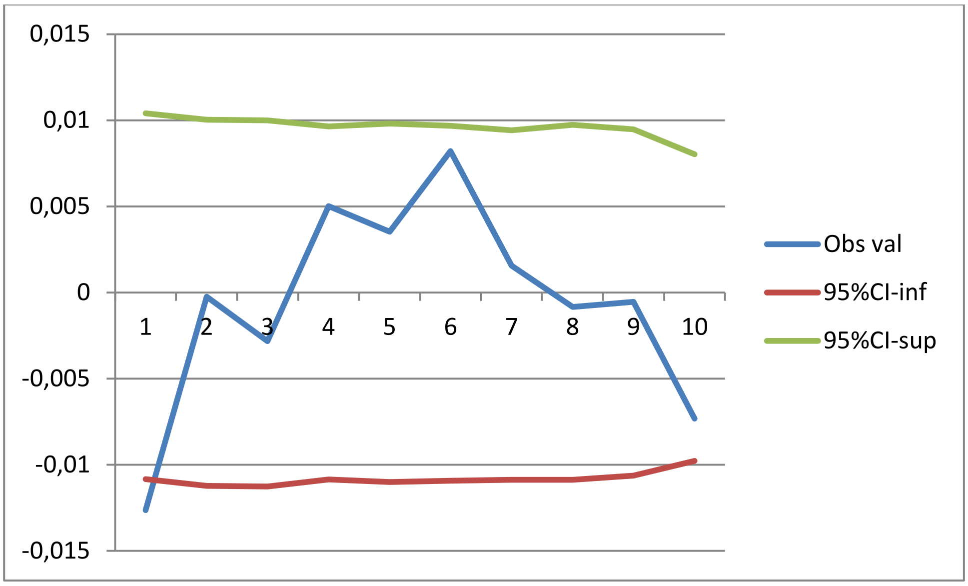


Fig.29o Spatial structuring of population T11.

Dist. classes	1	2	3	4	5	6	7	8	9	10
Max distance [m]	168	278	390	502	613	723	873	1035	1217	2023
Mean distance [m]	108	225	333	443	552	661	797	957	1118	1515

T12

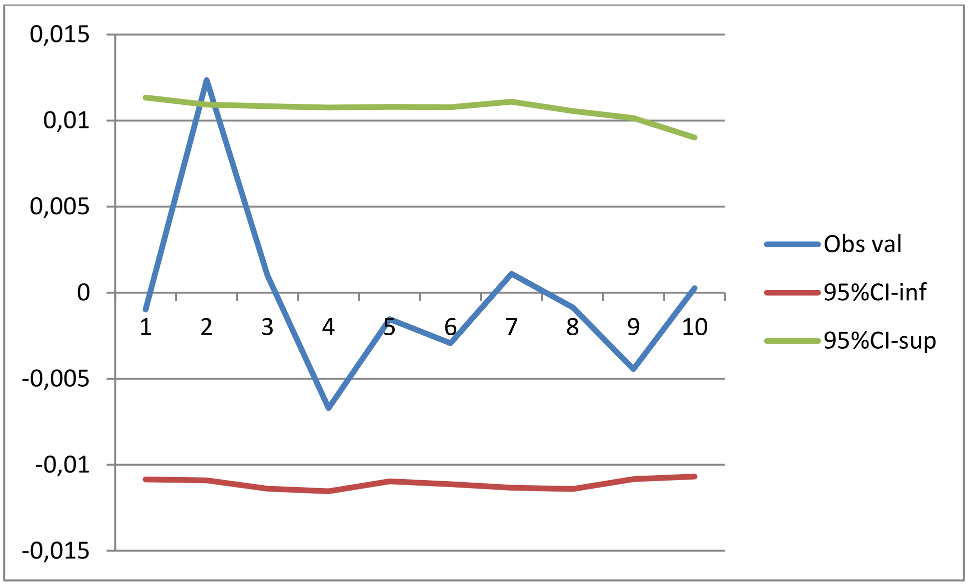


Fig.29p Spatial structuring of population T12.

Dist. classes	1	2	3	4	5	6	7	8	9	10
Max distance [m]	136	235	322	407	497	610	738	917	1059	1509
Mean distance [m]	83	187	280	363	451	554	677	820	993	1211

Genetic distance

Table 11 Pairwise population matrix of Nei's standard genetic distance (Nei 1972)

	R1(Adult)	R1(Juv.)	R2(Adult)	R2(Juv.)	R3(Adult)	R3(Juv.)	R4(Adult)	R4(Juv.)	ST5	ST6	ST7	ST8	T9	T10	T11	T12
R1(Adult)	0.000															
R1(Juv.)	0.020	0.000														
R2(Adult)	0.232	0.254	0.000													
R2(Juv.)	0.242	0.244	0.026	0.000												
R3(Adult)	0.551	0.528	0.516	0.515	0.000											
R3(Juv.)	0.570	0.532	0.557	0.568	0.047	0.000										
R4(Adult)	0.103	0.093	0.228	0.216	0.505	0.509	0.000									
R4(Juv.)	0.104	0.095	0.197	0.191	0.510	0.532	0.038	0.000								
ST5	0.624	0.600	0.546	0.539	0.082	0.090	0.585	0.576	0.000							
ST6	0.649	0.611	0.590	0.567	0.108	0.121	0.588	0.577	0.057	0.000						
ST7	0.615	0.583	0.515	0.514	0.110	0.134	0.565	0.566	0.069	0.084	0.000					
ST8	0.644	0.600	0.594	0.567	0.086	0.085	0.580	0.592	0.071	0.109	0.125	0.000				
T9	0.592	0.550	0.579	0.577	0.057	0.075	0.517	0.520	0.088	0.111	0.146	0.088	0.000			
T10	0.643	0.614	0.575	0.573	0.049	0.090	0.591	0.588	0.073	0.090	0.114	0.084	0.074	0.000		
T11	0.597	0.565	0.574	0.564	0.054	0.068	0.552	0.535	0.077	0.107	0.122	0.087	0.057	0.078	0.000	
T12	0.672	0.640	0.637	0.622	0.046	0.080	0.610	0.612	0.080	0.090	0.119	0.090	0.069	0.060	0.061	0.000

Table 12 Pairwise population matrix of Nei's unbiased genetic distance (Nei 1978)

	R1(Adult)	R1(Juv.)	R2(Adult)	R2(Juv.)	R3(Adult)	R3(Juv.)	R4(Adult)	R4(Juv.)	ST5	ST6	ST7	ST8	T9	T10	T11	T12
R1(Adult)	0.000															
R1(Juv.)	0.000	0.000														
R2(Adult)	0.210	0.233	0.000													
R2(Juv.)	0.218	0.220	0.004	0.000												
R3(Adult)	0.520	0.497	0.488	0.484	0.000											
R3(Juv.)	0.543	0.505	0.533	0.541	0.013	0.000										
R4(Adult)	0.076	0.066	0.204	0.190	0.471	0.480	0.000									
R4(Juv.)	0.076	0.068	0.173	0.164	0.476	0.503	0.008	0.000								
ST5	0.595	0.571	0.520	0.509	0.045	0.058	0.553	0.543	0.000							
ST6	0.621	0.583	0.564	0.539	0.073	0.090	0.557	0.546	0.023	0.000						
ST7	0.587	0.556	0.489	0.486	0.074	0.103	0.534	0.535	0.036	0.052	0.000					
ST8	0.615	0.572	0.569	0.539	0.051	0.054	0.549	0.561	0.038	0.077	0.093	0.000				
T9	0.564	0.522	0.554	0.549	0.022	0.044	0.487	0.489	0.055	0.078	0.114	0.056	0.000			
T10	0.616	0.588	0.551	0.546	0.015	0.061	0.562	0.559	0.042	0.060	0.084	0.053	0.044	0.000		
T11	0.569	0.537	0.549	0.537	0.019	0.038	0.522	0.505	0.044	0.076	0.091	0.055	0.025	0.048	0.000	
T12	0.644	0.614	0.613	0.595	0.011	0.051	0.580	0.583	0.048	0.059	0.088	0.059	0.038	0.031	0.031	0.000

Pairwise F_{ST} and R_{ST} values

Table 13 Pairwise R_{ST} values of 16 *Larix decidua* populations

Distance method: Sum of squared size difference (RST)

	R1(Adult	R1(Juv.)	R2(Adult)	R2(Juv.)	R3(Adult)	R3(Juv.)	R4(Adult)	R4(Juv.)	ST5	ST6	ST7	ST8	T9	T10	T11	T12
R1(Adult)	0.00000															
R1(Juv.)	-0.00470-	0.00000														
R2(Adult)	0.05356*	0.06310*	0.00000													
R2(Juv.)	0.04136*	0.03802*	0.00461-	0.00000												
R3(Adult)	0.10653*	0.10450*	0.03738*	0.04553*	0.00000											
R3(Juv.)	0.13559*	0.13654*	0.05226*	0.06567*	0.00520-	0.00000										
R4(Adult)	0.05774*	0.06204*	0.02173*	0.01237-	0.05106*	0.05682*	0.00000									
R4(Juv.)	0.01547*	0.02473*	0.01547*	0.00959-	0.06331*	0.08924*	0.01136-	0.00000								
ST5	0.14096*	0.14040*	0.06572*	0.07023*	0.00834-	0.01747*	0.04856*	0.07927*	0.00000							
ST6	0.09815*	0.09467*	0.03710*	0.03462*	0.00072-	0.01983*	0.03112*	0.04448*	0.00088-	0.00000						
ST7	0.12929*	0.12261*	0.08448*	0.07272*	0.02703*	0.05339*	0.06428*	0.08435*	0.02647*	0.02523*	0.00000					
ST8	0.11968*	0.11185*	0.05020*	0.05489*	0.00209-	0.02264*	0.05830*	0.07221*	0.01545*	0.00447-	0.04999*	0.00000				
T9	0.15675*	0.15435*	0.06087*	0.08035*	0.00030-	0.01756*	0.08065*	0.10032*	0.01575*	0.01545*	0.04871*	0.00240-	0.00000			
T10	0.13311*	0.14141*	0.04506*	0.07572*	0.01146-	0.04166*	0.08561*	0.07901*	0.03522*	0.02611*	0.07876*	0.02691*	0.01588*	0.00000		
T11	0.11565*	0.11579*	0.02747*	0.03893*	-0.00505-	0.01778*	0.05267*	0.06052*	0.01941*	0.00414-	0.03819*	0.00877-	0.00420-	0.00961-	0.00000	
T12	0.13384*	0.13061*	0.05171*	0.05894*	-0.00021-	0.01063*	0.04361*	0.07291*	0.00337-	0.00090-	0.01367*	0.01257*	0.00578-	0.03650*	0.00642-	0.00000

*, significant values at P <0.05 level; -, not significant values.

Table 14 Pairwise F_{ST} values of 16 *Larix decidua* populations

Distance method: No. of different alleles (FST)

	R1(Adult)	R1(Juv.)	R2(Adult)	R2(Juv.)	R3(Adult)	R3(Juv.)	R4(Adult)	R4(Juv.)	ST5	ST6	ST7	ST8	T9	T10	T11	T12
R1(Adult)	0.00000															
R1(Juv.)	- 0.00195-	0.00000														
R2(Adult)	0.09102*	0.09852*	0.00000													
R2(Juv.)	0.08614*	0.08715*	0.00298-	0.00000												
R3(Adult)	0.12622*	0.12345*	0.14905*	0.13600*	0.00000											
R3(Juv.)	0.13892*	0.13333*	0.16549*	0.15492*	0.00484*	0.00000										
R4(Adult)	0.02832*	0.02552*	0.08691*	0.07504*	0.11142*	0.12167*	0.00000									
R4(Juv.)	0.02791*	0.02571*	0.07446*	0.06429*	0.10514*	0.11869*	0.00344-	0.00000								
ST5	0.13899*	0.13650*	0.15581*	0.14172*	0.01227*	0.01814*	0.12575*	0.11687*	0.00000							
ST6	0.14682*	0.14218*	0.16729*	0.15050*	0.02058*	0.02775*	0.13024*	0.12111*	0.00713*	0.00000						
ST7	0.14110*	0.13722*	0.15324*	0.14063*	0.02073*	0.03162*	0.12601*	0.11881*	0.01062*	0.01571*	0.00000					
ST8	0.14411*	0.13870*	0.16560*	0.14822*	0.01436*	0.01744*	0.12736*	0.12169*	0.01095*	0.02238*	0.02653*	0.00000				
T9	0.13494*	0.12930*	0.16119*	0.14807*	0.00621*	0.01396*	0.11565*	0.10929*	0.01551*	0.02248*	0.03175*	0.01619*	0.00000			
T10	0.15069*	0.14718*	0.16850*	0.15562*	0.00563*	0.02009*	0.13560*	0.12778*	0.01359*	0.01909*	0.02596*	0.01691*	0.01404*	0.00000		
T11	0.13964*	0.13542*	0.16436*	0.15006*	0.00612*	0.01252*	0.12525*	0.11566*	0.01332*	0.02279*	0.02675*	0.01667*	0.00782*	0.01565*	0.00000	
T12	0.15391*	0.15037*	0.17884*	0.16334*	0.00430*	0.01664*	0.13761*	0.13023*	0.01441*	0.01793*	0.02588*	0.01814*	0.01206*	0.01028*	0.00998*	0.00000

*, significant values at $P < 0.05$ level; -, not significant values.

AMOVA results

Table 15 Groups according to PCoA and UPGMA

	FST			RST		
Source of variation	Sum of squares	Variance components	Percentage variation	Sum of squares	Variance components	Percentage variation
Adults						
Among groups	316.63	0.67	11.98	22032.89	41.63	5.89
Among populations within groups	119.82	0.09	1.57	18240.53	14.20	2.01
Within populations	5481.93	4.83	86.45	737926.39	650.40	92.10
Total	**5918.37**	**5.59**		**778199.80**	**706.22**	
Juveniles						
Among groups	41.59	0.24	4.87	2192.43	-4.20	-0.52
Among populations within groups	16.70	0.13	2.57	2953.66	22.32	2.73
Within populations	1683.45	4.57	92.56	213551.95	798.14	97.78
Total	**1275.85**	**4.93**		**218698.04**	**816.25**	

Table 16 Groups according to geographical proximity

	FST			RST		
Source of variation	Sum of squares	Variance components	Percentage variation	Sum of squares	Variance components	Percentage variation
Adults						
Among groups	190.91	0.34	6.33	13512.61	22.18	3.20
Among populations within groups	245.54	0.21	3.83	26760.80	21.13	3.05
Within populations	5481.93	4.83	89.84	737926.39	650.40	93.76
Total	**5918.37**	**5.38**		**778199.80**	**693.71**	

ΔK and LnP(K) method of Evanno et al. (2005)(Fig.30)

All 16 *Larix decidua* populations

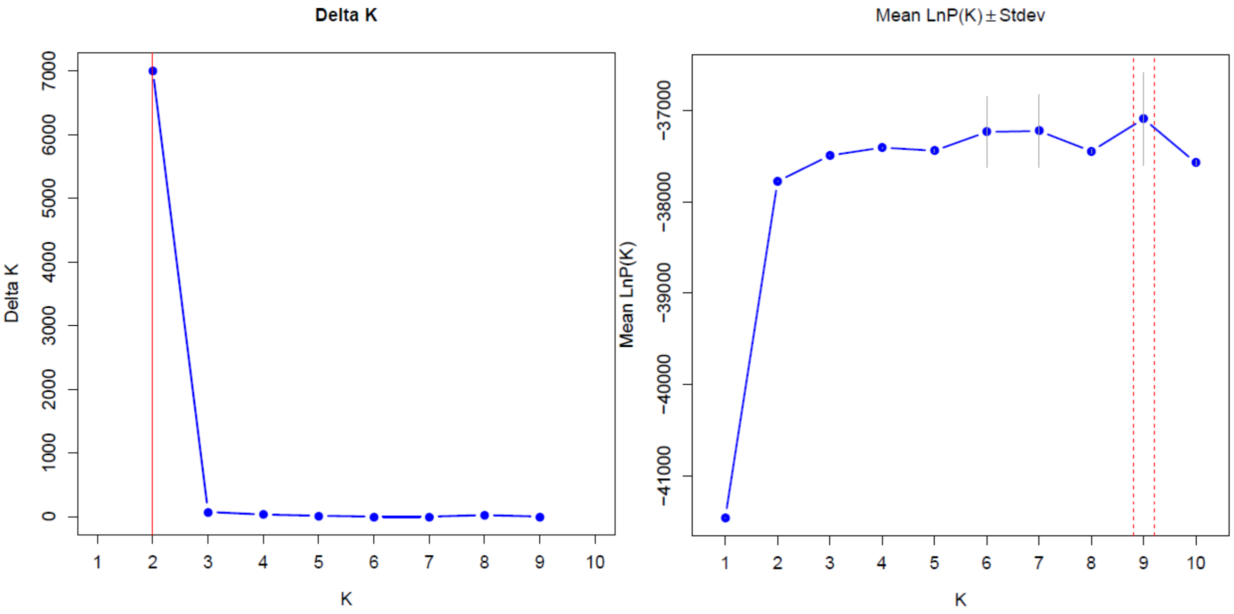


Fig.30a Plots for detecting the most appropriate number of clusters (*K*) in all 16 *Larix decidua* populations.

