

The influence of distance and landscape composition on the dispersal of water frogs (*P. lessonae* - *P. esculentus* system) in the Swiss lowlands

Master Thesis

Submitted to the Swiss Federal Institute of Technology (ETH) Zurich by Dorena Nagel, D-USYS



Supervisors: Dr. Felix Gugerli, PD Dr. Janine Bolliger, Swiss Federal Institute for Forest, Snow and Landscape Research WSL

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Abstract

The recent loss in amphibian biodiversity calls for effective conservation measures. Remaining populations need to stay connected to prevent further local extinctions. However, species-specific knowledge about what is hindering and what is enhancing the maintenance of gene flow between populations is often lacking. Therefore, this study identified how distance and different landscape classes between ponds affect the successful dispersal of water frogs (*P. lessonae* - *P. esculentus* system). The study was carried out in 19 ponds near Aargau in Switzerland.

Firstly, genetic distance between ponds, calculated with microsatellite data of 13 markers from 396 frogs, was analyzed to check whether isolation by distance (IBD) applied. As estimates for genetic distance, F_{st} , $F_{st}/(1-F_{st})$, and Nei's distance were used. Estimated F_{st} values ranged between -0.01 and 0.57 in the study area. A simple Mantel test showed that IBD is significantly contributing to genetic distance in water frogs. Secondly, the influence of landscape composition between locations was investigated with a corridor analysis using permuted multiple regression on distance matrices (MRM). MRM was carried out with two different measures for genetic differentiation ($F_{st}/(1-F_{st})$, and Nei's distance), two different subjective landscape classifications, and three different corridor types (200 m - 1'000 m, 300 m, 400 m - 2'000 m). This resulted in twelve full models containing the regression coefficients of the landscape classes and the straight-line distance. In addition, backward elimination of variables was applied to obtain reduced models containing only significant predictive variables. The full models showed that open land, particularly agricultural areas, tended to enhance gene flow in contrast to most other landscape classes. In the reduced models, Euclidean distance together with waters and wetlands exerted a significant, negative effect on gene flow. Thereby, variable corridor widths depending on the distance between locations provided the best model fits. A possible explanation for waters and wetlands hindering gene flow is that ponds attract dispersing individuals and make longer travel routes unnecessary. The positive effect of open land on gene flow could originate from the enhanced mobility of frogs in such a landscape.

To counteract further amphibian decline, I suggest to constantly improving conservation measures like for example the creation of stepping-stone habitats between ponds. Thereby, the results of studies such as this one can be used to find an adequate definition of a real stepping-stone for different amphibians and make the measure thus more efficient. Additionally, this study identified options to further develop studies applying corridor analyses to investigate landscape effects on gene flow. I recommend using variable corridor widths depending on the distance between locations instead of fixed corridor widths. Additionally, comparing several landscape classifications may reduce subjectivity in the analysis.

Introduction

The rapid decline in amphibians all over the world has reached an alarming extent. Progressing landscape and climate change are mainly held responsible for this recent biodiversity loss (Collins and Storfer 2003, Storfer 2003, Cushman 2006, Apodaca et al. 2012). These factors indeed seem to pose a particular problem, as amphibians are not known to be very flexible in their choice of habitat and therefore not predestined to easily adapt to changes. They exhibit relatively limited dispersal abilities compared to other animals of their size And, on top of that, show strong site fidelity (Gill 1978). Populations are thus threatened to become more and more isolated, which in turn is making them even more susceptible to other threats like competitive invasive organisms, diseases, and genetic as well as demographic stochasticity (Storfer 2003, Vittoz et al. 2013).

For these reasons, it is essential to know whether populations are connected by gene flow as well as to identify which parts of the landscape likely facilitate or hinder movement. Many scientific studies were conducted to investigate dispersal among populations for different amphibians (Bossart and Prowell 1998, Bohonak 1999). Thereby, dispersal can be determined with direct observations or indirect measurements. However, the direct approach has some disadvantages compared to the indirect one. On the one hand, direct measures of dispersal are limited in space and time and on the other hand, they measure only the movement of animals and not successful breeding (Slatkin 1987). In addition, the indirect measurement of dispersal has recently become even more attractive through vast progress in genetic analysis technologies (Segelbacher et al. 2010, Angelone et al. 2011, Keller et al. 2012). In earlier studies, the focus was thereby put on the investigation of habitat patches, stepping-stones and corridors. Later on, the focus shifted towards analyzing the effect of the whole landscape and not only subjectively allocated habitat patches (Rothermel and Semlitsch 2002, Goodwin 2003, Baum et al. 2004, Mazerolle and Desrochers 2005, Shirk et al. 2010). For amphibians, studying dispersal between subpopulations with indirect methods is straightforward as individuals from distinct ponds can be sampled and compared to each other (Manel et al. 2003). However, amphibian species are still most poorly studied with regards to the effects of the landscape on dispersal (Cushman 2006). The same conclusions are drawn by another review about landscape genetic studies in amphibians by Emel and Storfer (2012). They argue that until now only specific landscape variables were selected for analyses and therefore the effects of others are unknown (Emel and Storfer 2012).

The aim of this study is to contribute to gaining knowledge about amphibians and how they are affected by the landscape between ponds. This is achieved through the indirect measurement of dispersal with genetic analysis and the implementation of a corridor analysis for a nearly threatened water frogs (*Pelophylax* spp. system) (Schmidt et al. 2005). This study is part of a larger project (CCES-GeneMig), which investigates the role of landscape elements on species' distribution and genetic variation using landscape genetics analysis (<http://www.cces.ethz.ch/projects/sulu/genemig>). Specifically, permuted, multiple regression on distance matrices (MRM) and simple Mantel tests were applied to investigate the correlation between different landscape classes and the genetic pattern in water frogs. More precisely, the genome of water frogs was analyzed to answer the following research questions: (1) Is genetic structure shaped by isolation by distance (IBD)? (2) How do the different landscape classes influence dispersal and thereby genetic distance in water frogs?

Material and methods

Study system

The water frog system in central and eastern Europe consists of two parental species, *Pelophylax ridibundus* (genotype RR) and *Pelophylax lessonae* (genotype LL), and their hybrid, *Pelophylax esculentus* (genotype LR) (Uzzell and Berger 1975). The hybrids are not sterile as they are able to reproduce sexually through meiotic hybridogenesis. In this mechanism, only one of the parental genomes is selected for reproduction and after meiosis transmitted clonally to the gametes (Christiansen and Reyer 2009). However, offspring resulting from hybrid-hybrid mating is often not viable which is probably due to an accumulation of deleterious mutations on the clonally transmitted genome (Milinski 1994). The hybrid population maintains itself through backcrossing with individuals from their parental species. In Switzerland, the L genome is usually excluded from reproduction in hybrids, and individuals of *P. lessonae* are required to produce viable offspring. Therefore, in a habitat, the hybrid often co-occurs with *P. lessonae*. This mixed population is also called *P. lessonae* - *P. esculentus* (LE) system (Vorburger 2001). In addition, there exists a special type of reproduction mainly observed in all - hybrid populations around the Baltic Sea. These populations only consist of diploid (LR), triploid (LLR or LRR), and sometimes tetraploid (LLRR) *P. esculentus* individuals (Christiansen et al. 2005, Hermaniuk et al. 2013, Pruvost et al. 2013). Hermaniuk et al. (2013) recently even documented a pentaploid (LLLRR) froglet. All these polyploid individuals originate from LR eggs produced by hybrid females where the reduction mechanism described above (meiotic hybridogenesis) did not function properly (Christiansen et al. 2005). Even though, all-hybrid populations mainly occur in Northern Europe, polyploid frogs were also found in Central Europe (Pruvost et al. 2013).

Genetic sampling

During spring and summer of 2013, 999 water frogs were sampled in the cantons of Aargau, Thurgau, and Zürich as part of the GeneMig project. In this thesis, a subsample of 459 water frogs was used, collected from 25 ponds in the canton of Aargau. The goal was to catch around 30 water frogs per location. However, this was not always achieved as pond and population sizes varied greatly. Individuals were caught by hand during nights in benign weather conditions. Two saliva samples were taken with a sterile buccal swab (155C, Copan Diagnostics Inc., Italy) from each frog. Afterwards, all water frogs were released into their original ponds and the swabs were stored in a cooling box until the end of the night. All samples were stored at -20 °C until the DNA was extracted for further analysis.

Molecular analysis

DNA was extracted using the QIAamp 96 DNA Blood Kit (QIAGEN, Hilden, Germany) following the manufacturer's handbook with some minor changes. The adjustments were necessary because instead of blood, heads of the buccal swabs were used for DNA extraction. Firstly, in addition to 16 µl of QIAGEN Proteinase K stock solution, 320 µl of a PBS buffer were added to each sample. Whereby 500 ml PBS stock solution with a pH of 7.4 consist of: 4 g NaCl (71367, Fluka) + 0.19 g KCl (60130, Fluka) + 0.12 g KH₂PO₄ (60218, Fluka) + 0.865 g Na₂HPO₄ dihydrate (6580.1000, MERCK) solved in 400 ml H₂O dest (Milipore) and then filled up with H₂O dest to a total volume of 500 ml. Consequently, due to the increase in sample volume, the amount of AL Buffer and ethanol added to each sample in subsequent steps had to be increased to 320 µl as well. Furthermore, the incubation process was modified. Incubation temperature was decreased from 70 °C to 56 °C and incubation time was

increased from 10 minutes to eight hours (overnight) on a shaker. Lastly, the amount of AE buffer used to elute the DNA was decreased to 120 μ l.

All 459 samples from the canton of Aargau were amplified at 18 microsatellite loci using fluorescently labeled primers. Four to five loci were simultaneously amplified in multiplex polymerase chain reactions (PCRs), with specific annealing temperatures and cycle times for each multiplex as well as specific volumes of each forward and reverse primer (Appendix I). PCRs were performed in 10 μ l containing 2 μ l of DNA, 4 μ l 2x Multiplex PCR Master Mix (QIAGEN, Hilden, Germany), 1.1-2.3 μ l total primer mix and 1.7-2.9 μ l H₂O (MERCK) and were run on PTC-100 thermocyclers (MJ Research, Waltham, Massachusetts, USA). The five minutes of denaturation at 95°C were followed by 30 or 32 cycles of 30 s denaturation at 95 °C, respectively, 90 s of annealing at 55 °C or 58 °C respectively, 30 s of extension at 72 °C, and finally an extension of 30 min at 60 °C. PCR products were diluted with 20 μ l H₂O (MERCK). 1 μ l of each diluted multiplex PCR mix was added to 10 μ l of size standard GeneScan 400HD ROX mixed with HiDi - formamide in a ratio of 1 to 10 (Applied Biosystems, Carlsbad, California, USA), then analyzed on an ABI 3130 automated capillary sequencer (Applied Biosystems), and finally scored with GeneMapper version 5.0 (Applied Biosystems).

Genotyping of samples

In Switzerland, *P. ridibundus* is not native and was introduced from Eastern Europe (Semlitsch et al. 1996). Therefore, the present analysis focuses on the native *P. lessonae* and *P. esculentus*. The genetic diversity in this system is assessed using the L genome that is present in both *P. lessonae* and *P. esculentus* individuals. The unambiguous distinction between the three different water frog species is only possible through genetic analysis. Thus, during the sampling of water frogs it was not possible to selectively catch *P. lessonae* and *P. esculentus* individuals only. To find out what species had been collected, all sampled water frogs were genotyped.

Pelophylax ridibundus (RR) and *P. lessonae* (LL) individuals were genotyped using the microsatellite markers specific for either the L genome (Res20, RICA18, RICA1a27, RICA5) or the R (Re2Caga3, Res22, Rrid169A) genome. Based on alleles found in these individuals, genome specificity of alleles could be determined and, with this information at hand, all individuals could be unambiguously assigned to a genotype except one. However, two markers, Ca1b6 and RICA135A, had in each case one allele that occurred on the R as well as on the L genome. Therefore, for data analysis, individuals in which these alleles could not be attributed to a genome were treated the same as individuals with missing data for these markers. Furthermore, samples from two individuals did not amplify.

Selection of locations and samples

From the 25 ponds that were originally sampled, some had to be omitted and some had to be aggregated. In one pond, there were no individuals with an L genome and in the other one, there were only two frogs caught of which one could not be unambiguously matched with a genotype. Consequently, these two locations were omitted. Furthermore, due to technical reasons, ponds lying closer than 200 m from each other were aggregated. The remaining locations were then named with ascending numbers from 1 to 19 (Table 1).

