



SZENT ISTVÁN UNIVERSITY

PHD DISSERTATION THESIS

**GENETIC AND RINGING ANALYZES ON THE
HUNGARIAN BREEDING AND AFRICAN
WINTERING GREAT REED WARBLER
(*ACROCEPHALUS ARUNDINACEUS*) POPULATIONS**

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1. INTRODUCTION, AIMS OF THE STUDY

The bird migration is a unique natural phenomenon, which have long been interested people – and the biologists. We have now a lot of information about the ecological needs, reproduction, migration routes, breeding and moulting strategies of the different bird species. Bird ringing is an activity having unique and rich traditions, a big scientific value and very high educational power.

Through bird ringing we have information about the size of breeding populations, the direction and speed of changes and sometimes of their causes too; in case of the migratory birds about the migration routes, the timing of migration and about the accurate place of the resting and wintering areas. The analyzes on the breeding populations can help us understand the reproductive systems, the influencing mechanisms and it might be an example for the similar studies in other animal groups.

In addition to the traditional methods of bird ringing GPS-based tracking techniques are starting to become more widely used, especially for larger birds. For small songbirds there are technical limitations to use this method, but nowadays we try to replace the transmitters whit geolocator tracking methods. In addition, thanks to the latest laboratory techniques we could answer more specific ecological and ornithological questions. Such a new technical innovation is the use of different genetic analyzes, which can be used today for the different kinds of studies. Due to the genetic methods we are able to answer the question, from which population the birds are coming from. They are also useful for the analyzes of inbreeding, genetic drift, to measure genetic differentiation and give clues about their causes and effects on the breeding populations.

In our study we have used genetic methods beside the traditional and colour ringing techniques, which are able to estimate the natal and breeding philopatry of the Great Reed Warbler (*Acrocephalus arundinaceus*). We have tried to determine which European breeding populations are using the South-African wintering areas and to explore the extent and possible causes of the genetic differentiation between the different breeding populations.

1.1. Aims

In our studies we had the following questions:

1. What are the levels of juvenile natal- and the adult breeding philopatry based on the long-term bird ringing data on a macro (European) scale?
2. What is the level of the adult Great Reed Warbler breeding philopatry in the breeding population of Babatpuszta (micro, local scale)?
3. Which European breeding populations could use the South-African wintering areas?
4. To what degree are breeding Great Reed Warbler populations genetically differentiated on the European (macro) and Hungarian (micro) scale?

2. MATERIALS AND METHODS

2.1. Natal- and breeding philopatry of the Great reed Warblers according the European and Hungarian ringing databases

In this study we have used the data of birds ringed and recaptured in the breeding season (EURING and Hungarian Bird Ringing Databanks) .

According to the geographical location of the ringed and recaptured birds we divided Europe into three parts: southern part (hereinafter Region1: between 36°-43° latitudes); middle part (hereinafter Region2: latitudes 43°-49°) and northern part (hereinafter Region3: latitudes 49°-56°).

During the study we defined four breeding intervals (Table 1). Those birds were considered faithful to the area (natal- or breeding site philopatry), where location of capture and recapture were the same (distance: 0 kilometres and the elapsed time between the capture and recapture was at least 1 year.

Table 1: The four breeding intervals used in the tests.

	May		June			July						
int.	1-8	9-16	17-24	25-31	1-8	9-16	17-24	25-30	1-8	9-14	14-22	22-31
A	[Redacted]											
B	[Redacted]		[Redacted]									
C	[Redacted]								[Redacted]			
D	[Redacted]		[Redacted]									

We analyzed the natal- and breeding philopatry within and between the three regions as well as within the four intervals. To calculate the philopatry of juveniles (natal-) and adults (breeding philopatry), the following formula was used:

proportion of philopatric birds=[number of philopatric bird within region / number of philopatric and dispersing birds in the same region] x100.

Both the juvenile and adult birds were examined for the dispersion rate, more precisely, we examined, in which proportion the ringed birds chose a breeding area in the year after ringing within 20, 65 and 100 kilometres from the original ringing site. We calculated the ratio of birds dispersing more than 100 kilometres.

In the statistical analyzes *Chi-squared test* were used included in the STATISTICA 5.0 (StatSoft 1998) software package.