Within Tyrolean populations (including R3)

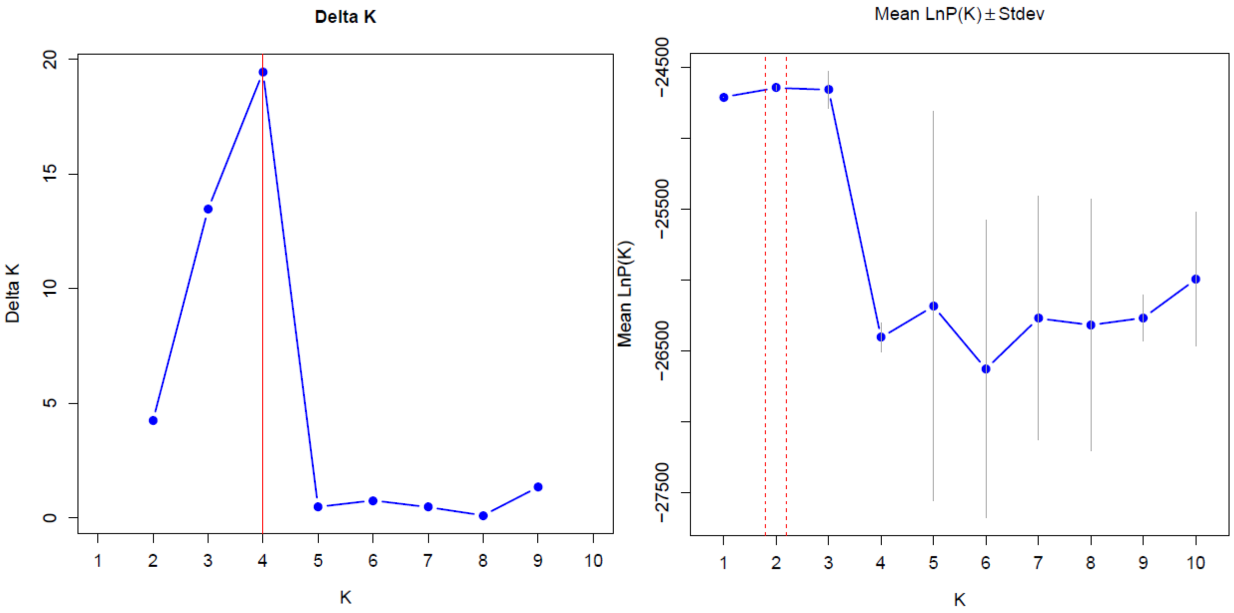


Fig.30b Plots for detecting the most appropriate number of clusters (*K*) within Tyrolean populations.

Within native Romanian populations

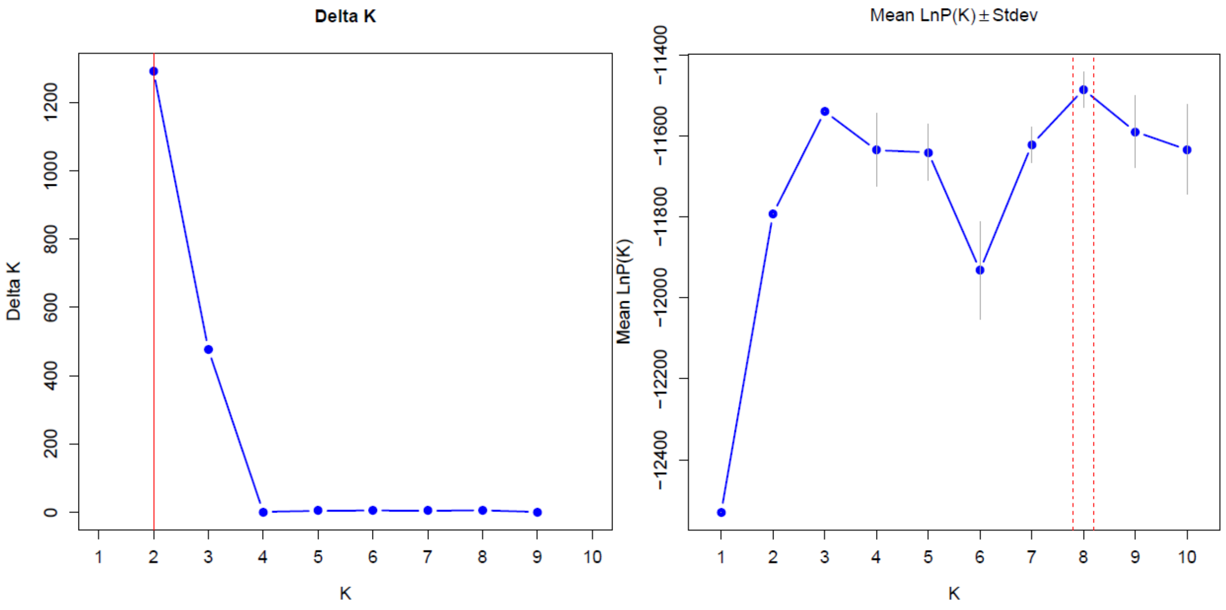


Fig.30c Plots for detecting the most appropriate number of clusters (*K*) within native Romanian populations.

Four statistics (MedMeaK, MaxMeaK, MedMedK, MaxMedK) of Puechmaille (2016)(Fig.31)

All 16 *Larix decidua* populations

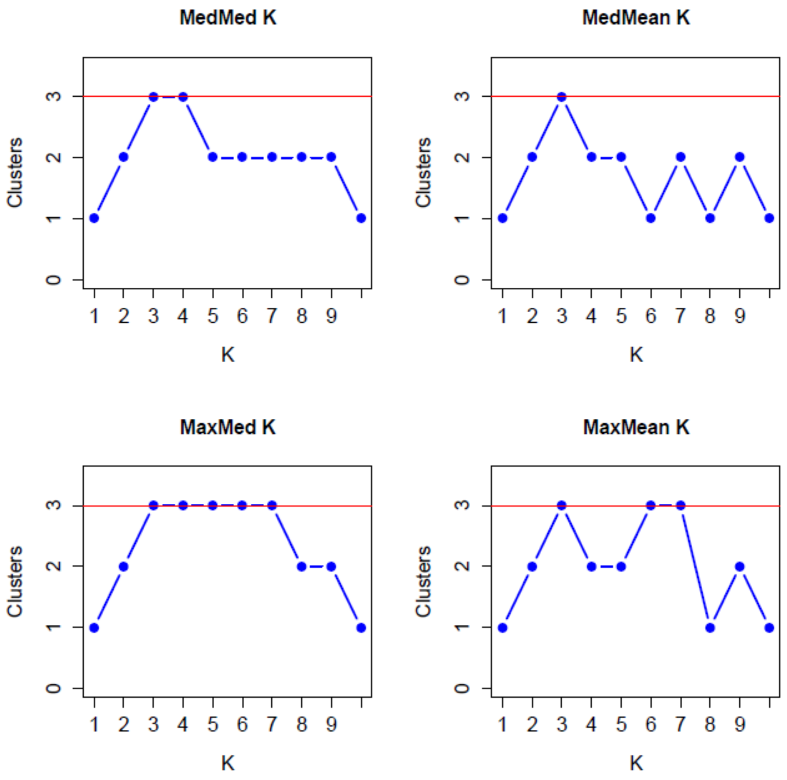


Fig.31a Plots for detecting the most appropriate number of clusters (*K*) in all 16 *Larix decidua* populations.

Within Tyrolean populations (including R3)

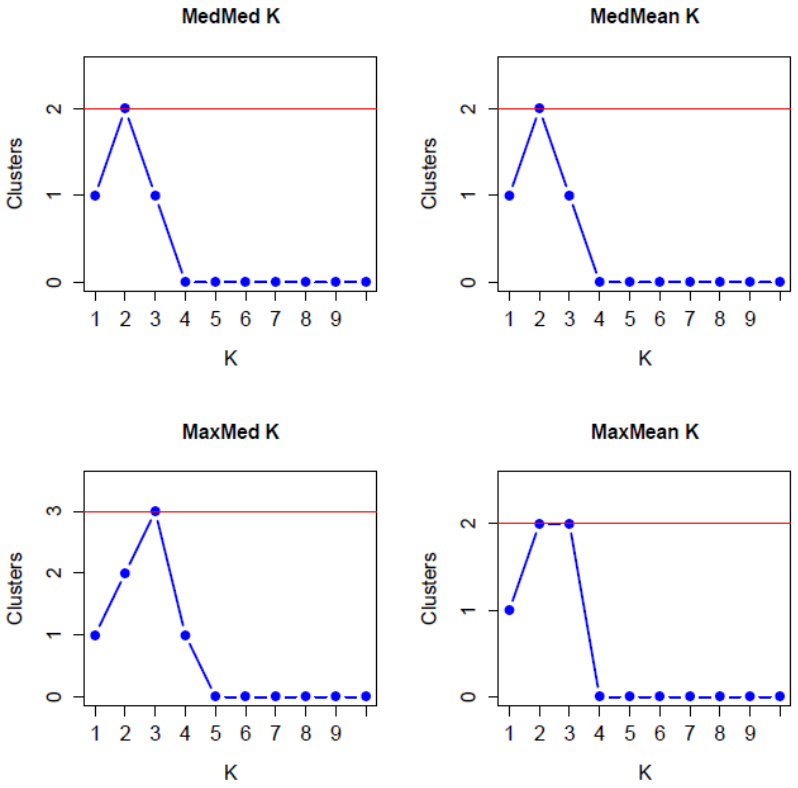


Fig.31b Plots for detecting the most appropriate number of clusters (*K*) within Tyrolean populations.

Within native Romanian populations

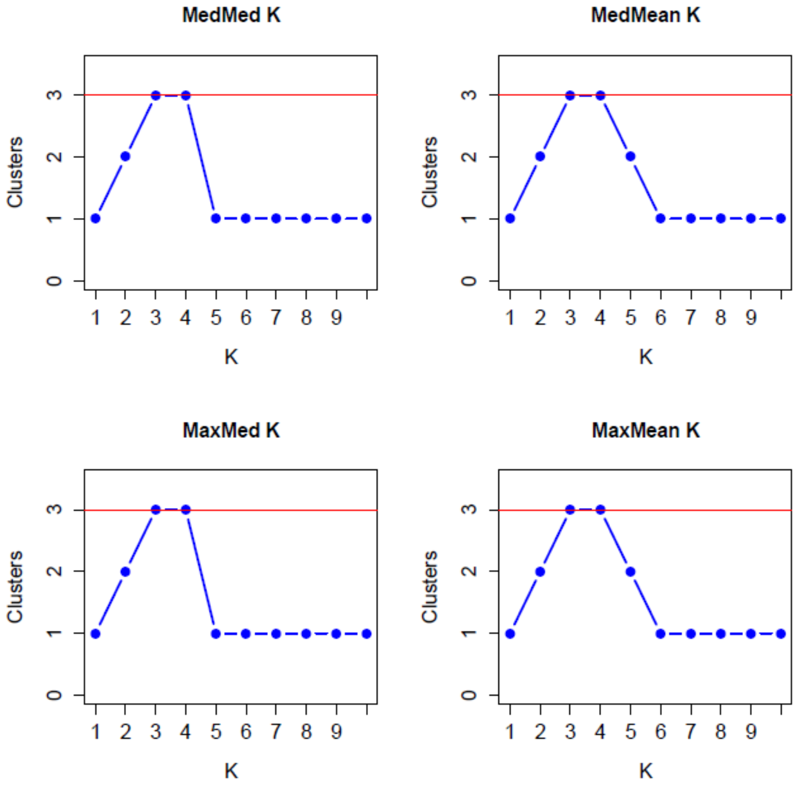


Fig.31c Plots for detecting the most appropriate number of clusters (*K*) within native Romanian populations.

Formulas for calculations

Effective number of alleles (N_e):

$$N_{\mathrm{e}} = \frac{1}{1 - H_{\mathrm{e}}}$$

Information index (I):

$$I = \sum p_i * \ln p_i$$

p_i, frequency of the *i*th allele.

Observed heterozygosity (H_o):

$$H_{\mathrm{o}} = \frac{\text{Number of heterozygotes}}{\mathrm{N}}$$

N, sample size.

Expected heterozygosity (H_e):

$$H_{\mathrm{e}} = 1 - \sum {p_i}^2$$

p_i, frequency of the *i*th allele.

Fixation index (F):

$$F = \frac{H_{\mathrm{e}} - H_{\mathrm{o}}}{H_{\mathrm{e}}}$$

Rarefaction and contribution of allelic richness (Petit *et al.* 1998):

$$r(g) = \sum_i \left[1 - \binom{N - N_i}{g} / \binom{N}{g}\right]$$

r(g), number of different alleles found.

g, number of sampled genes.

N, total number of genes at locus *i.*

$$C_T^{r(g)}(k) = \frac{r_{T(g)} - r_{Tk(g)}}{r_{T(g)} - 1}$$

$C_T^{r(g)}$, contribution of the *k*th population to total allelic richness.

$r_{T(g)}$, total allelic richness.

$r_{Tk(g)}$, total allelic richness when the *k*th population is excluded.

Kinship coefficient of Loiselle (1995):

$$F_{\mathrm{ij}} = \frac{Q_{ij} - Q_m}{(1 - Q_m)}$$

Q_{ij}, probability of identity by state between random loci for genotypes *i* and *j*.

Q_{m}, average probability of identity by state for loci from random genotypes in the population used to draw *i* and *j*.

Nei's standard genetic distance (Nei 1972):

$$D = -\ln \frac{\sum_{i=1}^{k} p_{ix} p_{iy}}{\sqrt{\left(\sum_{i=1}^{k} p_{ix}{}^2 \sum_{i=1}^{k} p_{iy}{}^2\right)}}$$

p_{ix}, frequency of the *i*th allele in population x.

p_{iy}, frequency of the *i*th allele in population y.

Nei's unbiased genetic distance (Nei 1978):

$$uD = -\ln \frac{\sum_{i=1}^{k} p_{ix} p_{iy}}{\sqrt{\left(\left(\frac{2n\left(\sum_{i=1}^{k} p_{ix}{}^2 - 1\right)}{2n-1}\right)\left(\frac{2n\left(\sum_{i=1}^{k} p_{iy}{}^2 - 1\right)}{2n-1}\right)\right)}}$$

p_{ix}, frequency of the *i*th allele in population x.

p_{iy}, frequency of the *i*th allele in population y.

***F_{ST}* value:**

$$F_{\mathrm{ST}} = \frac{\sigma_{\mathrm{S}}{}^2}{\sigma_{\mathrm{t}}{}^2} = \frac{\sigma_{\mathrm{S}}{}^2}{p(1-p)}$$

$\sigma_{\mathrm{S}}{}^2$, variance of allele frequency in subpopulation S.

$\sigma_{\mathrm{t}}{}^2$, variance of allele frequency in total population.

p, average frequency of an allele in total population.

R_{ST} value:

$$R_{\mathrm{ST}} = \frac{(S_{\mathrm{b}} - S_{\mathrm{w}})}{S_{\mathrm{b}}}$$

S_{w}, mean square difference in allele size for two genes from the same population.

S_{b}, mean square difference in allele size for two genes from different populations.

G'_{ST} value of Hedrick (2005):

$$G'_{\mathrm{ST}} = \frac{G_{\mathrm{ST}}}{G_{\mathrm{ST(max)}}} = \frac{\left(\frac{cH_{\mathrm{T}} - cH_{\mathrm{S}}}{cH_{\mathrm{T}}}\right)}{\left(\frac{(k-1)(1-cH_{\mathrm{S}})}{k-1+cH_{\mathrm{S}}}\right)}$$

cH_{T}, corrected total expected heterozygosity (H_{T}).

cH_{S}, corrected expected heterozygosity averaged across populations (H_{S}).

k, number of populations.