Table 1: Sampled locations in the canton of Aargau with the original pond names from the GeneMig project, respective coordinates (CH1903/LV03), number of water frogs caught, and date of sampling

Location	Original label	Longitude	Latitude	Sample size	Sampling date
1	AG01, AG02, AG03	645519	242270	32	08.04.2013
2	AG04, AG05	643724	241890	44	13.05.2013
3	AG06	645504	244636	19	14.05.2013
4	AG08	646629	241677	30	06.06.2013
5	AG09	642334	242455	28	06.06.2013
6	AG10	643015	243946	31	07.06.2013
7	AG11	643268	243854	30	07.06.2013
8	AG12	643824	243957	30	07.06.2013
9	AG13, AG15	645532	244167	32	08.06.2013
10	AG14	645913	244408	10	08.06.2013
11	AG16	651998	246630	30	11.06.2013
12	AG17	645751	240832	6	12.06.2013
13	AG18	649980	251355	5	14.06.2013
14	AG20	649634	251168	30	14.06.2013
15	AG21	649798	251276	8	14.06.2013
16	AG23	655950	251600	30	16.06.2013
17	AG32	644123	243624	18	26.06.2013
18	AG33	645388	244337	10	01.07.2013
19	AG34	654641	252199	9	02.07.2013

The 19 selected ponds were located near Aarau and were 200 m to 16'400 m apart from each other with a mean distance of 6'350 m (Fig 1).

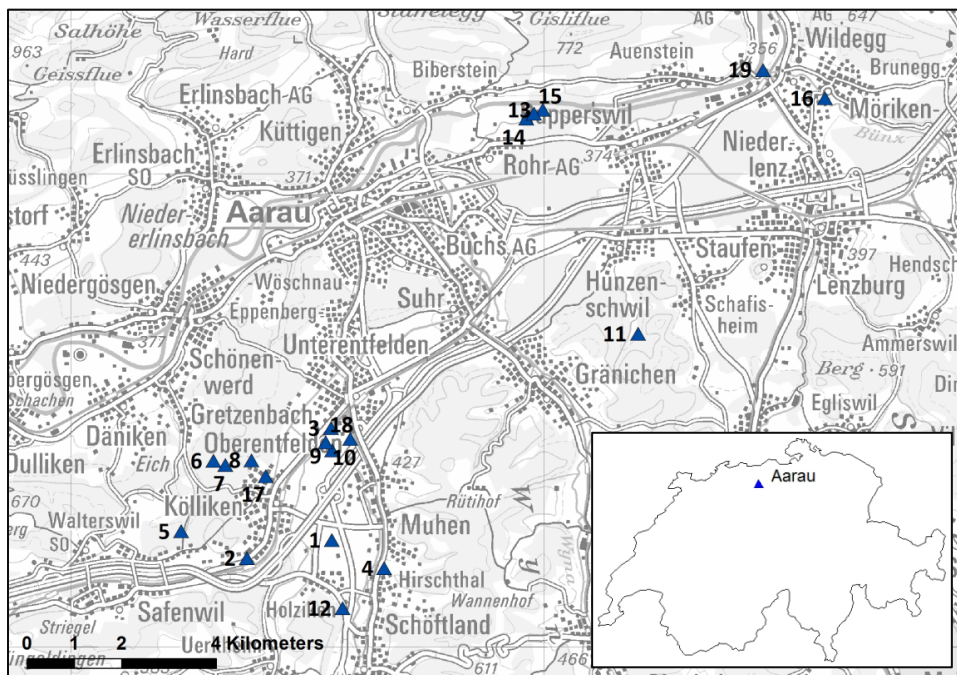


Fig 1: Map of the study area in the canton of Aargau in the north of Switzerland indicating the 19 sampling locations

The distribution of different genotypes over the 19 ponds varied greatly (Fig 2). In total, the individuals consisted of 35 *P. ridibundus*, 92 pure *P. lessonae* (LL), one triploid *P. lessonae* (LLL), 276 *P. esculentus* of the genome configuration RL, three triploids of the genome configuration RRL, 23 triploids of the configuration RLL, and two tetraploids (RRLL) (Appendix II).

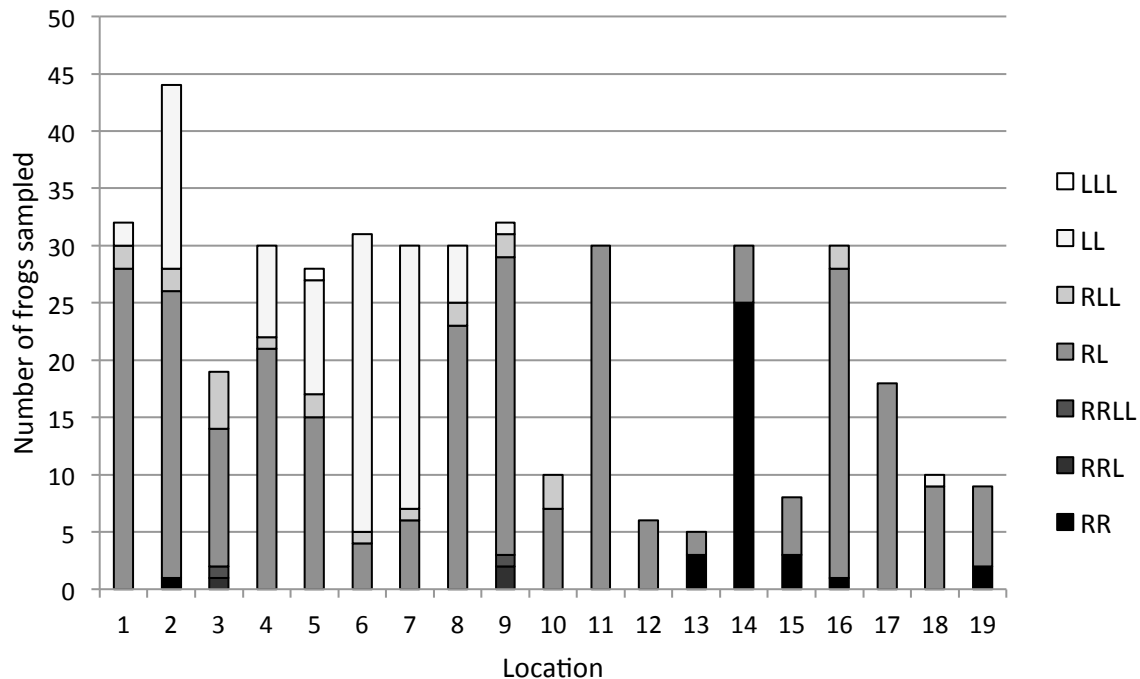


Fig 2: Genotype composition found in a total of 432 water frogs in 19 locations in the canton of Aargau (Appendix II)

From the 432 individuals that were unambiguously assignable a genotype, only the 396 individuals with at least one and maximally two L genomes were further investigated at 13 microsatellite loci polymorphic for the L genome (Ga1a19re., Re1CAGA10, ReGA1a23, Res16, Res20, RICA18, RICA1a27, RICA1b5, CA1b6, RICA2a34, RICA5, Rrid013A, Rrid135A) (Appendix II). All further analyses were conducted with allelic data from the L genome(s) of these 396 frogs.

Corridor analysis

Analyzing the influence of landscape composition on the genetic distance proceeded in three main steps: classifying the landscape, determining the proportion of each landscape class in the corridor area connecting two locations, and testing the explanatory power of the proportion of the landscape classes and Euclidean distance. The first two steps were conducted in ArcGIS (ARCGIS 10.1, ESRI, Redlands, CA, USA) and the last step was computed with R and its package “ecodist” (Goslee and Urban 2007).

In the first step, the landscape matrix between locations was classified. The Swiss land-use statistics from the year 2009, with a resolution of 100 m x 100 m served as basis for this step (Arealstatistik 2009, swisstopo). The original 72 classes were aggregated into nine classes. Thereby, classes which were considered of similar permeability for a frog and which may therefore affect its dispersal in a similar way were grouped (pers. communication B. Schmidt, karch, Neuchâtel). As this procedure is quite subjective, two alternative classifications (A and B) were tested separately. These two classifications differed slightly in almost all variables because some of the land-use classes were

difficult to assign (Table 2). The most important differences in classification B compared to A were the exclusion of railway from “linear elements”, the aggregation of “waters and wetlands”, and the separation of “forest and bushes”.

Table 2: Classification A and B composed of the basic categories from the Swiss land-use statistics 2009

<i>Classification A</i>		<i>Classification B</i>	
<i>Class name</i>	<i>Assigned basic categories</i>	<i>Class name</i>	<i>Assigned basic categories</i>
Settlement zone	1-14, 19, 22, 24-27, 29, 30, 32, 63	Settlement zone	1-14, 19, 24-27, 29, 30, 32, 63
Linear elements	15-18, 20, 21	Roads and highways	15-18
Mining	28	Mining	28
Green public areas	31, 33-36	Green public areas	31, 33-36
Agricultural land	37-41, 59	Open land	20-23, 37-41, 59
Grassland	23, 42-43, 45-46, 48-49, 60, 65-66, 68-72	Grassland	42-43, 45-46, 48-49, 60, 65-66, 68-72
Forest and bushes	50-57, 64	Forest	50-56
Waters	61, 62	Waters and wetlands	61, 62, 67
Wetlands	67	Bushes	44, 47, 57, 58, 64

The difference between the two classifications in the landscape composition of the study area was minor when visually comparing maps of both (Fig 3 and Fig 4). However, the proportion of the landscape classes lying between the 19 locations seems to be diverse with both classification A and classification B.