2.2. Philopatry analyses in Babatpuszta

We examined the breeding philopatry of the Great Reed Warblers in Babatpuszta located near to Gödöllő between 2007 and 2012. Between 2008 and 2012 we marked the birds caught in the breeding season with metal- and with colour rings.

Between 15 April and 20 May we made a territory mapping in 1-3 days in the study area between 2008 and 2012. During the territory mapping we registered the arriving order, the exact place of the arriving birds in the study area, as well as the birds having or not having colour and/or metal rings. We considered a territory occupied, if we saw or heard the same male warbler on three consecutive occasions in the same territory. In the next step after the territory mapping in the breeding season (20 May- 17 July) we started to catch and ring the birds. To catch the birds we used the standard mist nets. In June 2010 to 2012 we also made several observations in a 10 km diameter area around our study site, looking for Great reed Warblers with our colour rings.

To estimate our ringing success we counted the males breeding in the study area. For the calculation we used the following formula:

[total number = (number of caught males+ number of non caught males)].

Then we calculated the breeding success of the adult females and males according to the following formula:

$$[\textit{breeding success per sex (\%)} = \textit{number of ringed females or males} / (\textit{estimated total number of breeding birds} / 2) \times 100].$$

In the literature there are basically two calculation methods for the philopatry of birds. In our study we used both of them to investigate the breeding philopatry in case of the warblers of our study area.

According to the first method we calculated the breeding philopatry of the adults using the total number of ringed birds and the total number of recaptured birds. First we took the number of ringed birds and recaptured in the study area or within 10 kilometres around it after minimum 1 year from the ringing:

$$[\textit{proportion of recapture (\%)} = (\textit{number of recaptured adult birds} / \textit{total number of ringed adult birds}) \times 100];$$

then according to the number of birds, which were recaptured only in Babatpuszta we calculated the proportion of the philopatric- and dispersing birds.

In case of the second calculation method we used the data of adult birds, which were recaptured only after one year of ringing. So we determined the proportion of the breeding philopatric birds according to the following formula:

$$[\textit{proportion of the breeding philopatry (\%)} = (\textit{number (record) of the birds ringed and recaptured in Babatpuszta} / \textit{total recapture record}) \times 100].$$

Between 2007 and 2012 we examined in case of the birds ringed and recaptured

in Babatpuszta the place of the territory occupied and the distance between these and the previous years breeding territory of the same bird. In the statistical procedures we used the Chi-square test and the softwares STATISTICA 5.0, GoogleEarth, QuantumGIS, and MARK 7.1.

2.3. Genetic analyzes regarding migration and the South-African wintering areas of the species

For the genetic analyzes we collected blood samples from the Great Reed Warblers with help of bird ringers from 5 European breeding populations in the breeding season (10. May–15. July) and from a South-African wintering population (3 neighbouring locations) between 14. January and 4. April.

The blood samples were collected from adult Great Reed Warblers blood vessels except the Polish samples. These were collected from juveniles but from different nests. The DNA was extracted either with organic extraction (PCI: phenol-chloroform-isoamil-alcohol) or with the SOLEX 2T genomic DNA isolation kit. We amplified a 492 bp long part of the mtDNA (mitochondrial DNA) control region II D-loop using the BCML4 and 12SH2 primer pairs (Bensch és Hasselquist, 1999). We sequenced the purified and reisolated fragment with the original primer pairs (BCML4-12SH2) on ABI Prism 310 capillary sequencer.

We analyzed the aligned sequences calculating the haplotype diversity (H_d), the nucleotide diversity (π), the number of parsimony informative sites, and the gamma distribution. To consider the phylogenetic relationship we used the Neighbor-joining method with Tamura-Nei (Tamura és Nei, 1993) model. The phylogenetic relationships between the haplotypes were analyzed with the Median-joining haplotype network in NETWORK (Fluxus-Technology Inc.) software.

Besides the genetic analyzes we examined the migration routes and the possible wintering areas of the Great Reed Warbler according to the ringing and recapture data of the EURING Databank.

2.4. Genetic differentiation in the Hungarian breeding populations

The blood samples were collected in the breeding season (15. May-15. July) between 2007-2010 from five Hungarian populations (Fenekpuszta, Farnos, Babatpuszta, Izsák, Rakamaz), and we used the data of the five European breeding populations too. The Hungarian samples derived from adult breeding birds, the sex ratio was approximately 50-50%.