Nuclear raw data (microsatellites; Table 17)

		bcLK189		**Ld56**		**Ld30**		**bcLK263**		**bcLK228**		**bcLK211**		**bcLK253**		**Ld50**		**Ld31**		**Ld42**		**Ld45**		**Ld58**		**Ld101**	
Code	Pop.	L1	L2	L1	L2	L1	L2	L1	L2	L1	L2	L1	L2	L1	L2	L1	L2	L1	L2	L1	L2	L1	L2	L1	L2	L1	L2
72	R1(Adult)	167	171	242	242	129	129	213	247	197	207	231	233	211	215	183	197	145	147	184	184	213	213	159	159	198	198
78	R1(Adult)	159	161	238	242	133	133	233	233	175	197	207	233	223	223	183	183	139	143	184	186	213	220	157	159	198	198
80	R1(Adult)	167	167	244	244	133	133	215	215	201	207	195	201	211	221	179	183	137	143	184	184	0	0	151	151	198	198
82	R1(Adult)	159	161	242	242	133	133	215	215	207	211	195	195	213	215	183	197	137	147	186	186	213	220	159	159	198	198
86	R1(Adult)	159	169	238	242	129	129	193	215	209	211	195	195	213	213	197	203	143	147	182	184	211	213	151	177	198	198
87	R1(Adult)	159	167	238	238	129	133	215	217	207	211	219	227	211	229	185	195	141	143	184	186	213	213	155	169	200	200
89	R1(Adult)	159	159	242	242	121	133	215	215	195	211	191	227	223	223	183	185	139	141	184	184	213	220	159	159	198	200
91	R1(Adult)	159	163	238	242	121	129	211	211	183	209	219	229	211	215	185	197	143	147	182	184	0	0	151	159	198	198
92	R1(Adult)	159	165	238	238	121	133	249	249	203	213	195	199	211	225	175	199	143	143	184	186	213	213	159	175	198	198
94	R1(Adult)	159	163	238	238	121	133	215	223	203	207	195	195	213	223	193	193	137	137	184	186	213	220	159	161	198	198
95	R1(Adult)	167	167	242	242	0	0	0	0	197	197	195	195	213	213	181	197	145	145	184	184	213	213	159	159	198	198
98	R1(Adult)	159	159	238	238	121	129	193	215	193	207	195	219	213	223	185	197	139	147	184	184	213	213	159	161	198	198
101	R1(Adult)	159	159	238	242	129	133	211	211	207	211	195	227	211	223	183	197	143	147	182	184	213	220	161	169	198	198
102	R1(Adult)	161	163	238	238	121	129	215	223	207	207	195	219	213	223	193	199	121	139	184	186	213	220	161	169	198	198
103	R1(Adult)	159	161	238	238	121	133	211	233	211	213	195	199	221	229	185	199	137	143	184	184	211	211	151	177	198	198
107	R1(Adult)	159	159	238	242	129	135	215	215	185	207	195	195	213	213	183	197	139	147	184	184	213	220	161	169	198	198
113	R1(Adult)	163	171	238	242	129	133	207	215	207	211	191	207	213	213	193	197	139	143	184	186	213	213	161	175	198	198
118	R1(Adult)	159	165	230	230	133	133	207	219	209	209	195	197	211	225	189	189	143	143	184	188	213	213	159	159	198	198
121	R1(Adult)	163	167	238	242	133	133	193	233	207	207	207	229	213	223	183	193	139	139	184	184	220	220	159	161	198	198
122	R1(Adult)	167	167	230	238	133	135	213	213	207	211	195	233	211	229	185	197	137	147	184	186	213	220	169	175	198	198
126	R1(Adult)	159	165	230	238	121	121	193	211	193	209	195	195	211	215	183	185	121	143	184	186	213	213	159	169	198	198
127	R1(Adult)	159	159	238	238	121	129	219	225	203	209	195	199	211	213	183	193	127	143	184	186	211	213	157	161	198	198
130	R1(Adult)	167	169	248	248	133	133	211	215	195	207	195	195	221	223	185	193	143	143	184	188	213	213	165	175	198	198
136	R1(Adult)	159	167	248	248	121	133	211	211	193	203	0	0	211	225	181	199	143	147	184	184	210	213	161	169	198	198
138	R1(Adult)	159	169	238	238	121	135	215	267	183	207	195	201	211	211	193	199	137	139	184	184	220	220	159	159	198	198

140	R1(Adult)	163	167	230	242	121	121	207	217	193	207	225	233	215	221	193	199	137	143	184	184	213	220	151	177	198	198
141	R1(Adult)	159	167	238	238	121	129	219	233	203	209	191	199	211	223	199	199	137	143	184	186	220	220	151	151	198	198
143	R1(Adult)	163	171	242	246	121	121	207	211	201	207	195	243	211	215	185	193	143	147	186	186	213	220	161	161	198	198
145	R1(Adult)	159	169	246	246	129	133	217	247	183	207	195	229	211	215	193	193	143	143	184	184	211	213	159	169	198	202
150	R1(Adult)	159	159	238	238	129	133	215	215	207	213	195	229	211	223	193	195	137	141	182	184	220	220	159	161	198	198
151	R1(Adult)	159	161	238	242	121	121	215	247	211	211	201	231	213	223	185	193	137	147	184	184	213	213	159	159	198	198
158	R1(Adult)	159	163	230	238	121	129	217	217	201	203	195	225	211	229	195	197	143	143	184	184	213	213	159	169	198	198
160	R1(Adult)	163	167	238	246	121	121	211	211	203	207	193	237	221	223	185	195	139	139	184	184	213	220	165	181	198	200
163	R1(Adult)	163	167	238	238	133	133	193	211	193	207	195	201	221	225	191	199	133	141	184	186	220	220	151	175	198	198
167	R1(Adult)	159	167	238	242	129	133	193	225	175	207	201	231	221	229	193	201	131	137	186	186	213	213	159	169	194	198
179	R1(Adult)	159	163	238	238	119	127	209	225	201	207	219	243	211	213	197	199	133	143	184	184	220	220	159	159	198	198
181	R1(Adult)	159	167	238	238	121	133	225	225	207	213	195	231	221	225	179	193	137	147	184	184	218	218	151	175	198	198
182	R1(Adult)	159	159	238	238	121	121	209	269	203	209	195	247	223	223	183	193	143	147	184	184	211	211	159	169	194	198
186	R1(Adult)	159	167	238	248	121	133	215	225	205	207	195	229	211	213	185	197	143	147	184	186	220	220	161	161	198	198
190	R1(Adult)	159	159	238	242	129	133	215	215	211	217	195	201	223	225	185	185	143	147	184	188	213	213	159	159	198	198
191	R1(Adult)	167	169	238	246	133	133	209	263	183	213	195	207	211	213	197	199	139	147	182	184	213	220	159	159	198	198
198	R1(Adult)	163	163	238	242	133	133	217	235	193	207	225	243	211	215	193	195	143	145	184	184	0	0	159	159	198	198
202	R1(Adult)	163	169	238	242	133	133	193	193	193	211	201	245	211	223	183	185	143	143	184	186	211	213	151	159	198	198
207	R1(Adult)	159	159	238	238	121	133	193	215	211	211	201	229	211	229	193	195	143	147	184	184	211	213	151	159	198	198
208	R1(Adult)	159	167	238	242	121	133	223	223	207	207	195	229	211	211	193	199	137	143	184	184	220	220	159	159	198	198
211	R1(Adult)	159	165	238	242	121	135	233	267	197	209	195	199	223	229	193	199	139	143	184	184	221	221	151	169	198	198
702	R1(Adult)	159	169	238	242	133	135	193	213	207	207	207	227	213	223	197	197	139	143	184	184	213	220	159	161	198	198
116	R1(Juv.)	159	167	238	242	121	121	211	211	207	207	195	229	211	211	183	183	133	139	186	186	0	0	159	169	198	198
142	R1(Juv.)	159	167	238	238	129	133	193	253	207	207	195	219	213	215	185	189	143	143	184	184	213	215	161	175	198	198
176	R1(Juv.)	159	167	238	238	121	133	219	219	183	203	191	225	211	211	199	199	143	143	184	184	213	220	151	159	198	198
183	R1(Juv.)	161	161	238	242	121	133	215	215	211	221	195	219	213	225	195	197	139	147	184	186	220	220	159	159	198	198
629	R1(Juv.)	159	167	242	242	121	133	225	247	207	207	195	207	211	223	177	177	139	147	184	186	213	213	159	161	198	200
636	R1(Juv.)	163	167	238	238	121	129	207	219	203	221	201	219	223	223	185	197	139	147	184	184	213	220	155	177	198	198
644	R1(Juv.)	163	163	242	242	133	133	193	225	207	211	223	245	211	213	185	185	143	143	184	186	211	220	159	159	198	198

654	R1(Juv.)	159	159	238	238	133	133	211	213	207	213	195	219	215	223	179	193	139	147	182	186	213	213	159	169	198	198
657	R1(Juv.)	159	161	238	238	121	133	215	217	195	207	195	231	211	229	191	199	137	139	184	188	220	220	159	159	198	198
658	R1(Juv.)	159	163	238	238	121	121	215	217	183	209	195	217	211	223	195	197	143	145	182	184	220	220	161	169	198	198
660	R1(Juv.)	161	163	238	242	121	121	215	217	211	213	195	199	211	225	193	193	137	143	184	184	213	213	159	169	198	198
698	R1(Juv.)	163	167	238	240	133	133	211	225	207	207	195	239	221	221	197	199	133	143	184	184	220	220	161	175	198	198
699	R1(Juv.)	163	167	238	242	121	127	211	249	203	207	201	233	213	223	193	197	143	143	184	184	220	220	151	175	198	198
701	R1(Juv.)	159	167	242	242	131	135	211	225	197	213	195	239	213	223	177	199	141	143	184	186	213	213	169	175	198	198
710	R1(Juv.)	159	165	238	242	121	129	211	225	197	207	195	235	215	215	193	193	143	143	184	184	210	220	161	161	198	198
712	R1(Juv.)	159	159	236	246	131	147	211	225	197	203	197	223	215	231	185	197	137	137	188	188	215	220	167	183	198	198
714	R1(Juv.)	163	167	238	238	121	121	213	215	195	211	195	195	221	223	193	201	143	143	184	184	213	220	159	159	198	200
715	R1(Juv.)	159	159	230	242	133	133	193	215	203	209	195	195	211	223	185	193	143	147	184	184	213	220	157	169	198	198
717	R1(Juv.)	159	163	230	242	133	133	215	215	195	211	195	233	215	223	183	211	121	143	184	184	213	220	159	159	198	198
720	R1(Juv.)	163	165	238	246	133	133	207	249	203	211	195	233	215	225	175	177	143	143	184	184	0	0	159	175	198	198
722	R1(Juv.)	159	163	238	238	129	133	267	267	207	207	195	219	211	213	193	197	139	139	184	186	213	220	159	169	198	198
724	R1(Juv.)	159	173	238	244	121	135	217	217	207	209	199	235	211	223	185	195	147	147	182	186	213	213	169	169	198	198
726	R1(Juv.)	161	163	238	238	133	133	207	215	195	207	195	239	213	229	199	199	137	139	184	186	213	213	175	175	198	198
729	R1(Juv.)	165	171	242	242	121	127	215	229	207	209	195	223	211	225	199	211	141	143	184	186	211	220	159	161	198	198
730	R1(Juv.)	159	167	238	242	133	133	0	0	207	207	195	227	213	223	181	197	143	145	182	184	213	213	159	159	198	198
734	R1(Juv.)	159	167	238	238	121	133	223	247	207	207	195	231	211	213	185	193	137	143	184	184	220	220	159	159	198	198
735	R1(Juv.)	165	167	238	244	121	121	193	193	197	207	195	201	223	225	185	187	133	143	184	184	210	213	159	159	198	198
737	R1(Juv.)	163	163	238	238	121	129	215	225	193	195	195	195	213	223	185	197	141	141	186	188	213	220	169	169	198	198
742	R1(Juv.)	159	171	238	238	121	135	207	207	207	207	195	201	211	229	183	199	143	143	184	184	213	220	155	159	198	198
743	R1(Juv.)	159	163	238	238	0	0	193	209	207	211	195	245	211	213	183	183	143	147	184	186	211	213	159	161	198	198
745	R1(Juv.)	159	163	242	242	129	133	225	237	207	211	195	221	213	215	177	185	143	147	184	186	213	213	159	159	198	200
750	R1(Juv.)	163	163	238	245	121	121	213	217	183	197	195	235	211	223	183	195	137	137	184	188	210	210	151	177	198	200
758	R1(Juv.)	159	159	238	242	121	121	211	211	203	207	201	233	225	225	197	199	139	143	184	184	220	220	169	175	198	198
759	R1(Juv.)	161	163	238	242	121	133	193	211	197	207	195	237	223	225	197	197	137	147	184	184	211	220	159	165	198	198
762	R1(Juv.)	161	169	242	242	133	135	193	215	207	207	195	207	215	223	197	197	137	143	184	186	213	220	159	159	198	198
763	R1(Juv.)	165	167	238	238	133	133	215	215	211	213	199	229	211	223	175	197	143	143	184	184	213	220	159	159	198	198

764	R1(Juv.)	163	171	238	242	121	121	193	225	207	207	195	223	221	225	183	199	141	143	188	188	211	211	159	161	198	198
774	R1(Juv.)	167	167	238	242	133	133	207	211	207	211	195	195	213	225	197	199	133	137	186	186	220	220	151	175	198	198
779	R1(Juv.)	159	167	238	248	121	133	219	225	213	213	233	239	221	221	185	199	147	147	184	184	220	220	175	175	198	198
780	R1(Juv.)	159	159	238	242	127	127	213	215	203	207	195	195	219	223	183	197	141	143	184	186	220	220	151	161	198	198
783	R1(Juv.)	159	159	238	238	121	121	211	215	197	207	219	219	213	215	193	193	139	143	184	184	220	220	161	169	198	198
785	R1(Juv.)	159	167	238	248	121	135	215	215	183	213	195	238	211	229	193	199	137	143	184	186	220	220	159	159	198	200
788	R1(Juv.)	163	163	242	242	129	139	193	215	195	217	195	195	213	223	185	195	135	147	186	186	213	213	157	159	198	198
796	R1(Juv.)	159	165	242	246	121	121	209	219	201	203	195	229	223	229	185	203	133	141	184	184	211	220	159	175	198	198
802	R1(Juv.)	159	171	238	238	121	121	207	215	201	207	195	201	211	223	193	199	139	139	184	186	213	213	159	161	198	198
803	R1(Juv.)	159	165	230	238	121	121	193	219	193	195	195	221	211	215	185	195	139	143	184	184	213	213	151	159	198	198
805	R1(Juv.)	159	159	238	248	133	133	211	217	193	213	199	233	211	211	181	183	147	147	184	184	213	213	169	169	198	198
807	R1(Juv.)	159	167	238	242	129	129	211	215	195	211	195	195	223	223	197	197	121	143	182	184	213	213	159	161	198	198
668	SC1	149	159	236	250	129	133	225	225	197	197	195	225	225	227	183	193	139	151	184	186	215	215	149	159	198	198
792	SC1	163	169	240	250	129	131	211	213	183	197	195	195	211	213	195	199	137	137	186	188	218	218	155	171	198	198
109	SC2	163	163	240	246	117	129	193	237	183	195	195	195	213	227	185	185	139	149	186	188	213	218	171	171	198	198
112	SC2	163	165	248	250	133	161	215	221	195	205	195	199	213	229	183	193	135	137	186	188	218	218	159	165	198	198
128	SC2	149	163	240	246	119	127	211	219	195	197	195	199	211	223	185	193	147	149	186	188	218	218	165	173	198	198
154	SC2	163	163	246	250	119	133	211	221	183	195	199	227	213	223	193	195	135	149	186	188	218	218	164	165	198	198
166	SC2	163	163	246	246	131	139	225	231	183	211	195	201	211	215	185	195	127	137	188	188	218	218	151	177	194	198
1	R2(Adult)	161	163	238	242	121	129	207	217	197	209	191	195	215	223	185	195	137	143	184	184	213	220	159	161	198	198
27	R2(Adult)	159	163	238	242	127	129	229	229	201	203	195	195	223	223	183	193	0	0	184	188	213	218	151	161	198	198
32	R2(Adult)	159	163	242	242	129	129	215	265	195	195	195	195	223	223	185	193	137	137	184	184	213	213	161	169	198	198
37	R2(Adult)	161	163	238	242	121	129	207	215	197	201	197	227	213	213	193	197	125	137	184	184	213	220	161	169	198	198
43	R2(Adult)	159	167	232	242	129	129	217	217	175	195	207	219	213	223	183	211	137	137	184	184	213	218	161	173	198	198
54	R2(Adult)	163	165	238	242	129	129	207	207	203	209	193	195	223	227	183	193	137	137	184	184	213	213	161	173	198	198
59	R2(Adult)	161	165	242	242	99	129	209	219	195	209	191	195	215	223	193	193	137	137	184	184	213	213	161	173	198	198
62	R2(Adult)	165	165	242	242	127	129	217	219	195	209	193	195	223	223	193	203	137	139	184	184	218	218	161	161	198	198
63	R2(Adult)	159	159	242	242	121	127	215	215	205	205	195	195	213	223	193	199	125	125	184	184	213	213	161	161	198	198
64	R2(Adult)	161	165	242	242	129	133	209	215	175	203	195	195	223	227	183	193	137	145	184	184	218	220	151	161	198	198