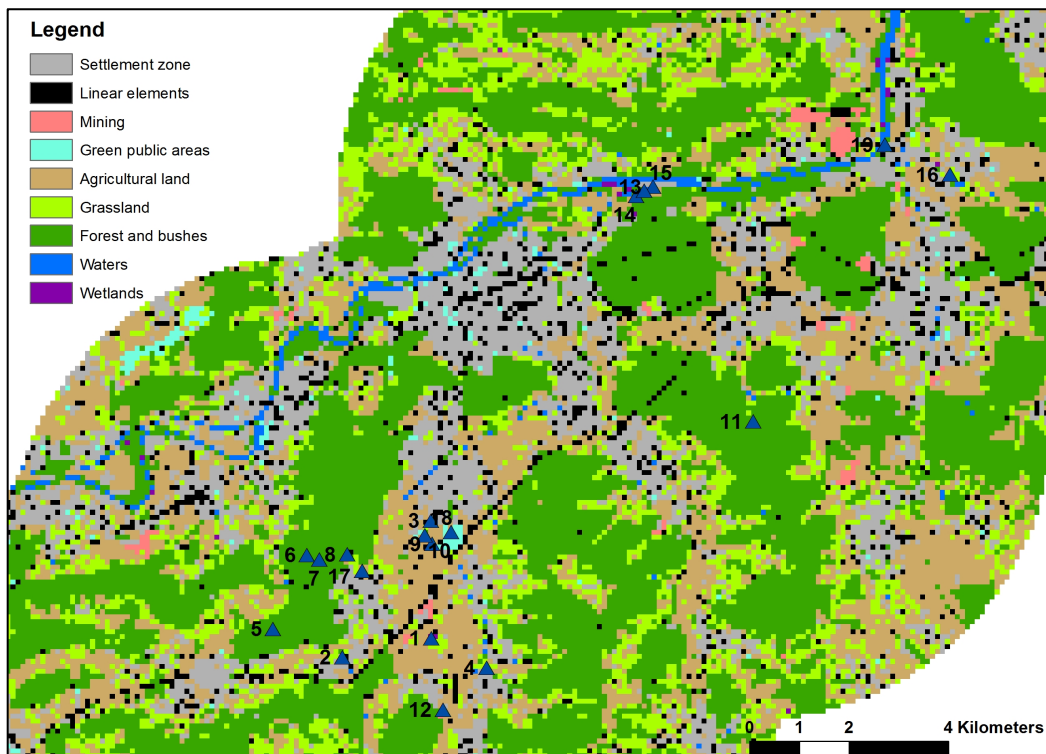


Fig 3: Study area with classification A in the canton of Aargau

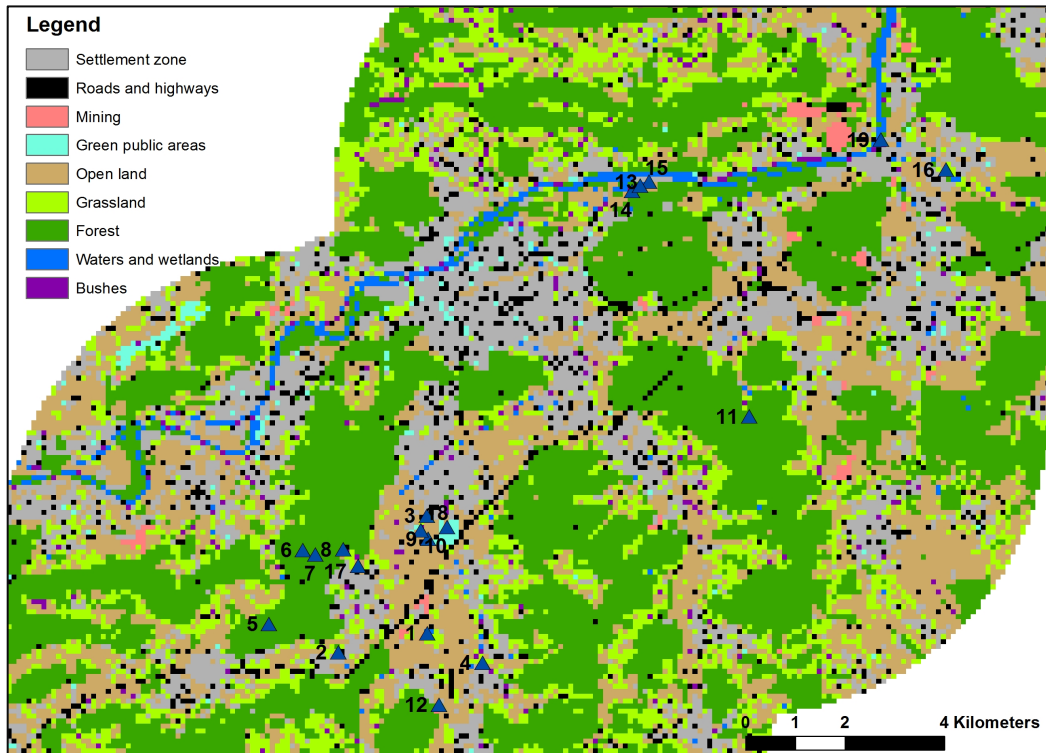


Fig 4: Study area with classification B in the canton of Aargau

In a next step, the proportion of all nine landscape types of both classifications between each pair of sampling sites was calculated as described in Emaresi et al. (2011). For this corridor analysis, a straight line between each location pair was drawn. The resulting corridors were constructed with three different corridor widths (Fig 5). This approach was chosen to evaluate the plausibility of the obtained results.

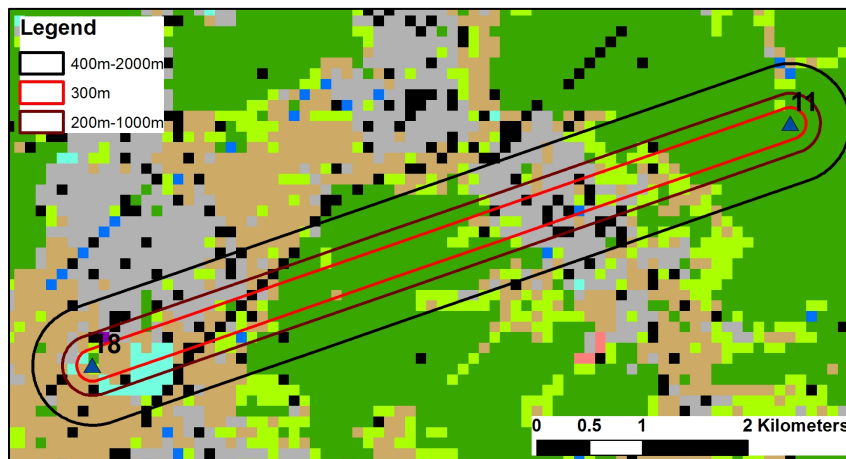


Fig 5: Example for the three different buffer-distances applied between all location pairs

One corridor width was fixed at 300 m for all 171 possible connections. The other two corridors were proportional to the Euclidian distance between two locations. This differentiated approach was chosen as some locations were relatively far apart compared to others which were closer. In such a case, a fixed corridor width would represent a rather unlikely dispersal path, as the frog's route through the landscape would likely deviate from a straight line the further apart the locations were. Corridor width was set to vary linearly between 200 m and 1'000 m ($\text{width} = 100 + (\text{Euclidian distance} - 100) * 400 / 14900$) in one case and between 400 m and 2'000 m ($\text{width} = 200 + (\text{Euclidian distance}$

- 200) * 800 / 14800) in the other case. The lower limit was chosen based on the minimal distance of 200 m between sampled locations and the upper limit based on the maximal dispersal distance recorded of *P. lessonae* lying between 1'000 m and 2'000 m according to Smith and Green (2005). The proportion of each landscape class within the different corridors was calculated in ArcGIS using the command "Zonal histogram" while iterating the 171 corridors due to overlapping stripe areas.

For the third step of the corridor analysis, pairwise F_{st} (Weir and Cockerham 1984), linearized to $F_{st}/(1-F_{st})$ as suggested by Rousset (1997) and D_s (Nei 1972) were calculated. Referring to Bohonak (1999) these estimates are an adequate representation of genetic distance between sampled locations. For this purpose, the program Spatial Pattern Analysis of Genetic Diversity (SPAGeDi) version 1.4 was used as it is able to handle data of any ploidy level (Hardy and Vekemans 2002). Significance of these estimates was tested with 10'000 permutations in SPAGeDi.

Pairwise F_{st} values were used to calculate mean global F_{st} for each location. To test for an IBD pattern, simple Mantel tests were conducted with $F_{st}/(1-F_{st})$ or D_s , respectively, and log-transformed Euclidian distance applying 10'000 randomizations (Rousset 1997). Both pairwise $F_{st}/(1-F_{st})$ and D_s were used as a response variable in a multiple regression on distance matrices (MRM) conducted in R with the package "ecodist" (Goslee and Urban 2007). The predictive variables used in this model were the arcsine-transformed proportions of all landscape classes and the log-transformed Euclidian distance between the ponds (Reimann et al. 2008). Thereby, from highly correlated ($r > |0.6|$) landscape variables, only one entered the model, the other one was omitted. In classification A, the variables "forest and bushes" and "agricultural land" had a correlation coefficient > 0.6 , and in classification B, the correlation between "forest" and "open land" was above this threshold. In each case, the former variable was omitted. With MRM, both a full model and a reduced model was calculated applying 1'000'000 matrix randomizations. In the full model, all eight remaining landscape variables and Euclidian distance were included. The reduced model only contained the variables left after stepwise backward elimination applying Bonferroni-corrected p-values ($p < 0.05$) (Legendre et al. 1994). The full model as well as the reduced model was calculated for each corridor width and for each classification.

Results

Population differentiation

Global mean genetic distance between locations ranged from 0.13 to 0.33 and was not correlated with the estimated population size at each location. The estimations for pairwise F_{st} values was between -0.01 and 0.57 and showed a strong linear correlation (MRM, $R^2 = 0.37$, $p < 0.01$) with distance (Fig 6). There were several outliers (comparisons between the locations 13-16 and 19 as well as comparisons between 13-15 and 11). However, the comparisons of the involved locations (11, 13, 14, 15, 16, 19) with other locations were normal and thus the locations were not excluded from the analysis.

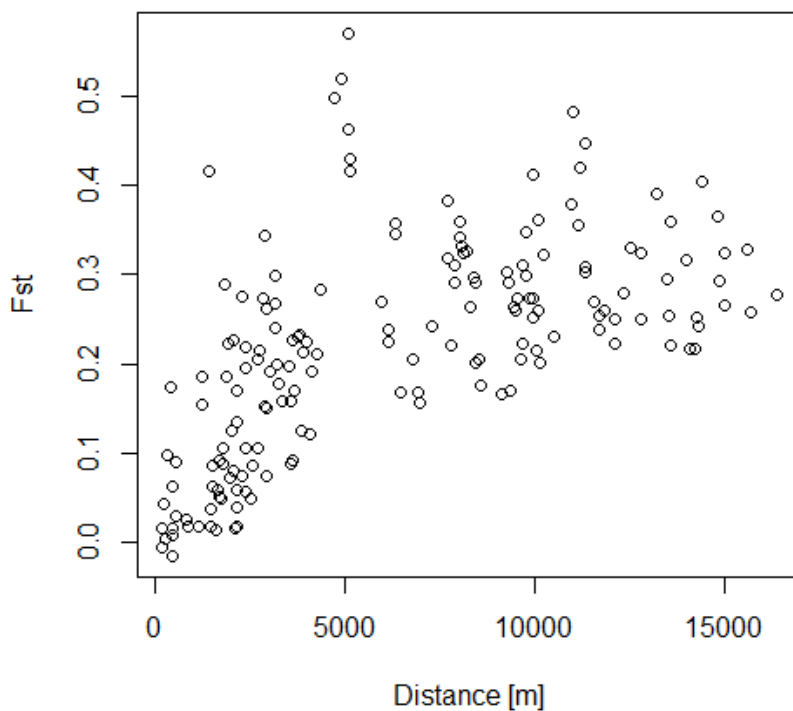


Fig 6: Pairwise Euclidian distance plotted against pairwise F_{st} values for all 171 comparisons between the 19 locations

Simple Mantel tests with genetic distance and Euclidian distance resulted in a significant ($p < 0.001$) Mantel r of 0.58 with $F_{st}/(1-F_{st})$ and 0.61 with D_s as dependent variable, respectively.

Corridor analysis

The full models including eight landscape variables and Euclidian distance resulted in an R^2 ranging from 0.51 to 0.66 (Table 3). All models were highly significant ($p < 0.01$), with Euclidian distance and landscape class “waters” / “waters and wetlands” always as significant predictor variables. Whether genetic distance was positively or negatively correlated with the predictor variables remained in most cases independent of the model. “Roads and highways”, “bushes”, “mining”, and “green public areas” showed once a slightly negative correlation with genetic distance in contrast to their otherwise positive correlation. “Settlement zone” and “agricultural land” / “open land” had mostly a reducing effect on genetic distance. Nevertheless, the regression coefficient of “settlement zone” was most of the time close to zero except in the models with the largest variable corridor. The landscape class “forest and bushes” / “forest” was not included in the models owing to its strong negative correlation with “agricultural land” / “open land”. When “forest and bushes” / “forest” was included instead, it had a positive regression coefficient.

Table 3: Regression coefficients for the nine predictor variables and respective R² for each corridor type, classification, and estimate of genetic distance

Corridor width	Classification	Genetic distance	Euclidian distance	Waters/ waters and wetlands	Linear elements/ roads and highways	Mining	Settlement zone	Agricultural land/ open land (Forest/ forest and bushes)	Grassland	Wetlands/ bushes	Green public areas	R ²
Fixed 300m	A	Ds	0.26 **	0.71 *	0.31	0.35	0.03	-0.18	0.16	0.42	0.07	0.51 **
	A	Fst ¹	0.24 **	1.06 **	0.25	0.54'	-0.04	-0.21'	0.33	0.31	0.09	0.59 **
	B	Ds	0.29 **	0.64 *	0.19	0.42	0.04	-0.20'	0.10	0.42	0.06	0.51 **
	B	Fst ¹	0.28 **	0.84 **	0.06	0.63 *	-0.05	-0.26 *	0.26	0.52'	0.08	0.57 **
Variable, 200-1'000m	A	Ds	0.22 **	0.82 **	0.39'	0.32	-0.05	-0.14	0.29	0.41	0.02	0.55 **
	A	Fst ¹	0.18 **	1.19 **	0.31	0.51'	-0.10	-0.11	0.46 **	0.18	0.01	0.63 **
	B	Ds	0.27 **	0.76 **	0.18	0.33	-0.02	-0.14	0.22	0.14	0.02	0.53 **
	B	Fst ¹	0.29 **	0.96 **	-0.05	0.55'	-0.09	-0.16	0.42 *	0.15	0.04	0.59 **
Variable, 400-2'000m	A	Ds	0.19 **	1.07 **	1.59 **	0.03	-0.32'	-0.31 *	0.31	0.71	0.06	0.60 **
	A	Fst ¹	0.16 **	1.47 **	1.18 **	0.37	-0.34*	-0.27'	0.63'	0.32	0.04	0.66 **
	B	Ds	0.24 **	1.14 **	1.16 **	-0.03	-0.20	-0.27'	0.30	-0.05	-0.11	0.57 **
	B	Fst ¹	0.23 **	1.39 **	0.67'	0.33	-0.25	-0.30*	0.71'	0.04	0.09	0.62 **

¹ stands for Fst/(1-Fst); ' marginally significant, p < 0.1; * significant at p < 0.05; ** significant at p < 0.01; intercept is not shown

The two classification types did not deliver substantially different results. Even though, classification A resulted in a slightly higher overall R². Differences between the two indirect measures for dispersal, Fst/(1-Fst) and Ds, were more pronounced. Models including Fst/(1-Fst) as dependent variable resulted in each case and in total in a higher R². However, the three different corridor types had the strongest impact on the outcome of the MRM analysis. The R² increased from the models with a fixed corridor width of 300 m to the model with a variable corridor width between 400 and 2'000 m, respectively. The regression coefficients for the independent variables “waters” / “waters and wetlands”, “linear elements” / “roads and highways”, “settlement zone”, and “grassland” did also show the same trend. Contrarily, Euclidian distance and “mining” showed an exactly inverse pattern. The remaining variables did not show any clear trend between the different corridor widths.