The DNA was extracted from 5-10 μ l blood either with organic extraction (PCI: phenol-chloroform-isoamil-alcohol) or with the SOLEX 2T genomic DNA isolation kit. We amplified the same 492 bp long part of the mtDNA (mitochondrial DNA) control region II D-loop using the BCML4 and 12SH2 primer pairs (Bensch és Hasselquist, 1999).

In case of the microsatellites we analyzed the following 11 microsatellites in 5 Hungarian breeding populations: Aar3, Aar8, Sjr4, Aar5, Aar2, G61, Ase7, Ase9, Ase11, Ase18, Ase46. The forward primers were labelled with 6-FAM, HEX or NED fluorescent dyes. To determine the sex of the birds in the laboratory we used the 2550F and 2718R primer pairs.

In case of the mtDNA analyzes we calculated the haplotype diversity (H_d), the nucleotide diversity (π), the number of haplotypes (H), the number of the parsimony informative sites, the average number of nucleotide differences, the Δ_{st} , G_{st} , and the level of the genetic differentiation. We determined the fixation-index between the populations (pairwise F_{st} calculation). According to the „best tree model test”, the gamma distribution, and the F_{st} values we draw the phylogenetic tree of the haplotypes.

In case of microsatellites we calculated the observed heterozygosity (H_O) and the expected heterozygosity (H_E), the mean alleles per locus, the fixation-index (F_{st}), the number of alleles per loci and determined the number of genetic clusters in the whole sample. The „isolation by distance test” was calculated based on

genetic (mtDNA and microsatellites F_{st} values) and geographic distances between the breeding populations.

3. RESULTS

3.1. Natal and breeding philopatry of the Great Reed Warbler based on ringing databases

There were no significant differences between the juveniles natal philopatry and the adults breeding philopatry except in the Region3 (all the 4 breeding intervals).

There were no significant differences in the adult breeding philopatry between the Region1 and Region2 except between Region1 interval A and Region2 interval B; and between Region1 interval C and Region2 interval B (Table 2). The adults ringed and breeding in Region3 were less faithful to their breeding sites, than the birds ringed and breeding in the other two regions. Significant differences were found between the Region3 A-D intervals and the Region 1-2 A-D intervals with one exception (Region1 D and Region3 D). In Region 3 no significant differences were found between the four breeding intervals, the proportions of the breeding philopatry were nearly the same (Table 2).

In the juveniles natal philopatry there were no significant differences except between the Region1 interval A and the Region2 A-D intervals (Table 2). The proportion of the philopatry in Region1 and Region2 differed in all cases from the results of Region3 intervals A-D. Some significant differences could be seen in case of Region3, depending on the breeding intervals (Table 2).

The results were the same in all cases considering only the capture-recapture date, where the elapsed time between the two events was 1 year (time between two breeding seasons).

Table 2: The differences between the juveniles and adults philopatry and between the different regions by breeding periods if the elapsed time between the capture and recapture is independent. Above diagonal: juveniles; below diagonal: adults. (Reg.: Region; p: significances; f.d.: few data - n< 10).

	Reg. 1A	Reg. 1B	Reg. 1C	Reg. 1D	Reg. 2A	Reg. 2B	Reg. 2C	Reg. 2D	Reg. 3A	Reg. 3B	Reg. 3C	Reg. 3D
Reg. 1A	1	f.d.	f.d.	f.d.	0.34	0.38	0.43	0.42	0.001	0.01	0.001	0.001
Reg. 1B	0.74	1	f.d.									
Reg. 1C	0.88	0.67	1	f.d.								
Reg. 1D	0.75	0.95	0.70	1	f.d.							
Reg. 2A	0.17	0.56	0.18	0.72	1	0.57	0.46	0.47	0.001	0.001	0.001	0.001
Reg. 2B	0.02	0.21	0.03	0.38	0.20	1	0.67	0.7	0.001	0.001	0.001	0.001
Reg. 2C	0.14	0.38	0.14	0.53	0.58	0.76	1	0.94	0.001	0.001	0.001	0.001
Reg. 2D	0.35	0.72	0.32	0.83	0.77	0.19	0.48	1	0.001	0.001	0.001	0.001
Reg. 3A	0.001	0.01	0.01	0.026	0.001	0.001	0.001	0.001	1	0.71	0.001	0.001
Reg. 3B	0.001	0.018	0.03	0.07	0.001	0.001	0.001	0.001	0.2	1	0.001	0.001
Reg. 3C	0.001	0.001	0.001	0.013	0.001	0.001	0.001	0.001	0.36	0.053	1	0.65
Reg. 3D	0.001	0.01	0.01	0.025	0.001	0.001	0.001	0.001	0.79	0.24	0.7	1