67	R2(Adult)	159	159	242	242	133	137	207	215	209	225	191	195	215	223	193	193	137	137	184	188	215	220	161	161	198	198
68	R2(Adult)	159	159	242	242	121	133	207	251	201	201	195	227	223	227	185	193	139	143	184	184	213	220	173	173	198	198
73	R2(Adult)	161	167	242	242	121	127	209	215	185	215	195	199	213	215	199	199	137	137	184	184	218	218	161	161	198	198
83	R2(Adult)	159	163	232	242	129	129	217	265	195	201	195	217	213	223	185	193	137	143	184	184	213	213	169	175	198	198
104	R2(Adult)	163	167	242	242	127	129	189	217	195	195	195	195	213	215	193	211	143	143	184	188	213	218	159	175	198	198
106	R2(Adult)	159	167	242	242	127	133	209	213	209	221	195	195	213	215	189	199	139	145	184	184	213	218	151	161	198	198
117	R2(Adult)	163	167	242	242	121	127	209	251	201	201	197	199	213	227	193	197	0	0	184	184	220	220	161	169	198	198
123	R2(Adult)	159	159	242	242	121	129	263	265	197	201	191	219	223	223	185	185	137	137	184	184	213	213	169	173	198	198
125	R2(Adult)	165	165	238	242	133	133	215	231	197	209	199	227	215	227	193	193	137	143	184	184	213	213	161	161	198	198
131	R2(Adult)	159	159	242	242	121	129	209	215	195	197	195	219	213	213	199	199	137	145	184	184	0	0	161	161	198	198
134	R2(Adult)	159	159	232	232	121	127	207	215	197	201	191	195	223	229	183	203	137	143	184	188	213	220	161	171	198	200
137	R2(Adult)	159	163	242	242	121	129	217	231	195	209	195	195	213	213	185	193	137	137	184	184	218	218	161	173	198	198
144	R2(Adult)	159	163	238	242	121	133	229	229	203	209	191	195	215	223	189	193	145	145	184	188	215	220	161	173	198	198
146	R2(Adult)	159	159	242	242	129	129	217	217	201	201	199	217	213	215	183	199	137	143	184	188	213	220	169	175	198	198
147	R2(Adult)	163	163	232	242	127	129	215	225	175	215	191	191	213	223	199	203	137	137	184	184	220	220	173	173	198	198
153	R2(Adult)	159	167	242	248	129	133	225	251	197	205	195	227	213	215	189	193	143	143	184	188	213	213	161	161	198	198
157	R2(Adult)	159	161	242	242	121	121	217	265	197	197	195	195	213	213	191	197	137	137	182	184	220	220	161	169	198	198
159	R2(Adult)	163	163	242	242	129	129	215	265	205	209	195	195	213	223	183	185	137	143	184	184	213	213	159	161	198	198
162	R2(Adult)	159	167	238	242	127	127	215	217	185	197	195	195	215	223	193	193	125	125	184	184	218	218	161	161	198	198
165	R2(Adult)	159	159	242	242	121	127	217	225	201	209	211	217	213	223	183	193	139	139	184	184	213	220	169	173	198	198
169	R2(Adult)	165	165	242	242	129	133	189	207	211	225	199	199	223	233	185	199	137	137	184	184	220	220	161	169	198	200
170	R2(Adult)	159	159	242	242	129	129	207	265	195	201	195	199	213	215	183	197	137	143	184	184	220	220	161	171	198	198
175	R2(Adult)	159	167	242	242	133	133	229	265	175	201	217	219	223	223	183	185	137	147	184	188	213	220	151	173	198	198
185	R2(Adult)	159	159	238	242	121	129	189	225	203	225	221	231	215	223	183	193	137	137	184	188	213	218	161	161	198	198
192	R2(Adult)	159	159	242	242	0	0	207	215	195	209	195	195	213	213	193	199	137	139	184	184	218	218	161	161	198	198
199	R2(Adult)	159	159	242	242	129	129	215	215	185	197	191	195	213	213	193	193	137	137	184	184	213	220	161	173	198	198
200	R2(Adult)	163	165	232	242	127	137	209	217	195	209	195	195	223	223	183	193	139	139	184	184	215	218	159	161	198	198
201	R2(Adult)	165	165	232	242	121	121	189	207	195	209	195	217	213	223	185	193	137	137	184	188	213	220	175	175	198	198
203	R2(Adult)	159	159	242	242	125	125	189	207	195	215	195	195	213	213	179	185	139	139	184	184	213	218	161	161	198	198

204	R2(Adult)	159	173	242	242	129	129	215	229	185	197	199	217	223	223	183	193	145	147	184	188	213	220	151	161	198	198
205	R2(Adult)	159	159	238	242	129	129	189	215	201	203	191	195	223	229	183	185	0	0	184	188	213	213	161	171	198	198
209	R2(Adult)	159	163	242	242	121	129	215	231	195	209	195	219	213	213	183	185	137	137	184	184	218	220	151	161	198	198
210	R2(Adult)	159	165	242	242	129	129	207	231	185	209	195	195	223	227	183	193	137	143	184	184	213	213	161	173	198	198
616	R2(Juv.)	163	173	238	242	121	121	189	217	197	207	195	195	213	227	179	193	137	143	184	184	218	220	161	173	198	198
630	R2(Juv.)	159	161	242	242	121	129	209	217	185	195	199	219	213	227	185	199	137	137	184	184	213	213	161	161	198	198
637	R2(Juv.)	159	163	232	242	127	129	207	217	195	197	191	195	215	223	183	185	137	143	184	184	218	220	161	175	198	200
648	R2(Juv.)	159	163	232	242	121	121	209	215	197	197	191	197	213	227	193	199	137	145	184	184	218	220	161	161	198	198
655	R2(Juv.)	159	163	242	242	121	129	189	207	197	201	195	211	213	223	197	203	137	143	184	188	213	220	159	173	198	198
659	R2(Juv.)	159	167	242	242	121	129	207	217	201	215	195	217	213	213	179	193	145	145	184	184	218	220	161	171	198	198
662	R2(Juv.)	159	173	242	242	0	0	189	217	209	221	195	219	213	215	197	199	0	0	184	188	213	219	161	173	198	198
667	R2(Juv.)	159	159	238	242	121	121	215	229	195	197	195	211	223	223	185	189	137	143	184	188	213	220	161	161	198	198
674	R2(Juv.)	159	165	242	242	133	137	215	229	203	209	211	219	223	223	179	189	143	143	184	184	220	220	159	173	198	198
677	R2(Juv.)	137	159	242	242	121	129	227	229	185	203	195	195	223	223	183	185	145	147	184	188	213	215	171	173	198	198
679	R2(Juv.)	159	161	242	242	129	129	209	219	195	201	199	199	215	215	193	193	145	145	184	184	213	220	161	169	198	198
683	R2(Juv.)	163	165	238	242	129	129	207	207	203	209	193	195	223	227	183	193	137	137	184	184	213	213	161	173	198	198
684	R2(Juv.)	161	163	242	242	121	129	215	231	195	201	195	199	215	223	185	193	137	145	184	184	213	220	161	169	198	198
688	R2(Juv.)	163	165	238	242	121	121	189	209	197	197	195	219	215	223	195	195	137	143	184	188	220	220	175	175	198	198
718	R2(Juv.)	163	165	242	242	121	129	189	207	185	209	191	191	215	223	193	193	137	137	184	184	213	213	161	173	198	198
725	R2(Juv.)	161	167	232	242	129	133	209	215	201	209	191	195	215	229	189	193	137	137	184	184	218	220	173	173	198	198
738	R2(Juv.)	163	167	242	242	121	133	215	251	197	209	195	217	223	223	183	199	137	137	184	188	215	220	161	161	198	198
739	R2(Juv.)	159	159	242	242	121	129	217	231	209	215	195	217	213	223	179	193	0	0	184	184	213	218	159	161	198	198
749	R2(Juv.)	163	173	242	242	121	121	189	219	203	225	191	197	223	223	197	199	139	139	184	184	218	220	151	173	198	198
754	R2(Juv.)	159	163	242	242	121	121	215	217	197	209	217	217	215	215	193	197	137	143	184	184	218	220	151	169	198	198
755	R2(Juv.)	163	163	238	242	127	129	207	217	201	203	199	211	213	223	183	199	143	143	184	184	213	220	161	175	198	198
757	R2(Juv.)	161	163	238	242	127	129	215	229	221	225	195	199	223	223	183	183	143	143	184	184	220	220	161	161	198	198
760	R2(Juv.)	159	165	242	242	129	133	215	231	185	203	191	195	223	233	183	193	137	137	184	184	213	218	151	161	198	198
761	R2(Juv.)	159	159	242	242	121	129	209	209	197	197	195	219	213	213	199	199	137	145	184	184	0	0	161	161	198	198
765	R2(Juv.)	159	159	232	242	127	129	215	225	197	209	191	195	213	229	183	183	143	147	184	184	213	218	161	171	198	200

767	R2(Juv.)	159	161	232	242	127	127	207	215	197	201	191	195	223	229	183	183	143	143	184	188	213	220	161	171	198	200
768	R2(Juv.)	163	165	242	242	127	129	215	251	209	209	195	227	213	215	185	185	143	143	184	184	213	215	161	169	198	198
769	R2(Juv.)	159	167	242	242	129	133	215	265	195	195	195	217	223	223	193	193	139	139	184	184	215	218	161	161	198	198
771	R2(Juv.)	159	163	238	242	121	129	209	225	201	203	193	231	215	215	193	199	137	137	188	188	218	218	161	161	198	198
775	R2(Juv.)	159	173	242	242	121	129	207	207	185	205	195	199	213	223	183	185	137	145	184	184	218	218	159	161	198	198
776	R2(Juv.)	159	165	242	242	121	127	219	229	185	195	193	195	223	223	199	203	137	145	184	184	218	220	161	169	198	198
778	R2(Juv.)	159	167	242	242	127	133	209	229	201	201	193	199	223	229	185	203	137	137	184	188	213	218	161	161	198	198
782	R2(Juv.)	159	173	242	242	129	133	189	229	203	209	195	219	215	223	183	193	0	0	184	188	218	220	161	169	198	198
786	R2(Juv.)	167	173	232	242	121	121	225	265	209	209	191	199	215	227	179	189	137	145	184	188	213	220	161	169	198	198
793	R2(Juv.)	163	163	232	238	127	127	189	215	175	209	195	217	223	227	185	193	139	139	184	184	220	220	161	161	198	198
794	R2(Juv.)	159	159	242	242	129	133	229	229	197	209	219	241	213	223	199	203	147	147	184	188	218	220	151	161	198	198
801	R2(Juv.)	161	163	242	242	127	129	229	249	201	209	195	195	215	223	183	199	139	147	184	184	213	218	169	171	198	198
804	R2(Juv.)	159	165	232	242	121	121	207	207	201	201	191	221	215	223	185	203	137	137	184	188	213	218	161	161	198	198
806	R2(Juv.)	159	173	232	242	121	121	209	229	201	201	195	217	223	223	183	185	137	137	184	184	213	218	151	173	198	198
619	SC3	169	171	246	248	117	127	207	207	197	197	223	223	211	231	195	195	135	149	188	190	213	213	157	157	198	198
748	SC3	163	163	244	246	117	131	205	223	183	201	195	199	211	215	195	195	137	141	188	188	213	215	171	171	198	198
773	SC3	149	169	238	248	117	121	207	235	187	211	195	223	211	217	183	185	135	149	190	196	213	215	157	157	198	198
3	R3(Adult)	149	169	242	248	129	131	209	223	201	207	195	219	211	221	181	197	127	137	186	190	218	220	169	177	198	198
12	R3(Adult)	171	171	242	242	0	0	211	219	187	187	195	195	211	215	193	195	137	147	188	188	210	210	173	175	198	198
13	R3(Adult)	169	171	244	250	131	133	205	241	201	203	197	201	215	219	181	193	127	127	184	186	210	215	165	171	198	198
17	R3(Adult)	169	171	248	248	131	131	209	221	197	201	195	195	219	229	185	195	147	147	188	188	213	217	157	179	198	198
18	R3(Adult)	161	163	242	244	111	131	193	231	183	205	195	225	219	225	183	195	137	139	186	190	215	220	171	179	198	198
20	R3(Adult)	163	165	240	248	131	131	221	223	203	203	205	225	215	227	187	195	137	147	186	186	210	215	164	167	198	202
30	R3(Adult)	163	163	238	240	127	133	207	213	183	197	199	211	225	231	183	193	137	137	184	186	215	215	163	175	198	198
31	R3(Adult)	163	165	240	248	117	131	213	223	197	203	195	195	219	225	175	195	135	135	188	190	213	218	163	167	200	202
35	R3(Adult)	149	163	244	250	127	131	231	233	183	197	195	223	211	219	187	195	137	137	186	190	210	215	165	173	196	198
36	R3(Adult)	149	149	246	246	129	133	225	225	197	203	195	201	219	219	185	185	127	143	196	196	215	217	167	167	198	198
40	R3(Adult)	149	163	240	248	117	131	225	233	201	205	195	195	213	215	195	195	137	139	186	188	215	220	157	169	198	202
41	R3(Adult)	165	169	248	248	131	131	217	227	211	211	195	205	213	215	185	187	137	137	186	188	215	218	167	171	198	198

45	R3(Adult)	165	165	244	246	119	127	223	227	201	207	195	199	227	235	195	195	137	137	188	196	215	215	165	173	200	202
47	R3(Adult)	149	157	246	248	129	133	209	217	197	201	219	225	217	227	185	197	135	137	184	186	213	218	165	175	198	202
49	R3(Adult)	161	167	244	250	131	131	193	223	201	205	195	195	211	219	195	195	129	139	186	190	218	220	171	177	198	198
50	R3(Adult)	149	149	246	248	129	139	219	241	197	201	195	227	225	227	195	195	137	147	184	188	213	218	151	171	198	198
57	R3(Adult)	149	149	248	248	131	131	213	223	197	203	211	211	215	229	191	195	137	137	184	184	215	215	0	0	198	202
60	R3(Adult)	165	169	238	248	131	131	209	239	195	199	195	225	229	229	183	195	137	137	186	188	210	218	169	177	198	198
66	R3(Adult)	163	171	238	246	127	131	209	213	183	197	193	195	211	215	185	185	137	147	186	188	210	215	173	173	198	198
69	R3(Adult)	149	149	248	250	127	131	217	227	195	197	195	197	211	211	189	195	137	137	184	190	215	220	167	171	196	202
70	R3(Adult)	157	167	238	246	131	131	223	241	183	201	195	195	213	227	193	195	137	147	188	188	218	222	151	173	198	198
71	R3(Adult)	149	165	238	242	117	131	227	231	183	205	195	195	211	225	185	195	137	137	188	196	218	218	161	173	198	202
74	R3(Adult)	159	163	246	248	129	131	199	211	197	203	195	201	213	231	185	189	137	137	190	190	215	218	177	177	198	202
76	R3(Adult)	163	171	246	250	131	131	223	225	199	203	195	215	211	217	183	185	137	149	188	188	218	218	171	175	198	198
77	R3(Adult)	161	165	238	248	121	133	211	213	199	209	195	255	211	227	185	189	137	147	188	196	204	213	151	171	198	198
88	R3(Adult)	163	163	238	240	131	131	211	223	199	201	195	199	211	215	185	185	137	149	188	188	210	218	165	173	194	198
93	R3(Adult)	163	165	238	240	111	131	211	235	187	203	195	197	215	231	183	187	137	151	186	188	215	218	161	177	198	198
97	R3(Adult)	163	169	238	248	121	131	199	205	201	203	195	195	217	229	185	187	135	149	186	188	213	220	157	175	198	198
99	R3(Adult)	163	163	238	244	127	129	211	241	195	201	195	199	219	221	183	187	127	147	188	190	213	215	157	164	198	198
105	R3(Adult)	149	161	240	248	129	135	211	215	183	207	201	209	211	227	183	199	137	149	188	188	213	218	161	175	198	198
108	R3(Adult)	171	171	238	246	127	131	209	223	183	195	193	195	213	213	185	195	137	151	186	190	210	218	173	173	198	198
129	R3(Adult)	163	163	238	246	125	131	205	217	183	203	195	195	215	227	183	185	137	139	188	188	218	220	171	177	198	202
133	R3(Adult)	165	169	242	246	131	139	193	217	185	197	195	217	211	221	183	185	137	137	188	188	213	215	151	163	198	198
149	R3(Adult)	149	169	246	248	131	131	193	217	197	199	195	197	211	233	185	189	137	137	186	188	215	215	173	173	198	198
152	R3(Adult)	149	163	246	248	131	131	223	235	187	201	205	219	215	223	185	185	137	149	188	190	210	218	173	175	198	198
164	R3(Adult)	169	169	238	238	131	131	209	211	187	211	195	215	215	219	183	195	139	141	184	188	213	218	167	177	196	198
172	R3(Adult)	149	169	246	250	127	131	217	235	183	197	195	209	211	227	185	195	135	137	186	188	213	218	171	173	198	198
177	R3(Adult)	169	169	238	248	129	131	199	229	197	201	195	221	215	219	183	195	137	141	184	184	218	218	165	167	198	198
178	R3(Adult)	157	167	246	248	121	129	211	223	201	203	195	195	219	225	195	195	137	149	184	188	210	220	171	179	198	198
187	R3(Adult)	163	167	244	244	129	147	211	213	197	197	209	227	217	219	185	185	137	147	182	184	215	215	149	155	196	198
188	R3(Adult)	157	163	238	246	131	131	199	199	197	201	195	215	215	227	185	195	133	141	186	188	218	218	165	173	196	198