The reduced models with the remaining predictor variables after backward elimination had a slightly lower R^2 of 0.48 up to 0.59 compared to the full models (Table 4). The variables Euclidian distance and “waters” / “waters and wetlands” were always included and had a positive effect on genetic distance.

Table 4: Regression coefficients of the predictor variables describing genetic distance best after stepwise backward elimination and respective R^2 for each corridor type, classification, and estimates of genetic distance

Corridor width	Classification	Genetic distance	Euclidian distance	Waters/ waters and wetlands	Linear elements/ roads and highways	Mining	R^2
Fixed 300m	A	Ds	0.12**	0.76**	-	-	0.59**
	A	Fst^1	0.11**	1.07**	-	-	0.52**
	B	Ds	0.14**	0.75**	-	-	0.48**
	B	Fst^1	0.13**	0.95**	-	-	0.51**
Variable, 200- 1'000m	A	Ds	0.11**	0.85**	-	-	0.49**
	A	Fst^1	0.09**	1.08**	-	0.66*	0.59**
	B	Ds	0.13**	0.80**	-	-	0.51**
	B	Fst^1	0.13**	0.95**	-	-	0.53**
Variable, 400- 2'000m	A	Ds	0.09**	1.04**	0.97**	-	0.55**
	A	Fst^1	0.08**	1.25**	0.88*	-	0.59**
	B	Ds	0.13**	0.88**	-	-	0.51**
	B	Fst^1	0.12**	1.05**	-	-	0.54**

¹stands for $Fst/(1-Fst)$; ' almost significant, $p < 0.1$; * significant at $p < 0.05$; ** significant at $p < 0.01$; intercept is not shown

Contrary to the full models, the reduced models showed the strongest changes in R^2 between the two classification types (Table 4). By reducing the predictor variables from nine to two, R^2 dropped by 0.02 to 0.06. The change in coefficients shows that the effect of Euclidian distance decreased remarkably compared to the full models.

Discussion

The present study, conducted in the densely populated Swiss lowlands near Aarau, shows that dispersal in the amphibian *P. lessonae* – *P. esculentus* system as measured by genetic distance, can be explained to a considerable extent by a combination of isolation by distance and the composition of the landscape between sampling locations. Most landscape variables exerted a hindering effect on gene flow. Thereby, the negative effect of “waters” / “waters and wetlands” is surprising. Only “agricultural land” / “open land” enhanced gene flow considerably which also needs closer examination.

Isolation by distance

The study area exhibited a wide range of values of genetic distance between sampled populations. Plotting these values against Euclidian distance between locations and the simple Mantel test revealed that dispersal in *P. esculentus* and *P. lessonae* was considerably characterized by IBD. Referring to Hutchison and Templeton (1999), the sampled locations showed a case-IV pattern. More precisely, this means that gene flow in the study region was more pronounced up to about 5 km and genetic drift gains in importance beyond this distance. Thus, populations were not in a state of regional equilibrium, in contrast rather in a state of expansion (Hutchison and Templeton 1999). (Keller et al. 2012) found a similar pattern of IBD in a wetland grasshopper just as Arens et al. (2007), who found such a pattern among moor frog populations.

Some of the pairwise comparisons did not fit the typical pattern of IBD described by Hutchison and Templeton (1999). This holds exclusively for pairs that include sampling locations 13, 14, 15, 16, and 19 situated beside the river Aare crossing the study area in the Northwest. This could be a coincidence, but the presence of the river could also be the explanation for this deviation. Additionally, it was striking that no *P. lessonae* was caught in these ponds, but all except one individual were *P. ridibundus* (Fig 2).

The river Aare might have enhanced long-distance dispersal of *P. ridibundus* and *P. esculentus* and, by the latter, brought in new L genomes or even lead to the colonization of new locations so far not inhabited by *P. lessonae*. This hypothesis is supported by a study conducted in Bratislava by Mikulicek and Pisut (2012). These authors found that populations of *P. ridibundus* showed enhanced dispersal along water paths compared to land. In addition, the different water frog taxa did not have the same habitat requirements, which could be the reason why *P. lessonae* did not occupy these locations near the Aare beforehand. *Pelophylax lessonae* prefers smaller ponds covered with vegetation, contrary to *P. ridibundus* which likes less vegetated but bigger ponds or even lakes. The hybrid between those, *P. esculentus*, can inhabit both pond types (Holenweg 2001). Actually, the ponds in the North of the study area were larger and less vegetated than the ones in the South (personal observation). This observation seconds the opinion that *P. lessonae* might have been absent in the North before. The colonization by water frogs could not have happened long ago because without *P. lessonae* present, *P. esculentus* has difficulties to reproduce. Therefore, gene flow between populations in the North could not be very pronounced, possibly resulting in relatively large genetic differences between close locations. However, pairwise genetic differences between these populations in the North and the *P. lessonae*-dominated populations in the South were within an average range found in this study. The reason for this supposed inconsistency in the hypothesis could be that the effect is vanished because distance between these populations is very large. According to Hutchison and Templeton (1999), another explanation could be that populations without gene flow can sometimes be genetically more

similar as genetic drift goes in any direction. Indeed, genetic drift and fixation of alleles might be a relevant factor in the L genome of these northern populations as there are hardly any *P. lessonae* to mate with. Therefore, those populations initially have low genetic diversity and no recombination in the L genome (Arioli et al. 2010).

In the future, the observed pattern of IBD and the outlier values of genetic distance are likely to change. Firstly, as already mentioned, the region seems to be in a state of disequilibrium. Secondly, triploid frogs of the genotype RLL were detected in the study area, which could lead to recombination in the L genome (Christiansen and Reyer 2009, Arioli et al. 2010).

Influence of landscape on dispersal

To assess the influence of landscape composition and distance on gene flow, multiple regression on distance matrices (MRM) with permutations was applied as an alternative to common multiple linear regression or partial Mantel test. The full models in MRM, containing the classified landscape together with Euclidian distance as predictor variables, reached a higher power to explain genetic distance than the reduced models. Thereby, most landscape classes and Euclidian distance restricted gene flow except for “agricultural land” / “open land” and “settlement zone”, which seemed to have an enhancing effect. However, the impact of “settlement zone” was in most models very small compared to other landscape classes. Although the coefficients of most landscape classes were not significant in the full model, the robustness of the observed pattern is demonstrated by the fact that neither the different classifications of land-use types nor the three types of corridor definitions or the indicators of genetic distance changed the resulting full models considerably. Nevertheless, models with classification A, pairwise $F_{st}/(1-F_{st})$ as an inversely proportionate estimate of gene flow, or the variable corridor ranging from 400 m to 2'000 m slightly outperformed the respective other model alternatives in their explanatory power, though this trend was not statistically supported.

The corridor analysis conducted in this study revealed that, apart from straight travel distance, also the composition of the landscape plays an important role in driving amphibian dispersal. The role of the respective landscape types, i.e. whether they act as a barrier or as an enhancer of gene flow, might not always be obvious by intuition. This conclusion is consistent with the results of other investigations concerning the effect of landscape lying between populations (Kamm et al. 2010, Angelone et al. 2011, Keller et al. 2012). (Keller et al. 2012) also discovered an enhancing effect of agricultural land on gene flow and a hindering effect of forest in a wetland grasshopper. Similarly, Angelone et al. (2011) found that forest hinders gene flow in tree frogs.

In conclusion, our study showed that agricultural or more generally open land seemed to enhance dispersal in water frogs. This contradicts findings of a study by Mazerolle and Desrochers (2005). The authors directly measured frog movement and found that frogs tend to avoid open surfaces and that they were less successful in reaching breeding habitat on such terrain. Nevertheless, the results in the present study imply that the advantage of moving faster through open fields outweighs the costs of being visible to predators and more prone to dehydration (Mazerolle and Desrochers 2005). Ultimately, it still remains difficult to disentangle if the effect resulted from forest hindering gene flow or agricultural land enhancing it, as these landscape classes were significantly correlated.

A much more counterintuitive discovery of this study was the barrier effect of waters and wetlands on water frog dispersal. The result contrasted findings of previous studies that attribute waters and wetlands a promoting effect on frog dispersal (Mazerolle and Desrochers 2005). However, other

authors that conducted corridor analyses did also discover an initially counterintuitive negative effect of wetlands, or in general a negative effect of suitable habitat on dispersal (Angelone et al. 2011, Keller et al. 2012). Adriaensen et al. (2003) formulated the hypothesis that suitable habitat for a species could also act as a sink for dispersing individuals because there is no need for them to move further. Applied to the present analysis, this could mean that gene flow between two ponds is lower if another pond is located between them, as compared to gene flow without a pond in a water frog's way. However, to fully decode why suitable habitat might restrict gene flow in the long run, the hypothesis needs to be extended. The attracting effect of such a pond located between two other ponds can only exert a negative effect on gene flow if it is also suitable habitat for adult water frogs but for whatever reasons not good for reproduction. In case of amphibians that spawn in waters, fish might be a considerable threat to successful reproduction (Ficetola and De Bernardi 2004). In this case, adult frogs might survive in the new habitat and breed there, whereas, as the resulting spawn and tadpoles are eaten by fish, there are no juveniles that could disperse to another pond. In frogs, juveniles are known to disperse more often than adults. Additionally, as population density in such a habitat will rather decrease than increase, there is no pressure on individuals to disperse (Berven and Grudzien 1990). In the long run, the habitat may act as a sink for dispersing frogs and therefore exert a barrier effect on gene flow. It needs further investigation if this is really the explanation for the unexpected negative impact of waters and wetlands on frog dispersal in the studied area.

An alternative explanation for the observed counterintuitive phenomenon and the fact that in the reduced models only “waters” / “waters and wetlands” remained from eight landscape classes could be habitat specificity and the differences in dispersal rates as well as dispersal abilities in the water frog system (Holenweg 2001). Therefore, the simple analysis of estimated gene flow between all ponds in an area does not fully reflect actual dispersal patterns. In order to exclude such an effect, future studies might focus on only one species of the water frog system and not on one genome. However, as hybrid water frogs are also contributing to the dispersal of the parental genome, this approach seems to be suitable. Another approach, which could probably enhance the meaningfulness of the resulting reduced model, is to look at the effect of different landscape classes at different spatial scales. Angelone et al. (2011) found that, depending on the spatial scale used, different landscape variables had a significant effect on gene flow. In the case of the water frog system, two distance classes — one for distances up to 5'000 m and the other one containing distances over 5'000 m — appear reasonable (Fig 6).

A further possibility to advance the here performed analysis is to choose more meaningful predictor variables to represent the landscape as the proportion of each landscape class is rarely a realistic representation of what a frog encounters between two ponds on its route through the landscape. An improvement would be to consider the configuration of each landscape class in the corridor area because small patches of unsuitable landscape can more easily be bypassed than large ones. For example, this could be implemented by standardizing the proportion of each landscape class with the mean number of connected landscape pixels per landscape class for each corridor. An approach that is supposed to better represent animal dispersal than simple corridor analysis is a least-cost-path analysis (Adriaensen et al. 2003). However, this method comes along with the disadvantage of increased subjectivity. The subjectivity originates in the a priori need of expert knowledge about the costs of the different landscape classes (Epps et al. 2007). Thereby, the counterintuitive results of the present study are a confirmation of the difficulties which could arise when trying to divide landscape into “good” and “bad” for dispersal a priori. Therefore, a combination of the approach used in this

study and the least-cost-path analysis seems to be a solution that could be considered (Van Strien et al. 2012).

Conclusions

To act against the decline in amphibians with meaningful conservation measures, species-specific knowledge about their dispersal is essential. Therefore, this study aims to provide insights about actual gene flow in the *P. lessonae* - *P. esculentus* system and how it is influenced by distance alone as well as by different landscape elements lying between ponds.

A clear pattern of isolation by distance was detected with ponds located further apart as they showed a higher degree of genetic distance than close populations. Thus, water-frog dispersal was limited by traveling distance. In the same way, waters and wetlands were restricting gene flow between different ponds. The only factor that seemed to enhance gene flow was the proportion of agricultural or more generally open land along the route of dispersing individuals. The direction in which the landscape classes affected frog dispersal may seem counterintuitive. However, if this is really the way the frogs experience the landscape matrix, it is very important to incorporate this knowledge in future conservation actions. For example, it could be applied in the planning of appropriate measures to improve connectivity between isolated populations such as stepping-stone-habitats. So far, this was rather based on expert knowledge than on results of studies investigating actual gene flow and the enhancing or hindering effect of different landscape elements.