3.2. The results of the philopatry analyses in Babatpuszta

Between 2007 and 2012 we ringed 135 Great Reed Warblers in Babatpuszta. In 2007 we used only the numbered metal ring, but from 2008 additional colour plastic rings were applied in individual colour combinations. During our work we marked 125 Great Reed Warblers (81 male, 44 female) with metal and colour rings between 2008 and 2012.

Among the caught and ringed birds 20 warblers were recaptured or identified at least two times (within 2-4 years) in the study area or within 10 kilometre distance.

In case of these 20 warblers 32 recapture records could be registered. Two birds were seen three times in another breeding site within 10 kilometre of the study site.

The earliest male arriving date in the last 5 years was the 22. April. The females arrived to the study site on average 1-1.5 weeks later than the males. During the time of study we estimated in all 113 territories within the study site the number of yearly ringed birds. So we expected that we could catch altogether 226 adult birds. However we caught 143 adult birds in this time, which means that the success rate of our ringing activity was on average 63.3% (males: 80.0-97.1%; females: 13.3-47.6%).

In the period between 2007-2012 15.1% (19 warblers; males: 20.7%, females: 4.5%) of the ringed birds returned and started to breeding in Babatpuszta or around its 10 kilometres after the first breeding years. If we consider the place of the recapture we could conclude that 13.5% (17) of the birds were philopatric, while 1.5% showed breeding dispersal behaviour.

90 % of the 31 recapture data originating from the 20 ringed and recaptured birds are recapture data from the same place (from the breeding site), so these birds were faithful to their previous breeding place.

During the investigation for the possible reasons of the territory infidelities we could utilize the data of those 17 adult breeding birds, which produced together 28 (26 male, 2 female) recapture events (records). The recaptured adult birds occupied after the first breeding season another breeding territory at the next breeding year around the first's 380 meter circle (30-150 meter). 30.8 % of the recaptured breeding males tried to occupy a territory in the next year close to the previous years breeding territory. The breeding territory of those males which tried to occupy a territory close to the previous year's territory was not depending on the time of the male's arrival date. In case of those breeding males which leaved their previous year's territory (dispersing males: 18 out of 26, 69.2%) in 66.6% of the instances (12 out of 18 males) the territories were already occupied by another male.

3.3. The result of the genetic analyzes regarding the migration and the South-African wintering areas

We amplified and sequenced a 492 base pair long part of the mtDNA control region II D-loop in case of 146 Great Reed Warblers. The samples came from five European breeding populations and from one South-African wintering population (3 close places). Altogether 51 different haplotypes could be distinguished, the haplotype diversity (H_d) was 0.912 and the nucleotide diversity (π) 0.00746.

On the phylogenetic tree („Neighbor-joining”) the samples produced two different haplogroups (“Eastern group” and “Western group”) where the bootstrap value was 72. There were two distinct peaks in the mismatch distribution where the maximum heights were at 1-2 and 6-7 base pair deviation which signals two distinct phylogenetic groups.

The proportion of the Eastern haplogroups was 23%, the haplotypes in this haplogroups could not be found in the Portuguese and German samples (Figure 1). According to the data in the EURING Databank (Figure 1) the most southern recapture data comes from 5° below the Equator.

We compared the haplotypes found in the South-African samples to the haplotypes found in the European breeding populations. We can establish that the two haplogroups (“eastern and western haplogroups”) occur in the South-African wintering population in nearly 50-50 percent.