193	R3(Adult)	149	163	242	246	111	127	213	219	183	203	197	215	215	219	187	195	137	151	182	188	215	218	171	177	198	198
195	R3(Adult)	163	169	238	250	131	133	205	211	203	207	197	199	215	219	185	193	127	127	184	196	210	220	165	173	198	198
196	R3(Adult)	169	171	246	250	121	131	209	239	183	203	193	195	213	215	183	185	127	137	186	188	218	218	175	179	198	198
197	R3(Adult)	169	169	238	240	129	131	205	225	207	211	199	201	215	215	185	193	127	147	184	184	220	220	165	173	198	198
614	R3(Juv.)	169	169	246	246	131	131	209	209	183	195	195	195	211	211	185	185	137	137	186	186	210	213	0	0	198	198
615	R3(Juv.)	161	163	238	248	121	121	211	213	187	199	195	195	211	227	195	203	137	137	188	188	210	222	151	163	198	198
617	R3(Juv.)	171	171	246	246	127	131	209	217	195	195	193	223	213	215	185	195	137	151	186	190	218	218	173	177	198	198
618	R3(Juv.)	163	163	246	250	129	147	215	217	201	203	195	201	217	223	183	195	127	132	186	186	210	218	164	164	198	200
620	R3(Juv.)	163	167	238	244	111	131	193	223	183	201	195	195	213	219	193	195	139	147	188	190	215	218	151	179	198	198
621	R3(Juv.)	149	165	246	246	127	127	211	227	195	207	197	199	211	235	195	195	137	137	184	188	213	215	161	173	196	200
622	R3(Juv.)	149	171	238	250	117	131	213	219	201	203	195	223	211	219	181	185	137	147	186	186	210	215	157	175	198	202
627	R3(Juv.)	163	163	248	250	127	127	213	217	183	197	195	195	211	211	195	195	127	127	186	190	215	218	171	171	202	202
628	R3(Juv.)	169	171	238	248	129	131	213	239	199	201	221	225	215	229	183	195	127	137	188	188	210	210	169	169	198	198
632	R3(Juv.)	163	171	238	250	127	131	213	219	197	203	195	223	211	213	185	185	137	139	184	184	215	218	149	173	198	198
634	R3(Juv.)	149	155	238	246	117	133	213	231	195	201	195	197	211	227	195	195	137	137	188	196	218	222	173	175	198	198
635	R3(Juv.)	169	171	238	246	131	139	193	205	185	199	195	223	211	211	185	185	137	147	186	188	210	215	149	151	198	198
638	R3(Juv.)	163	171	238	238	127	131	205	217	195	205	193	195	211	215	185	195	133	137	186	186	210	218	0	0	198	198
639	R3(Juv.)	161	171	238	242	133	133	197	213	197	197	195	221	215	217	185	185	127	147	188	188	210	210	149	149	198	202
641	R3(Juv.)	161	171	244	246	127	131	193	211	183	197	195	195	213	225	183	183	137	139	190	190	218	218	171	171	198	198
642	R3(Juv.)	157	169	238	238	131	133	205	223	183	185	195	195	213	215	193	195	137	147	188	188	215	222	173	173	198	202
646	R3(Juv.)	163	165	246	250	121	131	223	227	197	199	221	233	215	227	183	195	137	137	186	188	215	218	167	171	198	198
649	R3(Juv.)	159	163	240	250	131	133	209	217	183	195	197	201	211	213	183	183	137	137	186	196	215	220	173	175	198	198
651	R3(Juv.)	149	163	238	246	131	131	213	223	197	205	195	199	211	215	193	195	127	147	188	190	210	213	164	179	198	198
652	R3(Juv.)	163	165	238	244	117	133	213	213	199	203	195	221	219	219	185	195	137	147	186	188	210	218	151	173	198	198
653	R3(Juv.)	163	169	238	244	131	131	193	209	183	205	195	195	211	219	185	195	137	139	186	190	213	220	175	179	198	198
656	R3(Juv.)	165	167	238	248	129	131	205	211	197	199	195	205	211	229	185	193	137	147	186	186	210	220	149	173	198	202
663	R3(Juv.)	157	165	238	246	131	131	213	235	203	215	195	197	215	231	195	195	137	137	186	190	215	218	165	171	198	198
670	R3(Juv.)	171	171	238	246	131	131	209	217	183	183	195	195	211	211	185	185	137	137	186	190	210	213	175	175	198	198
671	R3(Juv.)	163	165	246	250	129	131	213	233	183	197	195	195	219	219	183	195	137	137	186	190	210	215	165	171	196	198

672	R3(Juv.)	149	149	238	248	117	117	221	231	197	197	195	195	211	215	195	203	137	147	188	188	218	222	173	177	198	198
675	R3(Juv.)	155	169	240	242	127	129	221	231	183	197	195	195	211	227	185	203	137	137	188	188	220	222	163	173	198	198
681	R3(Juv.)	169	169	238	244	131	131	217	217	183	197	195	195	211	215	185	195	139	141	184	190	210	218	177	177	198	198
685	R3(Juv.)	149	161	238	248	131	147	213	221	183	197	193	195	215	223	195	195	137	137	186	186	215	218	163	177	198	200
700	R3(Juv.)	157	161	244	244	111	129	211	231	183	197	195	225	217	219	195	195	137	147	184	190	215	218	171	171	198	198
704	R3(Juv.)	165	173	250	250	131	131	199	219	197	203	195	233	211	215	183	183	137	137	188	190	215	220	171	171	198	198
706	R3(Juv.)	163	165	240	248	131	131	197	217	197	211	195	195	213	213	183	195	137	139	188	188	210	218	167	175	198	202
708	R3(Juv.)	169	171	238	248	129	131	217	217	195	197	195	195	211	215	185	195	137	139	186	186	210	218	177	177	198	198
709	R3(Juv.)	163	165	248	250	127	131	213	219	195	197	195	195	225	229	185	193	137	137	186	186	215	222	177	179	198	198
713	R3(Juv.)	157	159	240	250	129	133	211	231	197	199	195	197	211	227	195	195	137	147	188	196	215	220	171	177	198	198
716	R3(Juv.)	161	161	242	246	121	133	211	221	195	199	195	197	227	227	183	185	137	149	186	188	222	222	149	163	198	198
719	R3(Juv.)	165	165	242	250	131	131	199	209	201	201	195	195	215	215	187	187	149	149	186	190	220	220	171	171	198	198
727	R3(Juv.)	149	163	244	244	117	121	211	213	195	197	195	195	215	219	187	195	137	137	188	188	218	218	164	177	198	198
733	R3(Juv.)	161	163	244	250	127	147	217	227	197	203	193	207	211	211	185	195	132	137	184	188	0	0	163	177	198	200
740	R3(Juv.)	163	163	238	242	127	131	211	211	199	203	195	221	215	229	185	195	137	147	186	188	215	215	171	177	198	198
744	R3(Juv.)	157	163	240	242	129	129	211	241	183	203	195	195	211	215	185	195	137	137	188	188	210	213	171	173	198	198
746	R3(Juv.)	149	165	244	248	127	147	213	227	197	213	195	207	211	223	175	195	135	149	186	188	0	0	163	177	198	198
751	R3(Juv.)	161	169	238	244	127	131	227	229	197	197	195	201	211	211	185	195	137	149	186	188	218	218	151	177	198	198
752	R3(Juv.)	149	165	240	242	131	131	227	235	187	205	195	205	211	215	185	195	127	137	188	188	218	218	167	173	198	202
753	R3(Juv.)	163	171	238	242	127	127	213	223	183	195	195	215	213	215	185	187	137	151	186	188	218	218	171	171	198	198
756	R3(Juv.)	165	165	248	250	131	131	213	213	197	199	195	197	215	215	185	185	137	147	186	190	215	218	164	173	198	198
766	R3(Juv.)	163	165	238	240	131	133	213	235	183	203	195	201	213	219	183	185	137	147	186	186	210	215	151	175	198	202
781	R3(Juv.)	161	163	238	238	127	127	213	227	201	203	197	221	211	219	195	197	127	147	184	190	215	215	169	173	198	198
790	R3(Juv.)	157	165	238	248	131	133	211	223	201	209	195	195	211	227	185	195	137	137	188	196	204	218	151	173	198	198
2	R4(Adult)	165	167	242	244	121	121	211	211	193	213	193	195	223	225	195	197	139	139	184	186	210	210	159	183	198	198
4	R4(Adult)	157	159	238	242	121	133	211	241	175	193	195	199	225	227	193	199	143	143	184	186	213	213	159	159	198	198
6	R4(Adult)	165	169	238	242	0	0	207	207	193	193	191	195	211	213	197	197	145	145	186	186	210	213	159	159	198	198
9	R4(Adult)	159	169	244	246	121	121	207	207	203	205	195	195	211	215	175	187	0	0	184	184	210	217	159	159	198	198
10	R4(Adult)	159	165	238	240	121	121	207	211	183	195	193	219	221	229	187	199	137	137	184	188	220	220	161	169	198	198

14	R4(Adult)	159	177	238	238	121	121	217	265	175	205	195	199	221	227	185	195	149	149	184	184	215	220	159	175	198	198
15	R4(Adult)	163	169	238	240	121	121	215	215	193	207	191	195	213	223	185	195	139	139	184	184	213	213	159	159	198	202
16	R4(Adult)	159	163	238	238	121	121	193	249	175	195	195	195	223	223	185	199	143	143	184	186	215	215	155	159	198	198
19	R4(Adult)	159	169	242	242	135	135	213	213	183	207	195	217	211	227	197	197	0	0	184	184	217	217	159	159	198	198
22	R4(Adult)	159	165	238	248	121	127	209	213	175	193	195	225	215	233	187	197	137	147	182	186	213	220	159	171	198	198
25	R4(Adult)	165	173	238	242	0	0	209	217	203	209	195	195	211	225	191	195	139	143	184	186	210	213	159	169	198	198
28	R4(Adult)	165	169	242	242	127	127	229	229	197	197	193	195	211	229	197	207	149	149	184	184	213	213	161	161	198	200
29	R4(Adult)	159	159	242	246	121	127	211	217	195	197	195	195	211	211	183	191	141	147	184	184	213	213	159	159	198	200
33	R4(Adult)	161	165	238	242	129	129	207	209	175	185	193	195	215	229	199	199	139	139	184	184	213	220	159	161	198	198
34	R4(Adult)	159	173	246	248	121	135	209	209	185	193	193	225	211	215	179	199	139	139	184	184	213	213	159	165	198	200
42	R4(Adult)	165	165	242	246	121	121	227	227	207	211	195	221	223	223	187	195	139	139	184	184	210	220	169	169	198	198
46	R4(Adult)	159	167	238	240	135	135	207	209	211	213	195	195	211	223	183	185	125	137	184	184	213	220	159	171	198	198
51	R4(Adult)	159	167	238	242	121	127	207	213	207	209	191	225	211	225	187	187	145	145	184	186	213	215	159	159	198	198
61	R4(Adult)	165	167	242	242	127	127	209	229	193	207	195	199	215	221	185	197	141	141	184	186	215	220	161	161	198	200
65	R4(Adult)	159	159	238	242	133	133	209	213	193	195	195	197	215	215	175	175	143	143	184	184	210	210	159	165	198	198
75	R4(Adult)	165	173	246	246	133	133	219	225	193	207	195	195	229	229	197	211	135	135	184	186	210	213	159	161	198	198
79	R4(Adult)	159	163	236	242	133	133	209	211	175	207	193	199	211	229	183	193	137	137	184	184	210	213	159	159	198	200
81	R4(Adult)	159	167	242	248	121	135	193	225	205	207	193	225	211	211	193	193	133	139	184	184	213	213	159	169	198	198
84	R4(Adult)	159	165	238	246	121	121	213	213	175	207	193	193	213	229	179	199	137	143	184	186	213	220	159	169	198	200
90	R4(Adult)	163	165	238	248	133	135	213	227	175	195	195	195	213	229	199	199	133	139	184	186	213	215	159	165	198	198
96	R4(Adult)	159	163	248	248	133	133	221	221	207	213	199	237	213	215	183	187	147	147	184	184	210	215	169	175	198	198
100	R4(Adult)	159	159	242	242	135	135	207	249	195	201	195	195	223	229	193	213	135	137	184	184	215	215	159	159	198	198
111	R4(Adult)	159	169	238	238	121	121	209	209	185	211	227	245	215	215	191	197	125	137	184	184	213	215	159	159	198	198
115	R4(Adult)	159	163	242	242	121	121	207	217	175	205	195	195	229	229	193	195	147	147	184	184	213	213	165	169	198	200
120	R4(Adult)	159	165	240	242	121	121	207	213	193	211	199	217	211	229	197	199	137	143	184	184	215	220	161	165	198	198
124	R4(Adult)	163	167	238	242	121	121	207	213	205	207	191	195	211	225	187	193	147	147	184	184	213	213	159	165	198	198
132	R4(Adult)	159	159	238	242	121	121	213	215	197	205	195	195	221	223	183	197	149	149	184	184	220	220	159	161	198	200
135	R4(Adult)	159	167	238	244	121	121	213	265	197	203	207	223	217	223	193	199	141	143	184	186	213	220	159	159	198	202
139	R4(Adult)	159	165	238	242	121	127	229	249	193	193	195	199	211	221	185	185	143	143	184	186	220	220	169	169	198	198

155	R4(Adult)	159	159	238	248	121	121	211	213	175	195	207	217	211	223	179	199	137	137	184	186	210	215	161	181	198	198
156	R4(Adult)	165	169	238	248	121	129	215	227	195	207	195	195	215	223	197	199	0	0	184	184	213	219	151	161	198	198
161	R4(Adult)	163	167	238	242	121	121	223	249	195	209	195	221	211	229	175	199	137	137	184	184	213	213	159	159	198	200
168	R4(Adult)	163	165	238	242	121	133	213	213	175	203	207	227	221	223	179	197	137	137	184	184	220	220	161	161	198	198
171	R4(Adult)	159	173	242	246	121	121	193	215	195	201	195	195	215	229	195	199	137	137	184	186	213	213	171	181	198	198
184	R4(Adult)	159	165	238	242	127	129	217	229	183	193	195	199	211	215	185	185	143	143	184	184	213	220	169	171	198	200
189	R4(Adult)	167	169	238	238	121	121	193	219	207	211	195	219	211	223	193	199	139	139	184	186	213	213	159	159	198	198
194	R4(Adult)	159	159	236	242	121	127	207	213	211	211	195	199	211	227	179	199	125	125	184	184	213	213	163	169	198	198
206	R4(Adult)	161	163	242	248	95	95	207	207	175	209	221	251	223	225	187	199	139	147	184	186	220	220	159	159	198	198
795	R4(Adult)	163	165	240	248	129	129	207	209	203	213	221	245	213	229	195	197	143	143	184	184	217	217	159	159	198	198
148	R4(Juv.)	163	163	238	238	121	121	215	217	207	207	191	195	213	213	183	185	139	139	184	184	213	220	159	159	198	198
623	R4(Juv.)	159	167	238	238	121	129	193	227	195	207	195	195	223	233	189	193	139	145	184	186	210	213	159	161	194	198
624	R4(Juv.)	159	163	238	246	129	129	207	235	203	213	195	209	215	227	179	185	137	137	184	188	218	219	155	161	198	198
625	R4(Juv.)	159	163	238	248	121	121	227	227	175	195	193	217	211	213	197	199	137	137	184	184	213	219	159	169	198	198
626	R4(Juv.)	159	169	242	246	121	129	215	247	205	213	193	195	211	211	175	195	137	137	184	184	210	210	159	161	198	202
633	R4(Juv.)	159	169	242	242	135	135	215	217	175	183	195	195	215	229	199	199	143	145	184	184	210	220	155	159	198	198
640	R4(Juv.)	169	169	242	246	115	121	209	265	195	213	193	199	225	225	193	193	139	139	184	184	210	220	151	157	198	198
643	R4(Juv.)	163	169	242	246	121	135	227	265	195	213	217	239	217	229	185	193	139	143	184	184	213	220	169	169	198	198
645	R4(Juv.)	165	169	238	242	121	129	213	227	175	207	195	227	223	223	199	199	147	147	184	184	210	213	151	159	198	198
647	R4(Juv.)	159	161	238	242	0	0	205	217	205	213	199	229	213	217	187	211	149	149	184	186	213	215	159	159	198	200
650	R4(Juv.)	163	167	238	240	133	135	207	207	197	211	193	199	211	213	197	199	137	147	184	186	213	221	159	161	198	198
661	R4(Juv.)	159	169	246	246	121	121	209	227	175	213	197	199	215	229	191	197	139	139	184	184	210	220	151	169	198	198
664	R4(Juv.)	165	167	242	246	121	133	225	249	207	207	195	251	215	221	175	193	147	149	184	184	210	215	159	169	198	198
666	R4(Juv.)	163	165	238	242	115	121	213	221	195	207	193	195	225	225	187	199	139	143	186	186	213	220	159	159	198	198
669	R4(Juv.)	159	159	246	246	135	135	217	265	193	205	207	211	223	223	197	199	137	139	184	184	220	220	159	161	198	200
676	R4(Juv.)	159	163	238	238	121	121	207	215	193	213	225	245	213	215	185	199	143	143	184	184	210	210	161	171	198	202
678	R4(Juv.)	159	159	246	246	129	129	227	265	175	183	195	199	211	223	193	193	139	139	184	186	210	210	159	159	198	198
680	R4(Juv.)	163	163	238	242	121	121	213	225	175	183	195	229	215	229	195	197	139	147	184	186	213	213	159	169	198	200
682	R4(Juv.)	159	167	238	242	99	121	209	209	195	211	195	195	211	223	185	199	145	145	184	186	213	213	159	169	198	198