The techniques used to conduct such landscape genetic analyses are continuously improved (Manel and Segelbacher 2009). Experience from this study showed that the use of $F_{st}/(1-F_{st})$ as dependent variable and the allocation of a variable corridor width between 400 m and 2'000 m depending on the distance between locations provided the best model fit. In addition, it is recommended to use several classification methods to further enhance the explanatory power of the results and to reduce subjectivity in grouping the landscape to a minimum.

There are still many uncertainties and challenges that future studies need to address. On the one hand, studies conducted in different regions would allow testing the general validity of the discovered landscape effects for the *P. lessonae* - *P. esculentus* system. On the other hand, a corridor analysis at different spatial scales could improve the significance of the observed pattern in the same region. To put it in a nutshell, it is crucial to gather further species-specific knowledge about dispersal because without such information, it is difficult to undertake effective measures to counteract global loss in amphibian biodiversity.

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Appendix I: Microsatellite primer pairs in multiplex PCR one to four

PCR	Locus	Sequence 5'-3'	Genome specificity	Sequenced by	Fluorescent label	Primer volume (μ l) [100 μ M]	Annealing temperature ($^{\circ}$ C)	PCR cycles
Primer mix 1	CA1b6	F: AAA CTC GCG GTT TCC CTT AG R: GAG CCA GGT TAA GAT AAC TGG AG	R + L	Arioli (2007), Arioli et al. (2010)	F: FAM	0.014	58	30
	RICA1b5	F: CCC AGT GAC AGT GAG TAC CG R: CCC AAC TGG AGG ACC AAA AG	R + L	Garner et al. (2000)	F: HEX	0.014	58	30
	Ga1a19red.	F: GCA CAC TAT TTC TGC TGT ATT GC R: CAG GGG ATT TTC CCA TCA G	R + L	Arioli (2007), Christiansen and Reyer (2009)	F: FAM	0.028	58	30
	RICA5	F: CTT CCA CTT TGC CCA TCA AG R: ATG TGT CGG CAG CTA TGT TC	(R +) L	Garner et al. (2000)	F: HEX	0.02	58	30
	Rrid064A	F: TGT ACG GGC CTT TAG ACT GG R: AAC TTT TTG AAG GCC CCT TG	R (+ L)	Christiansen and Reyer (2009)	F: ATTO550	0.028	58	30
Primer mix 2	Re2CAGA3	F: ATG TCG TTA GAG TTC ATA GG R: ATC TCA AGT AAT CTG TCT GTC	R	Arioli (2007)	F: HEX	0.005	55	32
	Res16	F: GAT CCT GAT TTC CTG CT R: GTT TAT TTA CTC TGT TCG TCT T	R + L	Zeisset et al. (2000)	F: FAM	0.01	55	32
	Res20	F: TTT GTA AAT ATT CCG CTG GTA R: CCG AGG TTG GCT GTC ATT A	L	Zeisset et al. (2000)	F: HEX	0.05	55	32
	RICA2a34	F: GCT CCA TGC CAA AAG TCT TC R: TTG GGT ATG ATA CTA CAA GCT ATG C	R + L	Christiansen and Reyer (2009)	F: ATTO550	0.05	55	32

<i>PCR</i>	<i>Locus</i>	<i>Sequence 5'-3'</i>	<i>Genome specificity</i>	<i>Sequenced by</i>	<i>Fluorescent label</i>	<i>Primer volume (μl) [100μM]</i>	<i>Annealing temperature (°C)</i>	<i>PCR cycles</i>
<i>Primer mix 3</i>	ReGA1a23	F: ATT GCT TTG GCA GTG AAG G R: TGA CAT CAC AGT GGG AGG AG	(R +) L	Christiansen and Reyer (2009)	F: HEX	0.014	58	30
	Res22	F: ATA CAG GGC TTA GTG AAA TGA A R: AAG GGG TTA AAG GTG TGA CTA T	R	Zeisset et al. (2000)	F: FAM	0.007	58	30
	Rrid013A	F: CGA GAA TCG AAG TGG AGA GG R: ACC CGT CTC CAC AAT ACT GC	R + L	Hotz et al. (2001)	F: FAM	0.0035	58	30
	Rrid059A	F redesigned: ACA CTT ACA CTA AAA AGG ACA TTT ACC R: CCC CAT ACA TAT TGT TGG TTC C	R (+ L)	Hotz et al. (2001)	R: HEX	0.0098	58	30
	Rrid169A	F: CGG AAC TCC GCT TTA ATC AC R: CCC ATG TTG TCG TTG AGC TA	R	Christiansen and Reyer (2009)	F: FAM	0.028	58	30
<i>Primer mix 4</i>	Re1CAGA10	F: CAT GTT TAC CGT CAC TTT AAG AAC AC R: CAT CTC TTC AGG TGG CTG GA	R + L	Arioli (2007)	F: HEX	0.014	58	30
	RICA18	F: CTC TGC TCC CTC AGC TAT GC R: AAA AAG TGG TCC TTT CAT TTT GAG	L (+ R)	Garner et al. (2000)	F: FAM	0.0126	58	30
	RICA1a27	F: CAA ATG GGT CAT CCA CAC C R: GTT CAA GGG GGT CGA AAT AC	L	Christiansen and Reyer (2009)	R: FAM	0.014	58	30
	Rrid135A	F: TCT TTT GTT TTA GCG CAC CT R: CTG CCC GTC TAA GCA AGT GT	R (+ L)	Christiansen and Reyer (2009)	F: HEX	0.014	58	30

Appendix II: Genotype table for 396 frogs at 13 microsatellite markers, where for every marker, a zero in the first column indicates that no second allele is present in this individual and a zero in the second column that the data is missing but there should be an allele

<i>Frogs</i>	<i>Pond</i>	<i>Genotype</i>	<i>Ga1a19re.</i>		<i>Re1Caga10</i>		<i>ReGa1a23</i>		<i>Res16</i>		<i>Res20</i>		<i>RICA18</i>		<i>RICA1a27</i>		<i>RICA1b5</i>		<i>CA1b6</i>		<i>RICA2a34</i>		<i>RICA5</i>		<i>Rrid013A</i>		<i>Rrid135A</i>	
01_01	01	RL	0	196	0	98	0	140	0	121	0	125	0	180	0	117	0	122	0	76	0	141	0	256	0	291	0	206
01_02	01	RL	0	227	0	98	0	134	0	121	0	127	0	180	0	117	0	148	0	90	0	155	0	262	0	291	0	206
01_03	01	RL	0	196	0	98	0	142	0	121	0	0	0	178	0	109	0	128	0	78	0	139	0	262	0	291	0	238
01_04	01	RLL	227	227	96	96	138	138	121	121	125	125	180	180	117	117	148	148	78	0	155	139	256	256	291	291	238	0
02_01	01	RL	0	227	0	98	0	140	0	121	0	125	0	180	0	117	0	148	0	78	0	155	0	256	0	291	0	238
02_02	01	RL	0	231	0	96	0	142	0	121	0	125	0	180	0	117	0	128	0	88	0	135	0	256	0	291	0	206
02_03	01	RL	0	196	0	98	0	142	0	121	0	0	0	178	0	117	0	122	0	76	0	139	0	256	0	291	0	206
02_04	01	RL	0	196	0	98	0	142	0	121	0	103	0	178	0	117	0	122	0	78	0	139	0	262	0	0	0	206
02_05	01	RL	0	196	0	98	0	142	0	121	0	121	0	178	0	109	0	128	0	76	0	139	0	256	0	291	0	206
02_06	01	RL	0	196	0	96	0	142	0	121	0	121	0	180	0	117	0	122	0	88	0	139	0	262	0	291	0	206
02_07	01	RL	0	196	0	98	0	142	0	121	0	103	0	178	0	109	0	128	0	78	0	135	0	256	0	291	0	206
02_08	01	RL	0	231	0	98	0	140	0	123	0	125	0	180	0	117	0	148	0	78	0	155	0	258	0	291	0	238
02_09	01	RL	0	196	0	98	0	138	0	121	0	121	0	180	0	109	0	128	0	76	0	135	0	256	0	291	0	238
02_10	01	RL	0	196	0	98	0	140	0	121	0	121	0	178	0	117	0	122	0	76	0	139	0	256	0	291	0	206
02_11	01	RL	0	196	0	96	0	142	0	121	0	125	0	184	0	109	0	122	0	78	0	135	0	256	0	291	0	206
02_12	01	RL	0	196	0	98	0	142	0	121	0	103	0	178	0	109	0	128	0	76	0	141	0	256	0	291	0	238
02_13	01	LL	196	196	98	96	142	138	121	121	103	103	184	180	117	117	122	122	88	76	141	135	262	256	291	291	238	238
02_14	01	RL	0	231	0	98	0	142	0	121	0	125	0	178	0	117	0	122	0	88	0	139	0	256	0	291	0	206
02_15	01	RL	0	196	0	96	0	130	0	123	0	125	0	182	0	97	0	124	0	88	0	155	0	262	0	291	0	206
02_16	01	RL	0	196	0	98	0	142	0	121	0	121	0	178	0	117	0	122	0	76	0	141	0	256	0	291	0	238
02_17	01	RL	0	196	0	96	0	142	0	121	0	103	0	184	0	117	0	122	0	76	0	139	0	256	0	291	0	206
02_18	01	RLL	196	196	98	98	142	142	121	121	121	103	184	184	117	109	122	122	76	0	139	139	262	262	291	291	238	0
03_01	01	RL	0	196	0	98	0	140	0	121	0	125	0	178	0	95	0	122	0	76	0	141	0	256	0	291	0	206
03_02	01	RL	0	196	0	96	0	0	0	121	0	125	0	178	0	95	0	122	0	76	0	141	0	256	0	0	0	206
03_03	01	RL	0	227	0	98	0	138	0	123	0	125	0	180	0	117	0	148	0	90	0	147	0	256	0	291	0	238
03_04	01	RL	0	196	0	96	0	140	0	121	0	0	0	184	0	109	0	128	0	78	0	141	0	262	0	291	0	238
03_05	01	RL	0	196	0	98	0	142	0	121	0	125	0	178	0	117	0	122	0	76	0	139	0	262	0	291	0	206
03_06	01	RL	0	227	0	98	0	140	0	123	0	125	0	180	0	117	0	148	0	78	0	155	0	256	0	291	0	238
03_07	01	LL	231	196	98	96	142	140	121	121	125	125	184	180	117	117	122	122	88	76	141	135	256	256	291	291	238	238
03_08	01	RL	0	196	0	98	0	142	0	121	0	125	0	178	0	117	0	122	0	76	0	139	0	256	0	291	0	206
03_09	01	RL	0	196	0	98	0	142	0	121	0	103	0	178	0	109	0	128	0	76	0	141	0	256	0	291	0	238
03_10	01	RL	0	196	0	96	0	142	0	121	0	121	0	180	0	117	0	122	0	76	0	141	0	256	0	291	0	238
04_01	04	RL	0	196	0	96	0	124	0	121	0	109	0	180	0	95	0	148	0	90	0	145	0	262	0	0	0	206
04_02	04	LL	231	196	96	96	130	130	123	121	121	109	176	176	103	95	148	122	90	90	145	145	262	233	294	291	0	0
04_03	04	RL	0	231	0	96	0	130	0	121	0	125	0	176	0	95	0	148	0	90	0	139	0	262	0	294	0	206
04_04	04	RL	0	196	0	96	0	130	0	121	0	109	0	176	0	103	0	122	0	78	0	109	0	246	0	291	0	206
04_05	04	RL	0	196	0	96	0	124	0	121	0	121	0	176	0	117	0	122	0	90	0	139	0	233	0	291	0	206
04_06	04	LL	235	196	96	96	138	124	121	121	121	109	182	176	97	95	148	122	90	78	145	145	262	246	291	291	179	179