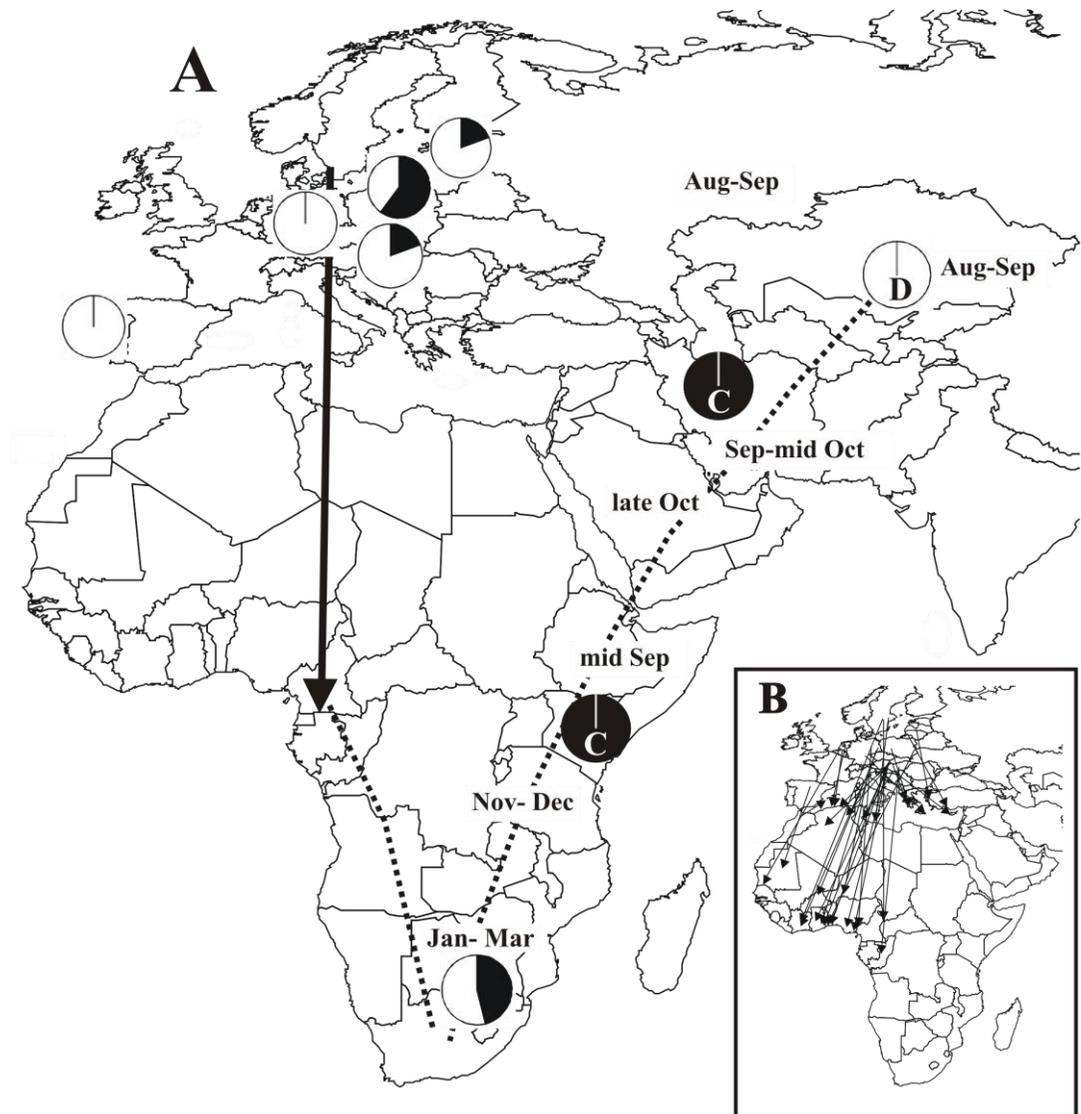


Figure 1: A: The distribution of the eastern and western haplotypes in the different populations. (C and D circles are results from Bensch and Hasselquist 1999). **B:** Map showing the African capture-recapture data of the EURING Databank. (Continuous arrow: broad front migration; dotted line: supposed migration routes).

3.4. The result of the genetic differentiation analysis in the Hungarian breeding populations

We amplified and sequenced a 492 base pair long part of the mtDNA control region II D-loop in case of 68 birds and investigated 11 microsatellite loci in case of 51 Great Reed Warblers. The samples were collected from five Hungarian breeding populations.