686	R4(Juv.)	169	169	238	242	99	137	193	225	195	207	195	207	223	227	199	199	0	0	184	184	220	220	159	159	198	198
687	R4(Juv.)	159	161	242	246	121	129	217	249	195	207	195	199	217	233	189	191	137	149	184	184	215	220	159	161	198	198
689	R4(Juv.)	159	165	238	242	99	121	211	265	207	215	201	225	215	221	185	199	137	143	184	184	218	218	159	181	198	200
690	R4(Juv.)	159	159	242	246	135	135	207	207	207	211	195	245	211	215	185	199	137	143	184	186	219	219	161	169	198	198
691	R4(Juv.)	159	163	242	242	121	121	215	227	201	213	195	195	225	227	185	195	147	147	182	184	220	220	159	159	198	198
693	R4(Juv.)	159	167	244	244	121	121	209	217	195	195	195	199	211	213	185	187	143	149	184	184	213	220	159	165	198	198
694	R4(Juv.)	159	165	242	248	121	135	217	217	193	207	197	235	215	227	193	199	147	147	184	186	213	220	159	161	198	198
695	R4(Juv.)	159	159	242	244	133	137	193	207	193	195	193	195	211	213	185	199	137	141	184	184	210	210	159	161	198	198
696	R4(Juv.)	159	169	238	242	121	121	213	249	207	211	195	195	213	227	191	191	0	0	184	184	220	220	151	161	198	202
697	R4(Juv.)	163	167	244	248	99	105	207	215	197	209	195	203	223	229	175	193	137	141	184	186	213	219	159	161	198	198
703	R4(Juv.)	159	169	238	238	121	129	215	227	207	209	195	195	215	223	193	195	139	143	184	184	213	220	159	159	198	200
705	R4(Juv.)	159	167	242	242	121	127	205	219	197	203	195	195	213	225	183	199	137	139	184	186	220	220	159	165	198	202
707	R4(Juv.)	161	165	246	246	135	135	209	225	207	209	195	195	213	223	179	197	139	143	184	184	215	220	159	159	198	198
711	R4(Juv.)	159	161	242	246	121	135	215	247	193	213	195	235	211	233	179	179	139	139	184	186	220	220	161	165	200	200
721	R4(Juv.)	159	159	242	242	121	133	207	211	193	195	193	229	211	229	197	199	139	149	184	186	213	213	161	161	198	198
723	R4(Juv.)	159	163	242	246	121	133	209	209	195	211	199	199	215	223	193	197	133	133	184	186	0	0	159	169	198	198
728	R4(Juv.)	159	163	242	246	115	135	207	227	175	213	209	217	215	215	185	213	137	139	182	184	213	219	159	161	198	200
731	R4(Juv.)	163	169	238	238	129	129	207	225	197	213	195	247	215	223	175	185	145	145	182	184	219	219	159	161	198	198
732	R4(Juv.)	159	165	242	246	121	133	209	209	195	207	195	207	225	229	195	199	141	143	184	184	213	217	159	173	198	200
736	R4(Juv.)	159	159	238	244	121	127	209	217	193	209	193	195	213	223	193	197	139	147	184	186	213	220	159	165	198	198
741	R4(Juv.)	163	167	244	248	0	0	207	215	197	209	195	203	223	229	175	193	137	141	184	186	213	220	159	161	198	198
747	R4(Juv.)	163	167	238	240	133	135	207	207	197	211	193	199	211	213	197	199	137	147	184	186	213	220	159	161	198	198
770	R4(Juv.)	159	163	238	246	135	135	209	217	203	207	197	211	223	225	179	197	137	137	184	184	213	213	159	161	198	198
772	R4(Juv.)	159	163	242	248	121	135	213	213	195	197	195	237	211	211	179	187	133	141	184	184	213	213	169	169	198	198
777	R4(Juv.)	159	167	240	242	137	137	209	247	201	207	195	229	223	225	187	197	137	137	184	186	213	220	159	161	194	198
789	R4(Juv.)	159	165	242	242	121	121	207	219	193	211	193	227	227	229	193	195	145	145	184	186	217	220	157	159	198	198
791	R4(Juv.)	159	163	238	242	121	129	213	225	201	211	195	223	213	229	185	199	141	143	182	184	220	220	159	171	198	198
797	R4(Juv.)	159	161	242	246	121	135	215	247	193	213	195	235	211	233	179	179	139	139	184	186	219	220	161	165	200	200
798	R4(Juv.)	159	165	238	242	121	137	207	211	197	207	211	221	211	215	179	199	125	149	184	186	210	213	159	183	198	198

800	R4(Juv.)	159	159	238	248	121	133	207	249	207	213	195	225	213	223	193	193	133	149	182	184	213	220	159	159	194	200
428	ST5	169	169	246	248	129	131	193	223	183	199	195	195	211	217	195	195	137	137	186	186	210	218	157	157	198	202
457	ST5	163	171	244	246	117	129	219	230	183	187	195	209	213	215	195	197	137	141	186	188	218	222	173	179	194	198
463	ST5	165	165	240	242	117	131	205	209	183	183	195	229	213	227	187	195	127	139	186	186	219	219	164	169	198	202
473	ST5	159	171	240	248	99	131	211	213	183	187	211	217	213	231	185	185	135	137	184	190	213	218	171	175	198	198
475	ST5	159	163	238	250	119	127	213	231	183	197	193	195	213	221	185	195	129	151	186	186	218	218	157	157	198	202
484	ST5	169	171	242	248	121	129	209	223	185	197	195	199	215	231	181	197	137	137	184	184	215	218	175	177	198	198
494	ST5	149	161	238	244	129	129	209	213	201	211	195	227	225	229	185	195	137	147	186	188	218	218	171	171	198	198
508	ST5	159	161	238	238	117	131	211	215	197	205	195	201	213	225	187	195	137	141	188	188	218	218	157	173	196	198
510	ST5	149	149	246	250	119	127	0	0	183	195	195	195	223	227	185	187	137	141	188	188	218	218	171	179	198	198
512	ST5	163	163	234	248	129	131	213	229	183	195	215	215	213	215	183	185	137	147	184	186	218	218	163	164	198	202
516	ST5	155	165	234	238	117	127	205	211	197	201	197	213	211	227	185	195	137	137	186	188	210	218	157	165	198	198
517	ST5	161	165	246	246	119	131	209	221	183	195	195	211	223	223	185	187	133	141	188	188	215	218	167	171	198	198
529	ST5	163	171	244	246	117	129	193	213	197	203	199	225	211	219	183	185	137	147	188	188	218	220	165	171	198	198
533	ST5	165	165	248	248	139	139	223	223	187	195	209	211	213	221	195	195	129	137	188	188	218	218	169	171	194	202
534	ST5	163	163	238	248	129	131	209	221	197	205	195	201	215	219	195	195	127	137	188	190	210	213	175	177	198	202
535	ST5	163	171	238	248	121	147	215	227	183	203	195	195	213	213	183	195	137	137	188	188	220	222	164	173	198	198
539	ST5	169	169	238	246	127	139	205	211	195	203	197	211	215	229	183	201	137	137	188	190	210	210	157	171	198	198
540	ST5	163	169	250	250	129	129	213	225	197	201	195	195	211	219	183	185	137	147	188	190	218	218	163	175	198	202
542	ST5	167	169	246	248	131	135	217	235	183	197	197	209	221	221	183	197	127	135	188	188	222	222	157	157	198	198
547	ST5	163	167	240	250	117	121	217	225	183	201	207	219	231	233	185	195	137	139	184	186	218	220	165	171	198	198
551	ST5	161	163	238	240	117	117	213	219	183	183	195	223	213	221	185	195	135	137	188	188	213	220	151	179	198	202
552	ST5	161	171	248	250	133	133	209	209	195	201	195	223	217	231	185	185	137	137	188	188	215	218	171	173	198	198
557	ST5	163	163	246	248	129	131	213	225	197	197	195	195	215	233	185	185	137	137	188	188	218	218	171	175	198	198
560	ST5	157	163	246	246	117	131	205	217	197	203	195	199	213	229	183	187	135	147	188	188	218	218	171	197	198	198
562	ST5	163	165	244	248	127	131	209	213	195	199	197	199	211	215	187	195	137	149	188	188	210	218	171	179	198	198
570	ST5	161	169	238	242	119	127	223	233	183	201	195	195	215	227	183	195	135	147	184	190	215	218	157	157	198	198
573	ST5	157	165	238	246	127	131	211	211	185	185	195	215	211	219	195	195	137	141	186	188	218	220	165	171	198	202
578	ST5	169	169	250	250	127	133	225	225	197	207	195	199	229	229	185	185	137	153	186	188	210	215	157	169	196	202

579	ST5	165	169	244	248	129	131	223	233	183	183	195	195	219	221	183	195	135	137	188	188	218	218	171	173	198	202
583	ST5	149	163	240	248	129	131	223	231	197	197	195	223	211	215	183	183	137	137	186	188	218	218	157	173	198	202
584	ST5	149	163	244	250	127	131	193	211	183	199	193	195	213	221	175	203	137	149	186	186	213	215	149	179	198	200
586	ST5	165	165	238	238	0	0	243	243	183	201	197	211	213	227	183	185	147	147	186	188	210	218	165	167	198	198
588	ST5	163	169	238	248	129	145	207	209	183	197	195	199	215	227	183	185	133	137	186	186	213	218	173	177	198	202
590	ST5	163	163	238	248	117	131	223	233	199	207	195	207	211	211	183	183	137	149	188	190	210	218	173	179	198	198
592	ST5	159	169	240	246	127	131	211	215	197	197	195	219	217	231	181	183	137	141	186	186	220	220	171	171	198	198
593	ST5	159	169	244	244	129	139	211	233	183	197	195	201	217	221	185	195	137	147	188	188	218	218	173	177	198	202
594	ST5	161	163	246	248	117	121	211	213	203	205	195	199	215	219	185	187	137	137	188	190	213	220	157	175	198	198
595	ST5	0	0	248	248	121	127	213	213	183	197	213	223	219	223	181	195	137	137	188	188	215	215	157	175	196	196
596	ST5	165	165	246	250	117	131	217	223	195	203	195	233	217	221	195	203	137	147	188	188	218	220	155	173	198	198
598	ST5	149	169	240	248	129	129	193	243	205	205	195	205	217	227	185	203	135	137	186	188	215	218	157	171	198	198
601	ST5	169	171	238	240	117	117	215	223	195	203	195	195	215	217	195	197	137	149	190	190	213	220	171	175	198	198
602	ST5	163	165	248	250	117	131	199	231	183	195	197	197	211	227	185	193	135	137	186	188	215	218	157	171	198	202
604	ST5	163	165	246	246	127	139	217	221	183	197	197	215	217	221	185	185	127	137	184	186	210	218	151	157	198	200
605	ST5	161	163	250	250	129	129	213	221	183	211	211	213	215	221	183	183	145	145	186	188	218	220	167	171	198	198
606	ST5	159	167	248	248	117	127	205	211	195	197	201	243	211	217	185	195	137	141	188	188	218	218	169	179	198	202
608	ST5	163	163	245	246	129	129	209	211	197	201	195	213	227	229	183	185	137	139	186	188	215	218	169	171	198	198
610	ST5	169	169	246	250	121	133	215	217	197	197	201	201	213	217	183	185	137	147	188	188	215	215	155	173	198	198
611	ST5	163	165	240	240	129	133	213	215	197	201	195	195	217	229	185	195	135	137	188	188	218	218	173	175	198	198
612	ST5	149	163	244	246	121	121	221	223	183	183	195	199	213	221	183	185	137	141	186	188	218	222	175	177	198	198
415	ST6	155	169	248	250	119	131	221	223	197	209	201	217	229	229	195	195	147	147	188	188	220	220	171	171	198	198
417	ST6	163	163	246	246	121	129	213	223	183	195	209	223	211	213	195	195	137	147	186	188	218	220	165	169	198	204
419	ST6	169	169	238	248	119	131	193	195	197	197	195	197	211	217	183	195	137	147	188	188	210	220	165	169	198	198
422	ST6	163	169	238	250	117	131	209	235	197	211	195	217	211	217	185	185	137	147	188	188	216	220	173	173	198	200
429	ST6	149	159	246	248	117	129	193	223	199	203	195	199	215	221	195	195	137	137	188	188	215	218	161	173	198	202
431	ST6	163	169	244	250	121	131	209	239	201	205	197	217	211	213	185	203	137	139	184	188	218	218	149	167	198	198
438	ST6	163	165	240	250	131	133	209	230	201	203	195	209	213	221	185	185	129	137	188	188	220	220	165	165	198	202
440	ST6	163	163	238	246	131	131	197	213	183	197	195	195	211	227	193	195	135	147	186	188	215	220	171	175	198	198

465	ST6	149	159	238	248	129	131	209	211	187	195	195	195	213	227	195	195	137	137	186	196	216	218	171	171	198	198
466	ST6	149	163	245	245	119	131	209	213	199	205	195	195	211	227	195	195	137	137	186	188	218	220	157	171	198	200
472	ST6	149	167	244	250	117	119	207	213	187	203	195	221	217	227	187	193	135	137	184	188	218	220	171	171	198	202
477	ST6	149	163	238	250	117	129	217	221	183	187	195	217	215	233	187	195	137	151	188	188	216	218	167	167	196	198
489	ST6	149	163	248	248	129	131	215	239	187	197	213	213	215	231	185	187	137	139	182	188	213	221	171	175	198	198
496	ST6	163	165	244	248	129	131	193	211	183	215	195	197	225	227	189	195	129	137	188	188	213	218	157	173	198	198
499	ST6	163	163	238	248	121	131	211	219	197	203	209	223	221	227	183	183	137	147	186	186	218	218	164	175	198	198
500	ST6	163	163	238	246	117	121	235	237	183	197	195	213	227	229	195	195	137	137	186	188	210	220	157	157	202	202
503	ST6	163	165	238	248	117	131	209	235	197	211	195	195	211	221	185	195	147	147	188	188	213	218	157	157	198	198
505	ST6	163	163	244	244	121	127	207	209	187	215	197	217	213	213	185	185	137	139	186	186	218	222	163	175	198	198
511	ST6	163	165	248	248	121	121	213	227	183	197	195	211	213	215	187	189	137	149	186	188	218	222	161	171	202	202
513	ST6	157	165	244	246	121	127	193	223	201	209	193	197	219	233	183	183	137	139	186	186	215	215	161	171	198	202
514	ST6	149	161	250	250	117	139	193	221	205	211	207	209	211	221	195	195	137	149	188	188	218	220	157	173	198	198
527	ST6	159	165	238	244	119	127	193	211	197	205	195	195	213	213	187	195	137	137	188	188	220	222	157	177	198	198
528	ST6	163	163	240	248	111	131	199	223	183	201	199	209	225	235	185	195	137	137	188	188	215	220	167	171	198	202
530	ST6	149	165	238	240	129	131	209	219	197	197	195	207	221	221	185	195	137	137	186	188	215	218	161	171	198	198
531	ST6	165	169	240	246	121	133	230	233	211	215	209	209	211	227	185	195	137	147	182	188	210	220	157	169	198	202
532	ST6	161	165	246	250	129	131	217	223	207	211	193	211	213	219	183	185	137	137	188	196	213	216	157	163	198	202
543	ST6	163	163	244	244	121	129	223	233	197	197	195	209	211	221	183	195	137	137	188	188	215	220	167	171	196	198
544	ST6	165	169	240	250	131	139	211	223	185	205	197	217	213	229	181	185	137	149	186	186	213	215	167	175	198	200
545	ST6	169	169	246	250	105	129	209	223	183	203	195	195	225	229	183	183	135	137	186	188	0	0	171	179	0	0
546	ST6	157	169	244	244	121	121	215	215	183	197	193	211	231	231	183	187	137	137	188	188	210	220	157	165	200	200
548	ST6	149	157	248	250	99	131	213	221	183	197	195	195	213	213	183	195	137	137	188	188	220	220	171	171	198	200
550	ST6	163	169	240	248	119	131	209	233	183	201	195	197	215	215	193	195	135	137	186	188	215	218	171	173	198	200
553	ST6	161	167	250	250	117	117	209	209	195	211	207	213	213	217	195	195	137	137	188	188	213	218	157	161	198	198
554	ST6	163	165	238	240	127	139	193	211	195	215	195	195	211	217	185	187	137	137	188	188	218	220	169	175	198	198
566	ST6	163	169	238	238	121	131	223	235	197	199	195	219	221	221	183	195	143	147	188	188	215	220	171	175	198	202
574	ST6	149	161	246	250	129	129	209	241	197	197	197	209	211	219	183	185	137	147	188	188	213	218	161	171	198	198
575	ST6	163	169	240	246	121	121	213	221	195	201	193	193	213	221	185	195	137	147	188	196	210	218	157	171	198	198