Frogs	Pond	Genotype	Ga1a19re.	Re1Caga10	ReGa1a23	Res16	Res20	RICA18	RICA1a27	RICA1b5	CA1b6	RICA2a34	RICA5	Rrid013A	Rrid135A
04_07	04	LL	196 196	96 96	124 124	121 121	109 109	180 176	117 103	148 122	90 78	145 145	262 246	294 294	0 0
04_08	04	RL	0 196	0 96	0 130	0 121	0 121	0 180	0 95	0 148	0 90	0 145	0 262	0 294	0 206
04_09	04	RL	0 231	0 96	0 124	0 123	0 109	0 176	0 103	0 122	0 90	0 145	0 246	0 291	0 206
04_10	04	RL	0 235	0 96	0 124	0 121	0 125	0 180	0 117	0 122	0 90	0 145	0 262	0 291	0 206
04_11	04	LL	196 196	96 96	130 130	121 121	121 109	182 176	117 117	148 122	90 78	145 139	256 256	291 291	0 0
04_12	04	RLL	196 196	96 96	130 124	121 121	121 121	176 176	117 95	122 122	90 90	139 139	256 256	294 294	206 206
04_13	04	RL	0 196	0 96	0 130	0 121	0 109	0 176	0 117	0 122	0 78	0 139	0 233	0 291	0 206
04_14	04	RL	0 196	0 96	0 124	0 121	0 109	0 176	0 117	0 148	0 90	0 139	0 256	0 291	0 206
04_16	04	RL	0 196	0 96	0 124	0 121	0 121	0 180	0 103	0 148	0 78	0 155	0 246	0 291	0 206
04_17	04	RL	0 235	0 96	0 130	0 121	0 125	0 176	0 97	0 124	0 88	0 139	0 262	0 297	0 206
04_18	04	RL	0 196	0 0	0 124	0 121	0 109	0 176	0 95	0 148	0 90	0 145	0 262	0 0	0 206
04_19	04	RL	0 196	0 96	0 140	0 121	0 109	0 176	0 117	0 122	0 78	0 145	0 262	0 291	0 206
04_20	04	RL	0 196	0 96	0 130	0 121	0 109	0 180	0 95	0 148	0 90	0 139	0 233	0 294	0 206
04_21	04	RL	0 196	0 96	0 130	0 123	0 109	0 176	0 103	0 122	0 78	0 109	0 246	0 291	0 206
04_22	04	RL	0 231	0 96	0 130	0 121	0 109	0 176	0 103	0 122	0 78	0 109	0 262	0 291	0 206
04_23	04	LL	231 196	96 96	130 124	123 121	109 109	180 176	117 103	148 122	90 90	145 139	262 262	291 291	0 0
04_24	04	LL	196 196	96 96	130 130	121 121	121 109	176 176	103 95	148 122	90 78	139 109	262 246	294 291	0 0
04_25	04	LL	231 196	96 96	130 124	123 121	109 109	180 176	103 95	148 122	90 78	145 109	262 262	291 291	0 0
04_26	04	RL	0 196	0 96	0 124	0 121	0 125	0 176	0 117	0 122	0 78	0 145	0 256	0 291	0 206
04_27	04	LL	235 196	96 96	140 124	121 121	109 109	176 176	117 95	148 148	90 78	145 145	262 262	294 294	0 0
04_28	04	RLL	235 235	0 0	140 140	121 121	125 109	182 182	117 117	122 122	90 90	145 145	262 262	291 291	206 206
04_29	04	RL	0 196	0 96	0 124	0 121	0 109	0 176	0 95	0 148	0 90	0 139	0 233	0 291	0 206
05_01	04	RL	0 196	0 96	0 124	0 121	0 121	0 180	0 117	0 148	0 90	0 145	0 233	0 294	0 206
05_02	04	RL	0 196	0 96	0 124	0 121	0 109	0 176	0 103	0 122	0 78	0 145	0 262	0 291	0 206
05_03	04	LL	235 196	96 96	124 124	121 121	121 109	180 180	117 103	148 122	90 78	145 139	262 246	291 291	0 0
05_04	04	LL	231 196	96 96	130 124	121 121	125 109	180 176	117 117	148 122	90 78	145 145	256 233	294 294	0 0
05_05	04	LL	235 196	96 96	130 124	121 121	121 121	182 176	117 117	148 122	90 78	145 139	262 233	291 291	0 0
05_06	04	LL	235 196	96 96	130 124	121 121	121 109	176 176	117 117	148 122	90 78	145 145	262 256	291 291	0 0
05_07	04	RL	0 196	0 96	0 130	0 121	0 121	0 180	0 95	0 122	0 90	0 139	0 233	0 291	0 206
05_08	04	LL	196 196	96 96	130 130	121 121	109 109	176 176	103 103	148 122	90 90	145 139	262 233	294 291	0 0
05_09	04	RL	0 235	0 96	0 130	0 121	0 109	0 182	0 117	0 148	0 90	0 145	0 262	0 291	0 206
05_10	04	RL	0 196	0 96	0 124	0 121	0 109	0 176	0 117	0 148	0 78	0 145	0 256	0 291	0 206
05_11	04	LL	235 196	96 96	124 124	121 121	121 109	180 180	117 103	148 122	90 90	145 139	262 262	294 294	0 0
05_12	04	RL	0 235	0 96	0 124	0 121	0 109	0 182	0 117	0 148	0 90	0 145	0 262	0 294	0 206
05_13	04	LL	235 196	0 0	138 124	121 121	121 121	176 176	103 103	148 148	90 78	145 145	262 246	291 291	179 179
05_14	04	LL	196 196	96 96	130 124	121 121	121 109	180 176	117 95	148 122	90 78	139 139	256 233	291 291	0 0
05_15	04	RL	0 231	0 96	0 124	0 121	0 109	0 176	0 103	0 122	0 90	0 109	0 262	0 291	0 206
06_01	06	RL	0 196	0 96	0 138	0 121	0 125	0 180	0 103	0 148	0 88	0 145	0 256	0 291	0 206
06_02	06	RLL	196 196	96 96	130 130	125 125	109 109	207 180	103 103	122 122	78 0	117 117	256 256	294 294	238 0
06_03	06	RL	0 196	0 96	0 138	0 125	0 125	0 176	0 0	0 0	0 78	0 145	0 246	0 291	0 206
06_04	06	RL	0 198	0 96	0 138	0 125	0 125	0 176	0 103	0 122	0 78	0 117	0 256	0 291	0 238
06_05	06	RL	0 196	0 96	0 138	0 125	0 125	0 176	0 103	0 122	0 78	0 145	0 256	0 294	0 206
06_06	06	RRL	0 231	0 0	0 0	0 121	0 125	0 180	0 117	0 148	0 88	0 145	0 262	0 291	0 238
06_07	06	RL	0 196	0 96	0 130	0 125	0 125	0 176	0 103	0 122	0 78	0 117	0 246	0 294	0 238

Frogs	Pond	Genotype	Ga1a19re.	Re1Caga10	ReGa1a23	Res16	Res20	RICA18	RICA1a27	RICA1b5	CA1b6	RICA2a34	RICA5	Rrid013A	Rrid135A
06_08	06	RL	0 196	0 96	0 130	0 0	0 125	0 176	0 103	0 122	0 78	0 117	0 246	0 291	0 238
06_09	06	RLL	198 198	96 96	120 120	123 123	109 109	208 176	117 117	122 122	78 0	117 117	256 256	291 291	238 0
06_10	06	RL	0 196	0 96	0 138	0 125	0 125	0 176	0 0	0 0	0 78	0 145	0 256	0 291	0 206
06_11	06	RL	0 196	0 96	0 138	0 121	0 125	0 180	0 103	0 148	0 78	0 139	0 246	0 291	0 206
06_12	06	RL	0 196	0 96	0 138	0 121	0 125	0 180	0 103	0 148	0 78	0 139	0 256	0 291	0 206
06_13	06	RL	0 196	0 96	0 130	0 125	0 109	0 176	0 103	0 122	0 78	0 145	0 246	0 294	0 206
06_14	06	RLL	196 196	96 96	138 138	0 0	125 109	176 176	103 103	122 122	78 0	117 117	256 256	291 291	238 0
06_15	06	RL	0 196	0 96	0 140	0 121	0 125	0 176	0 117	0 122	0 88	0 139	0 262	0 297	0 238
06_16	06	RRLL	0 0	96 96	140 140	0 0	0 0	207 207	117 103	122 122	90 90	145 145	0 0	0 0	206 206
06_17	06	RL	0 196	0 96	0 140	0 121	0 125	0 180	0 117	0 122	0 88	0 139	0 256	0 294	0 238
06_18	06	RLL	196 196	96 96	140 124	121 121	125 125	180 180	117 103	148 148	78 0	145 139	256 246	294 291	206 206
06_19	06	RLL	196 196	96 96	140 124	121 121	125 125	180 180	117 103	148 148	88 0	139 139	256 246	294 291	206 206
08_01	08	RL	0 196	0 96	0 140	0 121	0 121	0 184	0 117	0 122	0 88	0 141	0 262	0 291	0 238
08_02	08	RL	0 196	0 98	0 138	0 121	0 125	0 180	0 109	0 128	0 88	0 135	0 262	0 291	0 238
08_03	08	LL	231 196	96 96	142 138	121 121	121 121	184 180	117 95	128 122	88 88	141 135	262 256	291 291	238 238
08_04	08	RL	0 196	0 96	0 138	0 121	0 121	0 180	0 109	0 128	0 88	0 135	0 262	0 291	0 238
08_05	08	RL	0 196	0 96	0 140	0 121	0 125	0 180	0 95	0 128	0 88	0 139	0 262	0 291	0 206
08_06	08	RL	0 196	0 96	0 140	0 121	0 125	0 180	0 95	0 128	0 88	0 135	0 262	0 291	0 238
08_07	08	LL	196 196	98 98	140 138	121 121	121 121	184 180	117 95	128 122	88 88	139 139	262 262	291 291	238 206
08_08	08	RL	0 196	0 98	0 138	0 121	0 125	0 180	0 95	0 128	0 88	0 135	0 262	0 291	0 238
08_09	08	LL	196 196	98 98	142 138	121 121	125 125	180 178	117 109	128 122	88 88	141 139	262 262	291 291	238 238
08_10	08	RL	0 196	0 96	0 142	0 121	0 121	0 178	0 95	0 122	0 88	0 135	0 262	0 291	0 238
08_11	08	RL	0 196	0 96	0 140	0 121	0 121	0 178	0 109	0 128	0 88	0 135	0 262	0 291	0 238
08_12	08	LL	231 196	96 96	142 138	121 121	121 121	180 178	117 109	128 122	88 88	139 135	262 256	291 291	238 238
08_13	08	RLL	196 196	98 98	138 138	121 121	125 125	180 180	117 117	148 148	88 78	155 155	258 256	291 291	238 0
08_14	08	LL	196 196	98 96	142 140	121 121	121 121	184 180	95 95	128 122	88 88	141 135	262 262	291 291	238 238
08_15	08	RL	0 196	0 98	0 138	0 121	0 121	0 180	0 109	0 128	0 88	0 139	0 262	0 291	0 206
08_16	08	RL	0 196	0 98	0 138	0 121	0 125	0 180	0 95	0 122	0 76	0 139	0 256	0 291	0 206
08_17	08	RL	0 196	0 96	0 142	0 121	0 121	0 180	0 95	0 128	0 88	0 135	0 262	0 291	0 238
08_18	08	RL	0 231	0 98	0 140	0 121	0 125	0 180	0 109	0 128	0 88	0 135	0 256	0 291	0 238
08_19	08	LL	196 196	98 96	140 138	121 121	121 121	180 178	95 95	128 122	88 88	141 135	262 262	291 291	238 238
08_20	08	RL	0 196	0 98	0 140	0 121	0 125	0 178	0 117	0 122	0 78	0 139	0 256	0 291	0 206
08_21	08	RL	0 196	0 98	0 142	0 121	0 125	0 178	0 117	0 122	0 88	0 139	0 262	0 291	0 206
08_22	08	RL	0 231	0 98	0 138	0 121	0 125	0 180	0 109	0 128	0 88	0 135	0 256	0 291	0 238
08_23	08	RL	0 196	0 98	0 142	0 121	0 125	0 178	0 117	0 122	0 88	0 139	0 262	0 291	0 206
08_24	08	RL	0 196	0 98	0 138	0 121	0 121	0 180	0 95	0 122	0 88	0 139	0 262	0 291	0 206
08_25	08	RL	0 196	0 96	0 140	0 121	0 125	0 178	0 95	0 122	0 88	0 141	0 262	0 291	0 238
08_26	08	RL	0 196	0 98	0 140	0 121	0 125	0 184	0 95	0 128	0 88	0 135	0 262	0 291	0 238
08_27	08	LL	231 196	96 96	140 138	121 121	125 125	184 180	109 95	128 122	88 88	139 135	262 256	291 291	238 238
08_28	08	RL	0 196	0 96	0 138	0 121	0 125	0 180	0 95	0 122	0 88	0 135	0 262	0 291	0 238
08_29	08	LL	231 196	96 96	142 138	121 121	121 121	184 180	95 95	128 122	88 88	139 135	262 256	291 291	238 238
08_30	08	RL	0 231	0 96	0 140	0 121	0 121	0 180	0 95	0 128	0 88	0 139	0 256	0 291	0 206
09_01	09	RL	0 196	0 96	0 124	0 123	0 109	0 180	0 103	0 122	0 78	0 109	0 246	0 291	0 206
09_02	09	LL	231 196	96 96	140 124	123 121	125 125	180 180	117 103	148 148	90 78	145 109	256 233	291 291	238 238