The 68 sequences contained 26 different haplotypes, the haplotype diversity (H_d) was 0,885 and the nucleotide diversity (π) 0.00082. In case of the microsatellites the mean allele number per locus ranged between 4.18-4.9 in the five breeding populations.

In case of the mtDNA no genetic differentiation was found according to the F_{st} , the Δ_{st} and the G_{st} values in the five Hungarian breeding populations (Table 3). However, significant differences could be found in several cases between the European populations and between the Hungarian and European breeding populations (mtDNA F_{st} values).

In the paired fixation-index (F_{st}) analysis of the microsatellites performed for the five Hungarian breeding populations we could find 6 out of 10 significant differences pointing in direction of genetic differentiation in Hungary (Table 3). From the results of the paired F_{st} analyzes we produced the Neighbour-joining phylogenetic tree which divided the five Hungarian breeding populations in two groups (Farnos-Rakamaz-Izsák and Babatpuszta-Fenekpuszta). The assignment probability test implemented in STRUCTURE supported these results, because there were two distinct clades ($K=2$) in the whole Hungarian breeding Great Reed Warbler population.

Table 3: Paired F_{st} values in case of the 5 Hungarian and 4 European breeding populations. (P: Portugal; D: Germany; PL: Poland; RU: Russia; FAR: Farnos; BAB: Babatpuszta; IZS: Izsák; FEN: Fenékpuszta; RAK: Rakamaz; “—“: could not be calculated; below diagonal: mtDNA data; above diagonal: microsatellite data; **bold**: significant values at 0.05).

F_{st}	P	D	PL	RU	FAR	BAB	IZS	FEN	RAK
P		—	—	—	—	—	—	—	—
D	0.11738		—	—	—	—	—	—	—
PL	0.31834	0.25610		—	—	—	—	—	—
RU	0.11508	0.01408	0.14387		—	—	—	—	—
FAR	0.12513	-0.00443	0.19731	0.02103		0.16382	0.04959	0.18629	0.02932
BAB	0.07768	0.01475	0.20455	0.02130	-0.00917		0.22554	0.05922	0.21546
IZS	0.08120	-0.00096	0.10665	-0.02447	-0.02576	-0.04877		0.26258	0.02793
FEN	0.10820	0.01506	0.17757	-0.00792	-0.05060	-0.01707	-0.03477		0.23325
RAK	0.08389	0.01628	0.08237	-0.02357	-0.02634	-0.06574	-0.05004	-0.03502	

3.5. New scientific results

1. We analyzed the juvenile natal- and the adult breeding philopatry on European (macro) scale according to the ringing and recapture data of the EURING- and Hungarian Database. We could not detect significant difference between the natal- and breeding philopatry except for Region3, where the juvenile Great Reed Warblers were less faithful to their natal sites than the adult to their breeding sites. The time of the breeding interval had significant effect on the juveniles natal philopatry.
2. With the investigation made in Babatpuszta we determined the rate of the breeding philopatry on a micro (one breeding population) scale. 90% of the ringed and recaptured warblers were faithful to their previous breeding sites, while

10% of the birds hatched in other reed-beds located within a 10 kilometre circle from the study site. The spring arrival time of the male warblers had a basic influence on the philopatry.

3. To our knowledge this was the first study analysing the mtDNA polymorphism in a South-African Great Reed Warbler wintering population. We verified that 60% of the haplotypes found in the South-African wintering population were the same as the haplotypes of the Middle- and Eastern-European populations. Taking into consideration the African recapture data and the possible migration routes of the species we cannot exclude the possibility that the birds of the Near- and Middle-Eastern breeding populations (Kazakhstan, Iran/Turkey) could reach this area, and use it as a wintering site.
4. The genetic differentiation of the species was documented on a micro scale. Moreover we proved that the genetic differentiation on the mtDNA level could be found only on macro (European) scale. Finally we have not found isolation by distance neither on the mtDNA level nor on the microsatellites level.