576	ST6	149	163	248	250	139	161	237	239	187	201	195	213	231	231	185	187	135	137	188	188	219	221	173	175	198	202
577	ST6	165	169	244	246	121	121	209	219	199	203	195	237	217	233	195	195	141	147	184	188	210	215	151	163	196	198
580	ST6	159	163	250	250	117	127	221	241	209	215	193	209	211	227	185	195	137	139	188	188	218	218	171	175	198	202
582	ST6	155	163	246	248	121	129	193	213	201	211	197	197	211	213	185	195	135	137	188	188	210	213	157	169	198	198
587	ST6	163	169	248	250	121	129	209	237	183	183	195	215	213	215	185	185	137	137	186	186	213	218	163	171	198	202
589	ST6	163	163	246	250	131	161	213	237	197	197	195	195	227	231	183	185	137	137	188	188	218	220	164	173	198	202
599	ST6	165	165	238	248	121	131	209	221	187	197	195	229	211	227	195	195	137	137	188	188	210	220	171	171	198	198
600	ST6	149	165	238	250	121	131	209	223	183	183	195	229	213	233	193	195	137	137	186	188	218	220	171	175	198	198
603	ST6	163	169	244	246	129	131	211	223	195	197	195	225	211	213	183	183	137	137	186	188	210	215	171	173	198	198
607	ST6	149	165	240	240	121	139	209	223	183	197	195	217	211	211	185	185	137	147	188	188	218	218	157	169	198	198
613	ST6	163	169	238	248	127	127	235	237	183	197	199	209	211	227	187	195	147	147	184	188	220	220	171	173	198	202
414	ST7	165	165	246	246	117	117	209	223	183	203	195	195	213	227	183	197	137	137	188	188	218	218	161	163	198	198
416	ST7	165	169	238	240	129	131	211	223	183	197	201	209	215	227	187	189	127	137	186	188	210	218	157	177	198	198
418	ST7	149	149	240	248	133	161	213	219	195	197	193	195	213	231	183	195	123	137	188	188	213	218	157	164	198	198
432	ST7	163	171	240	246	139	139	193	207	195	203	195	209	213	227	183	185	137	147	188	196	215	218	173	177	198	198
433	ST7	149	163	246	248	129	133	211	211	185	207	193	201	215	217	183	185	137	137	186	188	215	215	169	171	198	198
434	ST7	149	167	246	248	127	129	213	243	183	183	195	195	211	219	183	185	127	151	186	189	215	220	163	175	198	198
446	ST7	149	169	238	240	121	127	209	213	183	187	195	211	219	233	185	185	137	137	188	188	215	218	161	179	198	198
447	ST7	163	165	238	246	131	131	207	213	183	195	217	223	211	215	183	185	137	137	188	188	215	218	169	171	198	200
448	ST7	149	163	238	250	127	133	209	217	195	195	193	195	217	235	183	195	135	137	188	188	213	220	161	171	198	202
451	ST7	165	165	246	248	117	117	219	219	183	183	195	209	229	229	185	185	137	147	188	190	215	218	165	171	198	202
452	ST7	149	149	250	250	129	129	213	215	201	211	195	219	215	229	185	185	135	137	186	188	213	213	149	159	198	200
467	ST7	149	161	238	246	127	133	207	221	195	201	223	223	211	217	183	183	137	137	186	188	213	215	173	173	198	198
468	ST7	149	163	242	244	129	139	193	203	195	195	195	195	211	225	185	195	137	147	186	188	218	218	173	173	198	202
470	ST7	159	163	238	250	121	131	207	207	199	217	195	195	213	225	183	195	137	137	186	188	213	218	173	173	198	198
471	ST7	149	149	246	248	161	161	211	211	201	203	195	195	227	227	195	195	137	155	186	188	215	218	149	163	198	198
479	ST7	163	163	238	248	129	131	207	213	201	201	209	223	213	231	185	195	137	137	186	186	213	218	173	173	194	198
488	ST7	163	163	242	248	129	129	209	211	195	209	215	215	215	235	185	195	137	137	188	188	213	215	169	173	198	200
490	ST7	149	163	250	250	129	129	213	239	195	199	193	195	213	217	185	185	137	137	186	186	215	218	0	0	198	198

491	ST7	149	161	246	250	121	139	211	225	201	205	209	209	227	227	185	185	127	137	188	188	215	218	149	161	198	202
493	ST7	159	167	246	248	127	127	225	225	195	197	197	209	227	233	183	185	137	147	186	188	215	220	155	155	198	198
495	ST7	161	165	246	250	127	161	211	211	197	201	197	197	227	231	181	195	137	149	188	188	215	218	155	171	198	198
497	ST7	149	149	238	250	129	131	199	221	183	199	195	217	221	225	181	183	137	157	186	188	215	220	157	167	198	198
498	ST7	163	163	246	248	131	131	235	257	197	211	195	217	217	217	185	197	137	139	188	188	218	220	173	177	202	202
501	ST7	161	163	248	248	121	139	197	217	183	183	209	209	213	229	195	195	137	137	184	188	215	220	161	163	198	198
502	ST7	169	169	246	248	117	133	211	215	197	207	195	219	221	233	183	183	147	149	188	188	218	220	157	163	198	198
504	ST7	149	165	246	248	127	131	225	225	183	197	195	197	225	233	185	185	137	147	184	186	215	215	149	149	198	198
506	ST7	165	165	246	248	117	117	219	219	183	183	195	209	229	231	185	185	137	147	188	190	215	218	165	171	198	202
507	ST7	163	163	238	250	121	129	193	207	183	195	223	223	213	213	183	183	137	137	188	188	213	215	177	179	198	202
509	ST7	149	149	248	250	121	161	211	211	197	201	195	197	225	231	183	199	137	149	186	188	215	220	155	173	198	198
515	ST7	163	171	240	248	121	127	221	235	185	203	195	215	219	227	187	195	137	151	186	196	213	215	157	177	198	198
518	ST7	159	169	238	248	117	121	213	217	185	199	195	219	211	221	183	195	137	137	188	188	218	220	171	179	198	198
519	ST7	149	149	240	240	121	139	219	219	183	199	195	207	215	221	183	187	147	155	188	188	218	218	151	161	198	198
520	ST7	167	167	248	248	131	139	209	227	0	0	221	223	217	231	195	203	137	137	188	188	218	218	177	177	198	202
521	ST7	149	157	246	246	133	137	211	221	187	203	193	209	217	223	183	183	137	137	188	188	222	222	171	173	198	202
522	ST7	149	169	238	246	99	117	209	211	197	203	213	213	217	225	187	187	137	137	188	188	218	218	155	169	198	198
526	ST7	149	163	244	250	121	139	203	219	187	201	193	207	215	217	185	195	137	137	186	188	210	218	173	177	198	198
538	ST7	149	163	238	245	129	139	211	215	197	203	209	209	227	227	183	187	137	155	188	188	215	220	157	169	198	198
556	ST7	161	163	238	248	121	133	193	211	183	199	195	223	227	229	195	195	137	137	188	188	218	220	155	155	198	200
558	ST7	149	159	238	244	121	161	207	209	195	199	195	209	213	221	183	183	135	137	186	188	213	218	173	173	198	198
559	ST7	149	163	240	246	137	139	193	193	199	199	195	195	213	229	189	195	137	137	188	196	213	218	173	173	198	202
561	ST7	161	163	244	246	131	133	207	213	183	195	199	213	225	235	185	185	132	155	186	186	215	215	165	175	198	198
563	ST7	161	163	248	250	117	117	211	213	199	199	195	199	221	227	181	181	137	137	188	188	213	215	165	169	198	198
564	ST7	169	169	240	248	0	0	211	229	183	185	195	223	213	229	187	189	137	147	184	188	218	220	173	173	196	198
565	ST7	149	165	246	246	129	131	213	213	197	197	209	217	211	217	183	203	132	137	188	188	213	218	155	171	198	202
568	ST7	161	171	244	248	129	129	193	223	185	187	211	217	213	233	185	187	137	155	184	188	218	234	161	161	198	198
571	ST7	149	149	242	246	117	129	211	223	195	197	193	195	209	231	183	195	137	155	188	188	215	220	163	175	198	198
572	ST7	159	161	238	246	127	133	211	223	197	209	195	215	227	235	185	203	137	143	186	188	213	215	163	175	198	202

581	ST7	149	167	245	246	133	139	211	213	195	201	195	213	227	229	185	187	137	137	186	188	218	220	173	175	198	198
585	ST7	165	165	238	242	121	129	217	217	195	195	197	197	219	233	195	195	139	139	186	186	215	216	0	0	198	198
591	ST7	163	169	240	242	121	133	213	227	203	211	195	223	213	227	185	185	135	137	186	186	215	218	161	171	198	198
420	ST8	161	163	240	248	121	131	211	223	201	205	223	245	225	225	183	185	147	147	186	190	210	218	171	177	198	198
421	ST8	163	165	238	250	121	129	197	223	195	199	195	195	211	219	183	195	143	149	188	188	215	218	163	163	198	198
423	ST8	157	163	248	250	127	127	223	223	197	209	195	199	211	227	183	185	127	137	188	190	215	218	171	175	198	198
424	ST8	161	161	238	240	129	131	221	233	197	201	195	195	221	229	185	187	135	147	184	188	213	218	171	177	198	198
425	ST8	161	169	242	250	117	131	235	235	197	199	195	197	215	219	185	203	139	149	186	190	218	218	173	175	198	198
426	ST8	149	163	238	246	127	127	211	213	203	211	195	205	215	229	175	195	123	137	188	188	216	218	167	171	198	198
427	ST8	155	169	246	250	119	133	205	230	183	197	195	195	217	227	181	181	137	147	188	188	210	218	157	177	198	198
430	ST8	155	165	240	248	127	131	217	245	195	215	195	195	223	227	195	203	137	139	188	188	213	218	151	177	198	198
435	ST8	161	165	240	250	111	121	207	217	197	197	195	197	215	215	185	203	133	149	188	188	215	218	169	171	202	202
436	ST8	149	159	238	238	131	131	205	219	195	195	195	197	211	217	181	183	127	147	184	184	220	220	171	173	200	202
437	ST8	165	169	242	250	121	129	213	219	197	197	195	223	211	223	185	195	137	139	188	188	215	222	157	157	198	202
439	ST8	149	169	244	244	133	133	231	233	197	197	195	199	211	221	185	203	127	137	186	188	215	215	171	181	198	198
441	ST8	159	165	240	246	121	131	197	231	197	197	195	235	221	229	181	187	135	141	186	186	218	218	173	175	198	202
442	ST8	151	165	238	240	111	129	219	223	197	209	199	211	219	229	195	203	137	137	188	188	215	215	175	177	198	202
443	ST8	149	161	240	248	129	131	205	225	197	197	197	215	211	217	183	203	133	137	186	188	218	220	169	177	198	202
444	ST8	161	165	238	242	131	131	217	223	197	197	195	199	211	221	195	195	137	141	188	188	210	215	175	175	198	202
445	ST8	161	165	248	248	121	131	213	223	197	205	195	223	211	213	203	203	135	143	184	186	218	220	165	165	198	198
449	ST8	161	169	248	248	121	133	211	213	197	205	195	195	221	227	203	205	137	137	184	186	215	215	171	173	198	198
450	ST8	161	163	238	250	119	121	223	231	197	201	195	195	215	219	185	193	139	147	184	184	216	220	177	177	198	198
453	ST8	161	165	244	246	131	131	217	223	203	215	195	195	221	227	185	185	137	149	188	188	215	218	151	169	198	198
454	ST8	165	165	238	240	119	121	225	233	197	197	0	0	221	225	183	195	141	141	188	188	213	215	164	177	198	198
455	ST8	149	163	244	244	127	131	213	217	197	203	195	195	211	227	195	195	137	139	186	188	218	218	163	171	198	198
456	ST8	161	165	240	242	129	131	193	205	183	201	197	215	215	229	183	193	143	147	184	188	215	222	165	175	198	198
458	ST8	161	161	246	248	117	139	213	217	195	197	197	197	213	217	183	203	137	147	186	188	215	215	151	169	198	198
459	ST8	157	161	248	250	129	133	205	217	195	211	195	195	225	227	185	185	137	149	186	188	218	220	171	175	198	198
460	ST8	169	169	238	244	131	131	211	221	195	199	211	223	211	221	185	203	127	137	186	188	218	218	163	177	198	202

461	ST8	163	169	246	246	111	129	209	231	195	197	197	223	215	215	185	185	137	141	188	188	215	218	157	173	198	202
462	ST8	163	169	246	250	111	133	211	235	197	217	195	195	219	221	185	195	137	139	186	188	218	218	164	169	198	202
469	ST8	149	163	240	250	129	131	209	219	183	183	217	225	223	229	183	195	127	137	188	188	210	220	171	173	198	200
474	ST8	161	169	238	238	127	127	209	233	197	201	195	195	213	221	195	195	139	139	186	188	215	218	171	171	198	198
476	ST8	163	169	240	248	127	131	209	233	197	197	211	225	217	233	183	195	137	137	188	188	213	215	159	173	198	198
478	ST8	161	169	242	246	129	131	213	235	195	197	195	223	215	217	195	195	137	147	188	188	218	218	177	177	198	198
480	ST8	149	161	238	240	121	129	217	231	205	209	195	221	211	215	203	203	127	147	186	188	218	218	177	177	198	202
481	ST8	149	161	246	250	117	133	207	223	183	183	223	227	217	223	185	203	127	137	186	188	215	218	171	171	198	202
482	ST8	163	169	248	252	131	131	205	205	197	199	195	195	215	225	185	185	137	137	186	188	215	218	175	177	194	202
483	ST8	155	169	246	248	131	133	205	205	197	197	195	197	211	217	181	187	137	147	186	188	210	218	177	177	202	202
485	ST8	161	165	238	244	127	131	217	217	211	215	195	219	211	227	185	195	137	149	188	188	215	218	151	173	198	202
486	ST8	161	163	248	250	121	121	193	223	195	197	195	223	215	215	187	203	137	137	188	188	215	218	175	175	198	200
487	ST8	155	165	238	250	119	131	207	211	197	197	195	195	225	229	203	203	127	139	188	190	218	218	171	173	198	198
492	ST8	155	169	240	242	131	131	199	211	199	199	195	223	217	217	187	195	137	147	188	188	213	218	171	175	198	202
523	ST8	169	169	242	250	131	131	209	231	183	199	197	221	219	221	185	195	127	141	188	190	215	220	173	175	198	198
524	ST8	169	169	238	238	119	131	207	227	195	203	195	223	211	229	195	195	137	137	184	186	218	218	173	175	198	198
525	ST8	161	163	238	248	131	131	209	231	183	187	195	217	215	229	181	185	137	141	186	188	218	218	171	175	198	198
536	ST8	169	169	246	246	131	133	211	235	187	195	195	195	215	227	185	203	137	137	186	190	218	220	171	177	198	198
537	ST8	149	161	246	248	129	131	211	235	187	195	195	205	211	221	185	203	133	137	188	188	218	218	171	175	198	198
541	ST8	163	169	238	246	119	119	227	232	197	197	195	197	215	217	183	195	137	137	190	190	215	218	171	177	198	198
555	ST8	161	163	244	244	121	129	217	221	195	197	197	197	217	221	181	195	137	143	186	188	215	218	169	173	202	202
567	ST8	157	169	246	246	131	131	205	211	197	205	195	195	219	221	183	183	137	147	186	188	218	220	173	173	198	198
569	ST8	163	171	238	240	117	117	213	221	183	197	195	231	211	215	185	191	147	147	186	188	215	215	175	175	198	202
609	ST8	157	163	240	244	119	129	211	223	197	205	195	213	211	221	185	195	141	141	186	188	215	218	165	175	198	198
236	T9	159	161	246	248	119	131	205	219	197	203	195	211	219	229	183	183	127	149	184	188	210	220	167	177	198	198
247	T9	163	169	240	246	121	131	223	231	197	197	195	207	211	219	185	195	137	149	186	188	210	218	167	171	198	200
259	T9	163	163	244	248	131	131	213	231	183	195	195	217	213	229	183	183	127	135	188	188	210	213	167	177	198	198
265	T9	149	163	240	250	117	131	197	209	183	203	195	253	215	217	195	195	127	141	184	184	210	215	171	179	198	198
267	T9	159	165	240	240	117	129	211	235	183	183	195	223	221	229	185	195	127	137	184	188	213	220	171	173	198	198