Frogs	Pond	Genotype	Ga1a19re.	Re1Caga10	ReGa1a23	Res16	Res20	RICA18	RICA1a27	RICA1b5	CA1b6	RICA2a34	RICA5	Rrid013A	Rrid135A
09_03	09	LL	231 196	96 96	130 124	121 121	109 109	182 180	103 97	148 124	90 90	145 145	256 256	294 294	0 0
09_04	09	LL	235 196	96 96	124 124	123 123	123 123	180 176	117 117	148 124	88 78	155 145	262 246	297 297	0 0
09_05	09	LL	231 196	96 96	138 124	123 121	123 123	180 180	117 103	148 122	90 90	145 109	233 233	291 291	0 0
09_06	09	LL	231 196	96 96	130 124	121 121	109 109	182 180	103 97	148 124	90 88	145 145	262 256	291 291	0 0
09_07	09	RL	0 196	0 96	0 138	0 121	0 109	0 180	0 97	0 148	0 78	0 139	0 262	0 291	0 206
09_08	09	RL	0 196	0 96	0 138	0 121	0 125	0 182	0 95	0 148	0 78	0 109	0 262	0 291	0 206
09_09	09	LL	196 196	96 96	140 138	123 121	109 109	180 176	117 103	148 122	88 88	145 109	262 246	297 291	0 0
09_10	09	LL	235 231	96 96	124 124	123 121	109 109	180 180	97 95	124 124	90 90	145 139	262 256	297 291	0 0
09_11	09	RL	0 231	0 96	0 124	0 121	0 109	0 180	0 95	0 124	0 90	0 155	0 262	0 297	0 206
09_12	09	RL	0 196	0 96	0 124	0 121	0 109	0 180	0 117	0 122	0 88	0 139	0 262	0 291	0 206
09_13	09	RL	0 196	0 96	0 124	0 123	0 123	0 180	0 103	0 122	0 88	0 155	0 246	0 291	0 206
09_14	09	RL	0 235	0 96	0 138	0 121	0 109	0 180	0 97	0 124	0 90	0 145	0 262	0 291	0 206
09_15	09	LL	235 231	96 96	138 124	123 121	125 125	180 180	117 97	148 122	90 90	155 145	262 256	291 291	0 0
09_16	09	RL	0 231	0 96	0 140	0 121	0 109	0 184	0 103	0 148	0 90	0 145	0 256	0 291	0 206
09_17	09	RL	0 196	0 96	0 138	0 121	0 125	0 180	0 117	0 148	0 90	0 145	0 246	0 291	0 238
09_18	09	RL	0 231	0 96	0 130	0 121	0 109	0 184	0 103	0 148	0 90	0 109	0 256	0 291	0 206
09_21	09	RL	0 196	0 96	0 138	0 121	0 125	0 180	0 103	0 122	0 78	0 145	0 262	0 297	0 206
09_22	09	RL	0 235	0 96	0 138	0 123	0 109	0 182	0 103	0 122	0 88	0 145	0 262	0 297	0 206
09_23	09	RL	0 235	0 96	0 140	0 123	0 125	0 180	0 103	0 148	0 90	0 109	0 262	0 297	0 206
09_24	09	RL	0 196	0 96	0 138	0 123	0 109	0 180	0 95	0 148	0 78	0 155	0 246	0 291	0 206
09_25	09	LL	196 196	96 96	124 124	123 123	109 109	182 176	117 95	148 122	90 78	155 145	256 233	297 291	238 238
09_26	09	RLL	235 235	96 96	140 124	121 121	109 109	180 180	103 103	148 148	90 90	155 145	262 262	297 297	206 206
09_27	09	RLL	235 235	96 96	130 130	121 121	125 109	176 176	97 97	122 122	78 0	139 139	246 246	291 291	206 206
09_29	09	RL	0 196	0 96	0 140	0 123	0 109	0 180	0 103	0 122	0 78	0 139	0 246	0 291	0 206
09_30	09	LL	235 196	96 96	144 138	123 121	125 109	180 180	103 97	148 122	90 88	145 139	262 256	291 291	0 0
10_01	10	LL	196 196	96 96	138 130	121 121	125 125	180 176	117 103	148 122	78 78	145 109	256 246	291 291	238 238
10_02	10	LL	235 196	96 96	130 124	125 121	125 125	180 180	117 97	122 122	90 78	155 109	262 246	291 291	0 0
10_03	10	LL	231 196	0 0	138 124	123 123	123 123	180 180	117 103	122 122	90 88	155 145	262 262	294 291	179 179
10_04	10	LL	235 196	96 96	144 124	121 121	125 125	180 180	97 95	124 122	90 88	145 145	262 262	297 291	0 0
10_05	10	LL	235 196	96 96	138 130	121 121	125 125	180 180	97 95	122 122	88 88	145 109	262 256	294 291	238 179
10_06	10	LL	231 196	96 96	130 124	121 121	125 125	180 176	97 97	122 122	90 78	145 109	256 256	291 291	0 0
10_07	10	LL	231 196	96 96	144 138	123 121	125 125	180 180	103 97	148 122	90 78	145 139	262 246	291 291	0 0
10_08	10	LL	231 196	96 96	144 138	121 121	125 125	180 176	117 117	122 122	88 88	155 155	262 256	297 291	238 179
10_09	10	LL	196 196	96 96	144 130	121 121	109 109	180 176	103 97	148 148	88 78	139 139	262 256	291 291	238 238
10_10	10	LL	235 196	96 96	140 138	123 121	123 123	180 180	117 97	148 122	88 78	109 109	262 256	291 291	0 0
10_11	10	LL	196 196	96 96	130 124	125 123	109 109	180 176	117 117	148 122	88 88	155 155	262 262	297 297	0 0
10_12	10	RLL	231 231	96 96	130 130	121 121	123 123	182 182	117 95	122 122	90 90	145 145	233 233	291 291	206 206
10_13	10	LL	196 196	96 96	140 138	121 121	123 109	180 176	117 103	148 124	78 78	109 109	262 262	297 294	238 238
10_14	10	LL	196 196	96 96	144 124	121 121	125 109	180 176	119 103	148 122	90 78	145 145	256 246	291 291	0 0
10_15	10	RL	0 196	0 96	0 124	0 123	0 123	0 180	0 103	0 122	0 78	0 155	0 262	0 297	0 206
10_16	10	RL	0 196	0 96	0 144	0 121	0 125	0 180	0 117	0 148	0 78	0 145	0 262	0 297	0 206
10_17	10	LL	231 196	96 96	138 124	121 121	125 125	182 176	103 95	122 122	78 78	145 145	262 256	291 291	0 0
10_18	10	LL	235 196	96 96	144 138	121 121	125 125	182 180	103 97	124 122	90 88	145 139	256 256	297 291	206 179
10_19	10	LL	235 196	96 96	138 124	121 121	125 125	182 176	117 95	124 122	90 88	155 139	262 256	297 291	0 0

Frogs	Pond	Genotype	Ga1a19re.	Re1Caga10	ReGa1a23	Res16	Res20	RICA18	RICA1a27	RICA1b5	CA1b6	RICA2a34	RICA5	Rrid013A	Rrid135A
10_20	10	LL	196 196	96 96	144 124	123 121	123 123	180 180	103 97	148 122	78 78	145 145	256 246	294 294	0 0
10_21	10	LL	231 196	96 96	138 130	123 123	123 109	180 180	117 97	148 124	90 78	155 155	262 256	291 291	238 238
10_22	10	LL	196 196	96 96	138 138	121 121	123 123	180 176	117 117	148 122	90 78	145 109	262 262	291 291	0 0
10_23	10	LL	231 196	96 96	138 124	125 121	125 109	182 180	117 117	148 122	78 78	145 139	246 246	291 291	179 179
10_24	10	LL	235 196	96 96	144 138	121 121	121 121	180 176	117 95	124 124	90 88	145 145	262 246	297 297	179 179
10_25	10	RL	0 196	0 96	0 138	0 121	0 123	0 176	0 95	0 148	0 78	0 145	0 256	0 291	0 206
10_26	10	LL	231 196	96 96	138 130	123 121	125 125	180 180	97 97	124 122	90 88	155 145	262 256	291 291	0 0
10_27	10	LL	235 196	96 96	138 124	121 121	123 123	180 176	97 95	124 122	88 78	145 109	256 256	291 291	0 0
10_28	10	LL	196 196	96 96	124 124	125 121	125 123	180 180	117 103	148 122	90 88	145 145	262 233	297 297	0 0
10_29	10	RL	0 196	0 96	0 124	0 121	0 125	0 176	0 117	0 148	0 78	0 145	0 262	0 294	0 238
10_30	10	LL	231 196	96 96	138 124	121 121	123 109	176 176	117 95	122 122	78 78	109 109	256 256	297 294	238 238
10_31	10	LL	196 196	96 96	138 124	125 123	123 123	180 180	103 103	122 122	90 88	145 139	256 246	291 291	0 0
11_01	11	LL	235 196	96 96	138 124	121 121	125 109	176 176	117 103	148 122	90 88	155 145	246 246	297 291	238 179
11_02	11	LL	196 196	96 96	138 138	121 121	125 125	0 0	117 97	122 122	78 78	145 139	0 0	291 291	0 0
11_03	11	LL	231 196	96 96	138 124	121 121	125 125	180 180	103 97	148 148	78 78	155 139	262 246	297 291	0 0
11_04	11	LL	235 196	96 96	130 124	121 121	125 109	182 180	97 95	148 122	88 78	145 145	262 262	291 291	0 0
11_05	11	LL	231 196	96 96	138 130	121 121	125 109	182 182	97 95	150 124	88 78	145 139	262 246	291 291	0 0
11_06	11	RL	0 235	0 96	0 124	0 123	0 109	0 180	0 95	0 148	0 88	0 155	0 262	0 291	0 206
11_07	11	RL	0 235	0 96	0 144	0 121	0 123	0 182	0 95	0 124	0 90	0 145	0 262	0 297	0 206
11_08	11	LL	196 196	96 96	138 124	121 121	125 109	182 176	117 97	122 122	78 78	145 145	256 246	291 291	0 0
11_09	11	LL	235 196	96 96	130 124	121 121	123 123	180 176	117 97	148 124	90 78	145 109	262 246	291 291	0 0
11_10	11	LL	196 196	96 96	130 130	125 121	121 121	180 176	103 103	148 148	90 88	145 145	256 256	291 291	0 0
11_11	11	LL	235 196	96 96	130 130	125 121	125 109	182 180	117 97	122 122	88 78	145 145	262 262	297 291	179 179
11_12	11	LL	231 196	96 96	130 124	123 121	123 121	180 176	117 103	148 122	78 78	145 145	262 246	291 291	238 238
11_13	11	LL	231 196	96 96	138 138	125 121	125 109	182 180	103 97	148 148	78 78	139 139	262 256	291 291	0 0
11_14	11	LL	235 231	96 96	138 138	121 121	109 109	180 180	117 95	148 122	88 78	155 139	262 256	291 291	238 238
11_15	11	LL	196 196	96 96	138 138	121 121	125 109	180 176	117 97	148 122	88 78	145 139	256 246	291 291	206 179
11_16	11	LL	235 196	96 96	138 124	121 121	123 123	182 176	117 95	148 122	90 88	155 155	262 246	291 291	0 0
11_17	11	LL	235 196	96 96	138 124	123 121	109 109	180 180	117 97	148 122	88 78	155 145	262 246	291 291	238 179
11_18	11	RLL	196 196	96 96	138 138	121 121	125 109	180 180	117 117	122 122	90 90	155 155	262 262	297 297	206 206
11_19	11	LL	196 196	96 96	140 130	123 121	123 121	180 176	117 117	148 122	88 88	145 145	262 256	291 291	0 0
11_20	11	RL	0 196	0 96	0 130	0 125	0 125	0 182	0 117	0 122	0 78	0 145	0 262	0 0	0 206
11_21	11	RL	0 196	0 96	0 124	0 123	0 109	0 182	0 103	0 122	0 90	0 139	0 262	0 297	0 238
11_22	11	LL	231 196	96 96	124 124	123 121	125 109	182 176	103 103	148 122	78 78	145 145	262 246	291 291	238 238
11_23	11	LL	231 196	96 96	138 138	125 121	123 123	180 176	117 103	148 148	78 78	145 145	262 262	297 291	0 0
11_24	11	LL	196 196	96 96	138 124	121 121	123 123	182 176	97 97	124 122	78 78	145 145	262 262	297 291	0 0
11_25	11	RL	0 196	0 0	0 144	0 121	0 123	0 176	0 97	0 148	0 88	0 145	0 246	0 291	0 206
11_26	11	LL	235 196	96 96	138 138	125 121	123 123	180 180	117 95	124 122	88 78	145 145	262 246	291 291	238 238
11_27	11	LL	235 196	96 96	138 138	125 123	125 125	182 180	117 97	124 124	88 78	145 145	262 262	291 291	238 179
11_28	11	RL	0 196	0 96	0 124	0 123	0 125	0 180	0 97	0 148	0 88	0 145	0 256	0 291	0 206
11_29	11	LL	231 196	96 96	138 130	123 121	125 125	182 180	97 95	150 124	78 78	145 145	262 256	291 291	0 0
11_30	11	LL	231 196	96 96	130 124	123 121	123 109	180 180	103 97	148 124	90 90	155 145	262 246	291 291	0 0
12_01	12	RL	0 196	0 96	0 144	0 125	0 121	0 182	0 103	0 148	0 90	0 145	0 246	0 297	0 206
12_02	12	RL	0 235	0 96	0 124	0 121	0 125	0 182	0 97	0 148	0 88	0 145	0 262	0 297	0 206