4. CONCLUSIONS

According to former publications the juvenile Great Reed Warbler's natal philopatry differs from the adults breeding philopatry. In contrast with this, we could not find any significant differences between the two age-groups regarding philopatric behaviour, except in case of the birds hatched in the northern breeding places (49°-56° latitudes; Region3) and in case of the four different intervals. So we can conclude that the birds ringed and breeding in Region1 and Region2 (approximately South- and Middle-Europe) are more faithful (90%) to their previous breeding places than the birds breeding in more northern places (Region3; 70%). Among the birds ringed in a juvenile age 47% returned to their place of birth after one or more years after ringing and started to breed. If we consider only those birds recaptured after one year, this ratio raises to 54.9%.

During our investigations at Babatpuszta we analyzed the breeding philopatry on a smaller micro-scale. We ringed every year on average 63.3% of the breeding adult birds but it succeeded to ring most of the breeding males (90%). Moreover we analyzed the ringed birds recapture rate too. During the time of our study 20.7% of the ringed adult male warblers and 4.5% of the ringed adult female warblers were recaptured at least one year after the ringing. In case of the adult males, 18.3% of the ringed birds were faithful to their breeding site, 2.4% of the ringed birds choose another breeding site in the 10 kilometre surroundings of the ringing site (Babatpuszta). We have no information about the remaining birds (81.7%), perhaps most of them died (not unusual in songbirds). We analyzed our ringing and recapture data of Babatpuszta another way, considering only the recapture data. This way 90% of the ringed and recaptured adult males were faithful to their previous breeding place and started to breed again, while 10% of the ringed and recaptured adult males choose another breeding place within 10 kilometres. One third of the ringed and returned males brood very close (0-10 meters) to their previous territory. In

case of birds hatched in another site, the territory of 66.6% was occupied by another male.

During the investigation of the migration routes- and the possible wintering areas of the Great Reed Warbler we analyzed the data of the birds arrival date to the stopover and wintering areas, the African recapture data and the mtDNA polymorphisms in the South-African wintering population. The warblers breeding in Portugal and Germany carried only the western haplotypes, while the warblers breeding in Poland, Hungary and Russia carried both the Eastern- and Western haplotypes in different proportions. Approximately 60% of the warblers caught in the South-African wintering area carried the haplotypes found in the Middle- and Eastern European breeding populations. We note that both the Eastern- and Western haplotypes could be found in the South-African wintering area, approximately in 50-50 ratio.

We know from previous publications that the Great Reed Warbler recolonised Europe from two distinct refugia after the last glacial period. According to our results there is no detectable difference in the mtDNA F_{st} values in contrast with the microsatellites, which verifies the genetic differentiation in the Hungarian breeding Great Reed warbler population. According the result of the paired F_{st} analyzes of the microsatellites the five Hungarian breeding populations belonged to two population groups/clusters. Among the two clusters the “BAB-FEN” branch represents probably the Western refugia and could prove the recolonisation from the western direction. The “IZS-RAK-FAR” group represents probably the Eastern refugia and could prove the recolonisation from the southern and south-eastern direction (Figure2).