270	T9	159	167	244	246	131	131	219	233	183	197	207	223	215	233	195	195	137	149	188	188	220	220	171	175	198	198
289	T9	163	165	238	250	121	131	211	233	183	201	195	209	221	227	185	185	137	147	186	188	210	213	175	179	202	202
290	T9	163	169	248	248	119	131	223	233	195	197	195	195	211	221	187	195	137	137	188	188	210	210	164	165	196	198
300	T9	157	163	246	250	121	131	213	221	197	207	195	195	211	215	183	185	137	147	186	188	210	215	157	175	198	202
304	T9	163	163	245	248	129	131	213	217	183	197	195	217	213	233	0	0	135	137	188	196	210	218	175	177	198	198
310	T9	149	159	246	250	121	131	219	223	195	197	195	199	215	221	195	195	137	149	186	186	210	218	171	173	198	198
311	T9	149	161	248	248	121	133	205	233	183	183	195	225	219	223	195	195	137	147	186	188	213	215	173	179	196	198
313	T9	161	163	238	246	127	131	205	227	197	199	195	195	215	219	185	195	137	137	186	188	210	218	167	171	198	202
314	T9	159	169	238	246	121	131	207	235	197	201	195	197	215	217	183	195	137	141	188	188	220	220	164	171	198	202
315	T9	163	165	238	240	127	129	219	231	183	197	197	197	213	213	185	195	137	137	186	188	210	215	164	171	198	198
319	T9	163	169	246	246	127	127	211	223	197	211	195	195	211	215	185	185	137	147	188	188	215	220	165	171	198	200
321	T9	149	167	238	250	131	131	205	211	183	199	195	195	211	225	193	195	147	147	186	186	215	215	161	167	198	198
322	T9	161	161	246	248	131	131	209	211	197	197	195	217	219	221	185	199	135	147	188	188	210	220	171	173	198	202
325	T9	149	165	246	248	131	131	211	213	183	211	195	209	221	233	183	183	127	137	186	186	210	218	167	179	198	198
327	T9	163	167	246	246	121	129	211	213	197	211	195	195	211	213	195	195	133	147	184	186	210	218	151	175	198	202
343	T9	157	165	246	248	131	131	223	229	183	197	195	197	215	221	185	195	147	147	188	188	220	220	173	173	196	200
347	T9	165	165	244	250	129	131	209	231	183	183	195	205	213	215	185	193	127	127	188	190	210	218	157	167	198	198
349	T9	163	167	244	250	131	133	239	241	197	207	195	195	219	225	193	195	135	139	188	196	215	218	171	173	198	200
350	T9	163	171	244	246	127	129	205	233	211	211	195	201	215	215	185	195	137	147	184	186	213	215	167	167	194	198
351	T9	159	165	246	248	127	131	199	213	195	201	195	197	221	225	195	195	127	127	184	188	215	218	175	179	198	198
356	T9	165	171	244	246	129	131	211	221	197	203	195	195	215	227	183	195	137	141	184	188	215	218	175	177	198	198
357	T9	163	173	234	246	109	127	211	231	183	197	195	205	215	217	181	185	137	151	184	184	218	222	175	179	198	198
363	T9	149	163	238	250	131	131	213	213	183	195	195	217	213	227	195	195	137	137	186	188	219	219	167	171	198	202
364	T9	167	171	246	250	127	131	197	221	197	215	205	261	211	215	183	195	127	127	184	188	215	215	175	177	198	198
365	T9	161	165	246	248	131	131	213	213	199	211	195	229	215	233	193	195	127	137	186	196	218	218	177	179	198	202
366	T9	157	163	246	246	121	127	223	231	195	197	195	195	219	221	183	187	127	149	184	196	210	218	171	175	198	198
367	T9	161	167	246	248	117	129	205	223	203	207	195	195	215	227	183	187	127	149	186	188	215	218	167	171	198	198
368	T9	163	169	246	246	131	131	211	213	203	211	195	195	211	221	185	185	137	137	186	186	210	215	161	167	198	198
370	T9	163	163	248	250	127	127	233	235	207	211	199	219	225	227	183	185	137	137	184	184	213	220	171	171	198	202

373	T9	157	165	238	240	129	131	207	217	201	203	195	199	221	233	185	195	137	137	184	188	215	215	175	175	196	198
374	T9	159	165	248	250	117	131	197	223	183	195	193	199	225	227	185	193	137	137	186	186	218	218	171	173	198	198
377	T9	149	165	238	240	129	131	213	237	197	203	195	195	221	221	185	195	137	147	188	188	210	218	167	173	196	198
380	T9	149	159	238	244	121	121	211	223	195	197	195	223	215	219	185	195	127	137	188	188	213	215	164	173	198	198
382	T9	163	163	238	240	131	131	205	235	195	195	195	195	215	219	185	187	127	147	186	186	218	218	171	177	198	202
383	T9	149	159	238	250	139	139	213	213	195	203	195	195	211	219	185	203	127	137	186	188	213	218	175	175	198	198
386	T9	149	157	238	240	129	129	213	223	183	211	195	197	217	225	187	195	137	147	186	190	215	215	175	179	198	202
391	T9	163	163	240	248	131	139	205	223	197	215	195	195	211	219	187	187	137	149	186	188	213	213	179	179	194	198
393	T9	161	161	248	248	129	131	231	241	183	201	195	195	221	221	185	195	127	135	186	190	218	220	167	167	198	198
396	T9	149	163	246	248	121	121	213	231	195	197	197	209	215	233	185	187	127	143	186	188	215	218	167	171	198	198
399	T9	149	163	240	246	131	131	223	223	197	197	195	195	221	233	185	185	141	149	184	186	220	220	164	177	196	202
402	T9	159	163	248	250	131	131	205	209	195	197	195	215	215	217	185	185	147	149	184	188	215	218	167	171	196	200
406	T9	169	173	240	250	127	129	211	231	183	201	195	197	221	225	183	185	133	149	184	188	210	213	175	179	198	198
409	T9	163	169	238	250	129	131	213	221	183	197	197	225	217	221	183	185	127	137	184	188	210	220	164	177	198	198
410	T9	167	171	238	248	131	131	197	235	183	211	195	197	213	219	183	185	127	135	186	190	215	218	169	179	198	198
411	T9	159	163	250	250	129	131	205	217	197	211	197	217	211	215	183	195	127	137	188	196	216	219	165	171	196	198
413	T9	149	163	246	248	127	131	223	223	183	215	195	211	219	227	195	195	127	137	188	188	218	220	175	179	198	200
215	T10	149	169	240	248	129	129	223	241	195	201	195	195	219	221	193	195	137	137	184	190	210	218	173	173	198	198
228	T10	163	163	238	244	131	131	223	235	197	203	205	205	215	217	185	189	137	137	184	188	210	215	151	175	198	202
257	T10	161	163	238	246	121	129	199	223	185	211	195	217	221	227	185	185	137	137	188	188	213	213	173	175	198	198
264	T10	149	169	238	248	131	131	209	219	195	197	197	205	215	217	195	195	127	141	186	188	215	220	177	177	198	198
266	T10	163	163	242	248	131	133	223	241	195	197	227	227	217	225	185	185	127	127	184	188	215	218	165	171	198	198
269	T10	163	163	238	246	121	129	213	223	197	199	195	195	221	229	185	185	127	137	188	196	210	220	167	173	198	202
272	T10	149	169	240	246	129	129	209	213	197	211	201	223	217	221	185	185	147	149	186	186	210	215	157	165	198	202
279	T10	171	171	246	250	129	131	221	223	203	209	195	225	211	219	183	187	137	137	188	188	210	215	161	171	198	198
284	T10	163	163	248	250	127	131	223	227	197	211	195	211	215	215	181	183	137	137	188	188	215	218	169	171	198	198
285	T10	149	161	246	248	113	129	219	223	195	213	195	219	217	221	185	185	137	141	188	188	215	218	157	167	198	198
292	T10	149	165	238	240	129	133	213	223	205	211	199	221	217	227	183	185	137	139	186	196	210	210	157	157	198	198
296	T10	157	165	248	248	121	131	223	225	197	197	195	195	219	227	185	195	137	137	186	188	210	215	157	167	198	198

301	T10	149	163	238	246	121	121	209	221	195	215	195	195	215	229	185	195	137	147	184	188	213	218	161	179	198	198
307	T10	161	173	238	244	119	133	207	233	205	205	215	225	215	215	181	195	127	135	186	190	215	220	165	175	198	198
308	T10	163	163	238	240	127	129	219	227	197	201	195	201	217	221	185	195	137	149	184	188	218	218	165	173	198	202
309	T10	169	169	238	240	127	133	223	233	183	205	195	195	213	215	185	185	137	147	188	190	215	222	171	171	198	202
312	T10	161	163	244	250	111	131	233	239	187	195	195	223	217	229	183	185	137	137	188	190	218	220	163	173	198	198
316	T10	149	169	238	248	131	131	231	235	195	201	195	201	219	229	185	185	137	147	188	188	215	222	159	165	198	202
317	T10	163	165	246	248	129	129	223	223	187	201	201	217	215	231	185	195	137	137	188	188	215	220	165	171	198	202
318	T10	163	163	240	248	131	131	219	231	195	211	195	201	215	219	195	195	137	137	184	184	218	218	169	169	198	198
323	T10	163	169	244	250	117	129	211	223	195	197	195	211	217	217	181	185	137	149	186	188	218	220	167	171	198	198
326	T10	169	169	248	248	121	131	211	213	195	195	195	197	211	219	181	203	137	147	184	196	215	218	167	173	198	198
328	T10	149	163	240	246	131	131	223	227	197	197	195	205	217	227	185	195	137	137	184	186	218	218	157	165	198	198
332	T10	157	169	240	250	119	131	209	233	183	183	195	207	217	219	183	185	137	139	184	188	213	222	173	175	198	202
338	T10	163	163	246	250	131	131	215	221	201	203	195	215	215	221	185	185	127	127	188	188	220	220	167	177	198	202
344	T10	149	163	238	240	121	131	211	241	203	209	195	195	217	219	185	195	137	137	186	190	213	218	167	175	198	198
345	T10	169	171	238	248	127	133	223	233	201	201	195	199	219	227	185	195	137	137	184	196	218	234	171	171	198	202
346	T10	149	169	240	248	127	129	209	223	183	183	195	217	213	225	183	185	137	137	188	188	215	222	157	171	198	198
348	T10	169	169	240	248	131	131	199	225	197	203	195	201	211	215	185	195	137	137	188	188	210	210	171	179	198	202
352	T10	163	165	238	238	131	131	227	235	199	201	195	195	215	219	183	203	137	147	186	188	210	210	173	177	198	202
353	T10	149	163	246	246	129	131	213	217	183	205	195	197	221	227	183	183	137	137	188	188	210	215	175	177	198	202
355	T10	163	169	246	250	131	133	227	241	197	203	215	223	211	227	181	195	137	137	188	190	213	216	171	171	198	198
358	T10	171	173	240	246	121	129	223	223	199	207	209	223	211	215	185	195	137	139	188	188	215	218	164	173	198	198
359	T10	165	165	240	246	129	131	199	211	199	203	195	213	215	219	183	195	137	141	188	188	217	220	165	167	198	202
369	T10	149	163	240	248	131	131	227	231	195	201	199	201	221	221	183	195	137	147	186	188	210	218	165	165	198	202
371	T10	165	169	240	240	127	133	223	239	195	197	195	205	215	229	185	195	137	137	188	188	218	218	173	173	198	202
372	T10	161	169	238	240	129	133	223	227	195	211	195	205	211	213	185	195	143	147	188	190	218	218	175	177	198	198
375	T10	163	169	238	246	129	131	223	223	183	201	195	197	219	227	183	195	137	137	184	190	217	218	164	165	198	202
376	T10	165	165	238	240	131	131	205	205	183	195	195	195	217	227	185	195	135	137	188	188	210	215	164	171	198	202
385	T10	163	169	240	250	131	131	193	213	183	205	195	195	213	225	183	203	127	127	186	188	218	220	157	175	198	198
387	T10	161	163	248	250	131	131	225	241	195	205	195	195	219	233	183	185	137	137	188	188	210	218	169	177	198	198

388	T10	163	163	248	248	121	131	223	223	183	195	195	205	217	219	183	185	137	137	188	188	210	210	173	173	198	198
390	T10	163	165	238	248	129	131	211	233	185	199	195	195	211	219	181	195	127	137	188	190	218	218	165	173	198	198
392	T10	163	163	240	250	131	131	223	223	199	209	195	205	211	211	185	187	137	147	188	188	210	220	171	175	198	198
394	T10	165	169	248	250	129	131	223	223	197	205	195	195	211	229	183	187	147	149	186	186	215	218	157	157	198	200
401	T10	163	169	244	246	129	131	211	223	197	197	195	205	219	233	181	185	137	137	188	188	215	215	157	175	198	198
403	T10	169	171	240	250	121	131	211	239	197	201	195	223	217	219	181	181	137	137	184	188	210	220	165	167	198	198
404	T10	163	171	238	246	127	127	215	223	185	195	195	197	211	221	185	185	127	141	186	190	210	218	173	179	198	198
405	T10	163	171	238	248	131	131	223	223	197	201	201	205	221	229	181	195	137	137	186	188	213	213	175	175	198	198
408	T10	163	169	238	246	129	131	209	227	197	211	197	197	219	229	185	195	147	151	188	190	218	220	167	171	198	198
214	T11	149	149	238	246	131	131	209	235	197	207	211	215	227	233	185	193	129	137	186	186	218	218	169	175	198	198
217	T11	157	163	238	246	121	131	223	231	199	207	195	195	221	227	183	195	137	151	188	190	213	218	157	175	198	198
218	T11	167	167	246	246	133	133	223	235	183	199	195	211	211	215	193	195	137	137	184	186	218	220	161	167	198	198
221	T11	169	169	240	245	121	131	217	223	197	197	195	195	223	225	183	195	137	137	184	188	213	220	171	181	198	202
222	T11	159	161	246	250	121	131	193	221	197	201	201	215	215	215	187	195	147	147	186	188	210	218	169	177	194	200
229	T11	163	165	240	246	131	131	205	217	183	183	195	223	215	215	195	195	137	137	186	186	210	218	155	171	198	198
237	T11	149	161	246	250	131	131	209	209	187	197	195	197	231	231	185	185	135	147	186	188	210	218	177	179	198	198
240	T11	149	161	238	246	119	131	205	213	201	203	195	195	219	227	183	195	137	147	186	188	210	215	173	177	194	198
244	T11	161	163	246	248	131	133	211	213	195	215	195	225	221	225	195	195	127	137	186	188	218	218	167	167	198	198
253	T11	165	171	240	240	117	133	209	213	197	197	195	227	211	227	185	195	137	141	186	190	218	218	157	177	198	198
258	T11	161	165	238	246	117	127	213	223	197	207	201	209	215	217	185	187	129	137	186	186	210	210	169	171	198	198
262	T11	157	165	240	246	129	131	197	213	199	203	197	197	215	219	185	185	137	137	184	186	213	213	163	167	198	198
263	T11	161	161	238	248	117	131	199	211	201	201	195	195	219	221	183	185	137	147	186	186	210	215	157	171	198	198
268	T11	157	163	246	250	131	131	199	233	197	197	195	225	219	227	185	195	141	151	188	190	215	218	164	173	198	198
271	T11	149	163	238	246	117	131	211	235	199	207	195	201	227	233	187	195	137	149	186	188	213	215	149	164	198	200
273	T11	157	163	238	248	129	131	235	235	183	203	201	235	215	219	181	183	139	149	186	188	218	218	164	171	198	198
275	T11	149	159	246	250	131	133	209	235	195	203	201	201	221	233	195	195	137	137	186	186	210	220	164	171	198	198
278	T11	159	169	246	248	117	139	197	233	197	207	195	195	211	229	185	185	137	141	184	188	210	218	171	177	198	198
283	T11	163	163	238	250	121	121	219	235	197	203	205	213	215	219	195	203	137	137	188	188	218	220	164	167	198	202
286	T11	149	149	240	240	129	131	209	213	201	211	195	195	215	227	193	195	135	137	186	188	210	220	161	165	198	202

293	T11	159	161	244	250	127	129	211	231	197	199	195	201	219	229	181	181	137	137	186	188	213	218	171	173	198	198
295	T11	149	163	246	246	129	145	221	231	199	201	195	221	211	213	183	183	127	127	186	188	215	218	155	157	198	198
297	T11	157	169	240	250	131	131	213	235	197	207	205	221	215	227	185	195	135	137	188	188	215	215	161	171	198	202
298	T11	163	163	248	250	125	129	205	211	183	199	195	201	213	231	195	195	135	147	186	186	218	220	171	173	198	198
299	T11	157	159	238	246	121	131	213	215	182	195	195	195	211	227	183	193	137	137	186	186	215	222	164	169	198	202
302	T11	161	161	244	246	129	131	193	211	187	197	195	195	215	225	185	193	137	147	184	186	215	218	151	171	198	198
303	T11	155	165	240	246	131	131	223	233	183	197	195	195	221	225	181	181	147	151	188	188	210	215	173	175	198	198
306	T11	149	159	246	246	129	129	209	213	183	197	195	209	213	217	185	185	137	137	186	188	218	222	149	171	202	202
320	T11	163	163	240	250	131	131	221	230	197	199	195	195	215	227	185	185	139	151	188	188	215	218	164	167	198	202
329	T11	171	181	240	246	131	131	235	241	197	199	195	211	213	219	181	183	127	137	188	188	215	218	171	173	198	198
331	T11	165	165	238	248	131	131	223	230	197	203	195	201	215	231	183	185	137	137	184	184	210	215	175	177	198	198
333	T11	163	171	240	248	121	129	209	211	207	207	195	195	211	219	185	195	135	147	186	188	218	218	167	175	198	198
335	T11	161	165	246	246	131	139	209	211	195	203	195	195	219	227	185	203	141	147	184	188	210	218	167	171	196	198
336	T11	149	169	248	250	129	131	193	211	197	207	207	223	215	229	183	195	135	141	184	188	218	222	167	179	198	200
340	T11	165	165	246	248	117	117	213	223	207	207	195	195	219	221	185	195	137	137	186	188	220	220	157	161	198	198
341	T11	157	167	238	238	129	131	227	235	183	197	195	195	211	215	193	195	135	135	186	188	210	218	173	181	198	198
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