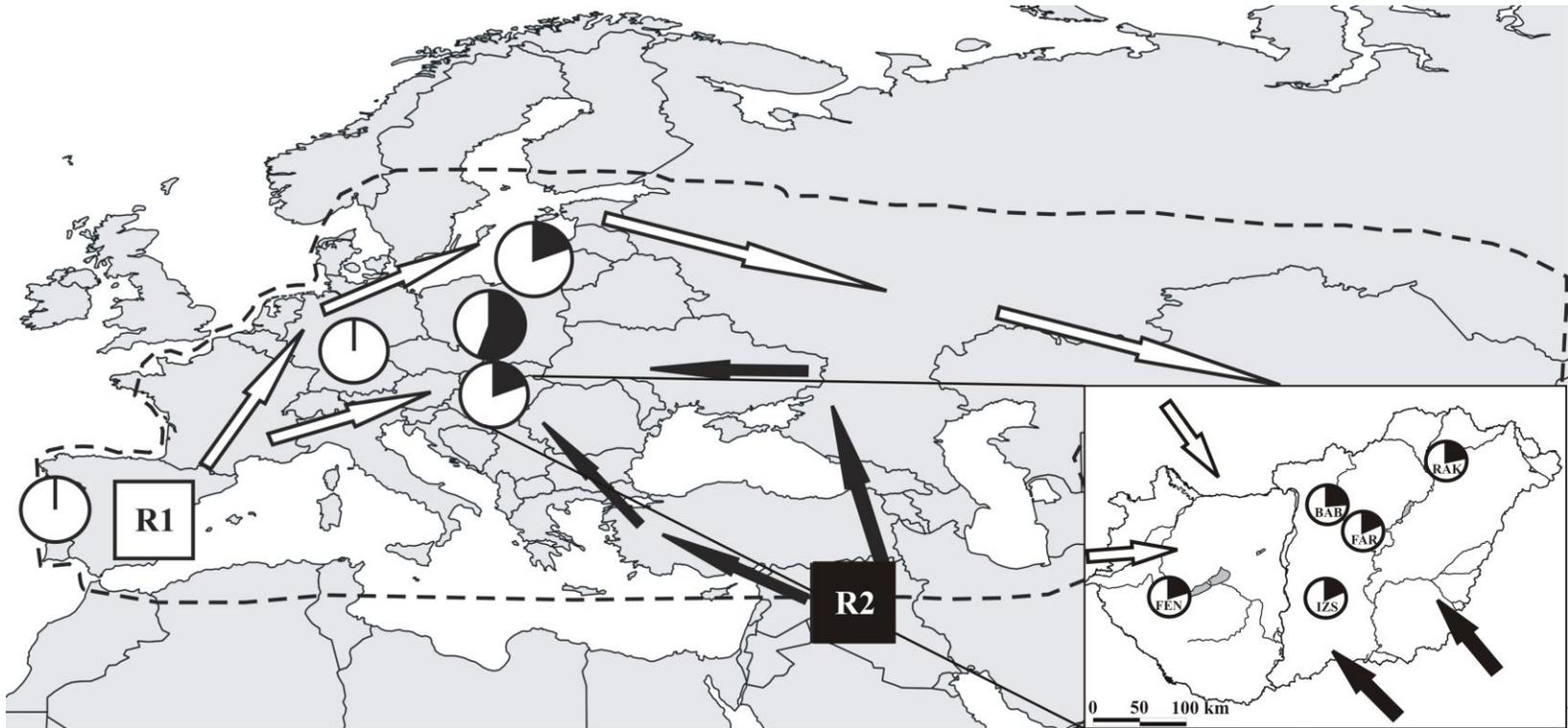


Figure 2: The presumable refugia (R1 and R2) of the two haplogroups in case of the Great Reed Warbler and the possible recolonisation routes (Hansson et al. 2008). The circles show the ratio of the two haplogroups (eastern and western) in case of the different breeding populations; the arrows show the directions of the possible recolonisation routes (white arrows: western haplotypes, black arrows: eastern haplotypes).

Based on our results we think that the analysis of the microsatellites could give better and reliable results if we analyze the small geographic scale which results from the recolonization history. From these results it seems that the mtDNA sequencing methods give only reliable results when geographical, ecological or other factor plays a role in the subdivision of populations (allopatric fragmentation), but in case of a continuous range and intermixing populations, like that of the Great Reed Warbler, only large scale studies are appropriate. With microsatellites some significant substructuring can be shown even in such cases and the correlations of the two methods depend on the features of the organism investigated.

5. PUBLICATIONS IN THE SUBJECT OF THE DISSERTATION

Scientific publications with IF

Mátrai, N., Gyurácz, J., Lenczl, M., Hoffmann, Gy., Bakonyi, G., Mátics, R. (2012a): Philopatry analysis of the great reed warbler (*Acrocephalus arundinaceus*) based on ringing data in Europe. *Biologia*, 67(3): 596-601. **(IF:0.609)**

Mátrai, N., Bakonyi, G., Gyurácz, J., Hoffmann, Gy., Rajmakers, K., Neto, J.M., Mátics, R. (2012b): Do the European Great Reed Warblers (*Acrocephalus arundinaceus*) reach South Africa during wintering? *Journal of Ornithology* 153: 579-583. **(IF:1.297)**

Neto, J.M., Arroyo, J.L., Bargain, B., Monrós, J.S., **Mátrai, N.**, Procházka, P., Zehndjiev, P. (2012c): Phylogeography of a habitat specialist with high dispersal capability: The Savi's Warbler *Locustella luscinioides*. *PlosOne* 7(6): e38497. **(IF:4.411)**

Scientific publications without IF

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