Frogs	Pond	Genotype	Ga1a19re.	Re1Caga10	ReGa1a23	Res16	Res20	RICA18	RICA1a27	RICA1b5	CA1b6	RICA2a34	RICA5	Rrid013A	Rrid135A
12_03	12	RL	0 196	0 96	0 138	0 121	0 125	0 182	0 117	0 122	0 78	0 155	0 262	0 291	0 206
12_04	12	RL	0 196	0 96	0 124	0 121	0 125	0 180	0 103	0 122	0 88	0 109	0 262	0 291	0 206
12_05	12	RL	0 235	0 96	0 140	0 121	0 125	0 176	0 117	0 122	0 90	0 145	0 256	0 291	0 238
12_06	12	RL	0 231	0 0	0 142	0 121	0 125	0 180	0 117	0 122	0 88	0 145	0 256	0 297	0 206
12_07	12	RL	0 196	0 96	0 130	0 121	0 109	0 180	0 97	0 148	0 88	0 145	0 262	0 291	0 206
12_08	12	RL	0 196	0 96	0 124	0 123	0 125	0 176	0 103	0 122	0 78	0 155	0 262	0 291	0 238
12_09	12	RL	0 231	0 96	0 144	0 121	0 109	0 180	0 117	0 148	0 90	0 145	0 246	0 291	0 206
12_10	12	RL	0 235	0 96	0 140	0 121	0 125	0 180	0 103	0 122	0 90	0 145	0 256	0 294	0 206
12_11	12	RL	0 196	0 96	0 138	0 121	0 125	0 180	0 117	0 148	0 90	0 109	0 262	0 291	0 206
12_12	12	RL	0 231	0 96	0 140	0 121	0 121	0 176	0 95	0 122	0 90	0 139	0 262	0 291	0 238
12_13	12	LL	196 196	96 96	138 130	121 121	123 123	180 176	117 97	124 122	90 78	145 109	262 256	291 291	0 0
12_14	12	LL	235 231	96 96	138 124	121 121	125 109	176 176	117 117	148 122	90 88	145 109	262 246	297 291	0 0
12_15	12	RL	0 235	0 96	0 140	0 121	0 109	0 180	0 103	0 122	0 90	0 155	0 262	0 291	0 206
12_16	12	LL	231 196	96 96	140 138	123 121	125 109	180 180	117 97	124 124	90 88	155 155	262 246	297 297	206 206
12_17	12	RL	0 235	0 96	0 138	0 121	0 125	0 180	0 97	0 124	0 88	0 139	0 262	0 291	0 206
12_18	12	RL	0 196	0 0	0 142	0 121	0 125	0 180	0 117	0 124	0 90	0 145	0 262	0 297	0 206
12_19	12	RL	0 231	0 96	0 124	0 121	0 125	0 176	0 95	0 122	0 90	0 155	0 262	0 291	0 206
12_20	12	LL	235 231	96 96	138 138	125 121	125 109	180 176	103 103	148 148	90 78	145 145	256 246	297 291	238 238
12_21	12	RL	0 235	0 96	0 140	0 121	0 121	0 182	0 117	0 122	0 90	0 155	0 262	0 297	0 206
12_22	12	RL	0 235	0 96	0 124	0 125	0 125	0 176	0 95	0 122	0 90	0 155	0 262	0 291	0 206
12_23	12	RL	0 231	0 96	0 124	0 121	0 125	0 180	0 103	0 122	0 90	0 145	0 256	0 291	0 206
12_24	12	RLL	196 196	96 96	124 124	123 123	109 109	176 176	95 95	122 122	78 0	155 145	262 262	297 297	238 0
12_25	12	RL	0 196	0 96	0 138	0 123	0 125	0 182	0 103	0 124	0 78	0 109	0 262	0 291	0 206
12_26	12	LL	196 196	96 96	138 138	123 123	109 109	180 176	103 95	148 122	88 78	145 139	256 256	291 291	238 238
12_27	12	RL	0 196	0 96	0 138	0 121	0 125	0 182	0 95	0 122	0 78	0 109	0 256	0 291	0 206
12_28	12	RLL	196 196	96 96	138 124	121 121	121 121	176 176	117 117	122 122	78 0	155 155	246 246	291 291	206 206
12_29	12	RL	0 196	0 96	0 124	0 125	0 109	0 180	0 95	0 122	0 90	0 145	0 262	0 291	0 206
12_30	12	RL	0 196	0 96	0 138	0 121	0 125	0 180	0 97	0 124	0 78	0 139	0 262	0 291	0 238
13_01	13	RL	0 196	0 96	0 140	0 121	0 125	0 176	0 117	0 122	0 88	0 139	0 256	0 294	0 238
13_02	13	RL	0 196	0 96	0 138	0 121	0 109	0 180	0 117	0 122	0 78	0 145	0 262	0 291	0 206
13_03	13	RL	0 196	0 96	0 124	0 123	0 121	0 180	0 95	0 124	0 78	0 109	0 256	0 294	0 238
13_04	13	RL	0 196	0 96	0 138	0 121	0 109	0 182	0 117	0 122	0 78	0 145	0 262	0 291	0 206
13_05	13	LL	231 196	96 96	140 138	123 121	125 109	182 182	103 97	124 124	90 78	155 145	262 262	291 291	0 0
13_06	13	RL	0 196	0 96	0 140	0 121	0 125	0 180	0 117	0 122	0 88	0 145	0 256	0 294	0 206
13_07	13	RL	0 196	0 96	0 130	0 123	0 109	0 180	0 95	0 124	0 78	0 145	0 256	0 294	0 206
13_08	13	RL	0 196	0 96	0 138	0 123	0 109	0 182	0 97	0 148	0 78	0 155	0 262	0 291	0 206
13_09	13	RL	0 196	0 96	0 140	0 121	0 125	0 176	0 117	0 122	0 88	0 139	0 262	0 294	0 238
13_10	13	RL	0 231	0 96	0 138	0 121	0 125	0 180	0 97	0 122	0 88	0 139	0 262	0 291	0 238
13_11	13	RLL	198 198	96 96	138 138	121 121	109 109	207 180	117 117	122 122	78 0	117 117	256 256	291 291	238 0
13_12	13	RRL	0 196	0 96	0 130	0 121	0 109	0 180	0 95	0 124	0 78	0 109	0 246	0 294	0 238
13_13	13	RL	0 196	0 96	0 138	0 121	0 109	0 180	0 117	0 122	0 88	0 109	0 262	0 291	0 206
13_14	13	RL	0 196	0 96	0 140	0 121	0 125	0 180	0 117	0 122	0 88	0 145	0 256	0 294	0 206
13_15	13	RRL	196 196	96 96	140 130	123 123	125 125	180 180	117 103	124 124	88 0	145 145	256 246	294 291	206 206
13_16	13	RL	0 196	0 96	0 140	0 121	0 125	0 180	0 117	0 122	0 88	0 145	0 262	0 294	0 206

Frogs	Pond	Genotype	Ga1a19re.	Re1Caga10	ReGa1a23	Res16	Res20	RICA18	RICA1a27	RICA1b5	CA1b6	RICA2a34	RICA5	Rrid013A	Rrid135A
13_17	13	RL	0 196	0 96	0 124	0 121	0 125	0 180	0 117	0 122	0 88	0 139	0 256	0 297	0 238
13_18	13	RL	0 196	0 96	0 124	0 121	0 125	0 180	0 117	0 122	0 88	0 145	0 256	0 294	0 206
13_19	13	RL	0 196	0 96	0 138	0 121	0 109	0 180	0 117	0 122	0 88	0 109	0 262	0 291	0 206
13_20	13	RL	0 196	0 96	0 140	0 121	0 109	0 176	0 117	0 124	0 78	0 109	0 246	0 297	0 206
13_21	13	RRL	0 196	0 96	0 130	0 121	0 109	0 180	0 95	0 124	0 78	0 109	0 246	0 294	0 238
13_22	13	RL	0 196	0 96	0 140	0 121	0 125	0 176	0 117	0 122	0 88	0 145	0 262	0 294	0 206
13_23	13	RL	0 196	0 96	0 138	0 121	0 125	0 182	0 117	0 148	0 78	0 117	0 252	0 291	0 238
13_24	13	RL	0 196	0 96	0 140	0 121	0 125	0 176	0 117	0 122	0 88	0 139	0 262	0 297	0 238
13_25	13	RL	0 196	0 96	0 124	0 121	0 125	0 176	0 117	0 122	0 88	0 145	0 256	0 294	0 206
13_26	13	RL	0 196	0 96	0 140	0 121	0 125	0 176	0 117	0 122	0 88	0 139	0 262	0 294	0 238
13_27	13	RLL	198 198	96 96	138 138	121 121	125 125	207 180	103 103	122 122	78 0	139 139	256 256	291 291	238 0
13_28	13	RL	0 196	0 96	0 124	0 121	0 125	0 180	0 117	0 122	0 88	0 139	0 256	0 297	0 238
13_29	13	RL	0 196	0 96	0 138	0 121	0 125	0 180	0 97	0 122	0 90	0 139	0 262	0 291	0 206
13_30	13	RL	0 196	0 96	0 140	0 121	0 125	0 176	0 117	0 122	0 88	0 145	0 262	0 294	0 206
14_01	14	RLL	198 198	96 96	138 138	125 125	125 125	207 180	117 117	122 122	78 0	139 139	256 256	291 291	238 0
14_02	14	RL	0 196	0 96	0 138	0 0	0 125	0 176	0 0	0 0	0 78	0 117	0 256	0 294	0 238
14_03	14	RL	0 196	0 96	0 138	0 121	0 109	0 182	0 117	0 148	0 78	0 109	0 246	0 291	0 206
14_04	14	RLL	196 196	96 96	124 124	125 125	125 109	180 180	117 117	122 122	90 90	109 109	262 262	291 291	206 206
14_05	14	RL	0 196	0 96	0 138	0 121	0 125	0 180	0 117	0 148	0 88	0 139	0 256	0 291	0 206
14_06	14	RL	0 198	0 96	0 138	0 121	0 125	0 176	0 117	0 122	0 78	0 139	0 252	0 291	0 206
14_07	14	RLL	196 196	96 96	140 140	121 121	125 109	176 176	117 117	122 122	88 0	145 145	256 256	294 294	206 206
14_08	14	RL	0 198	0 96	0 120	0 121	0 125	0 176	0 117	0 122	0 78	0 139	0 252	0 291	0 206
14_09	14	RL	0 196	0 96	0 124	0 121	0 125	0 180	0 103	0 148	0 88	0 145	0 246	0 291	0 206
14_10	14	RL	0 196	0 96	0 124	0 121	0 125	0 180	0 117	0 122	0 88	0 139	0 256	0 294	0 238
15_01	13	RL	0 196	0 96	0 138	0 121	0 125	0 180	0 103	0 148	0 78	0 109	0 262	0 291	0 206
15_02	13	RL	0 235	0 96	0 130	0 123	0 109	0 182	0 97	0 148	0 88	0 139	0 262	0 291	0 206
16_01	16	RL	0 196	0 96	0 134	0 121	0 127	0 176	0 117	0 122	0 88	0 135	0 256	0 291	0 206
16_02	16	RL	0 196	0 96	0 134	0 125	0 109	0 182	0 117	0 122	0 78	0 141	0 246	0 291	0 238
16_03	16	RL	0 196	0 96	0 138	0 125	0 125	0 182	0 117	0 122	0 78	0 141	0 246	0 291	0 238
16_04	16	RL	0 231	0 96	0 134	0 121	0 125	0 184	0 117	0 122	0 88	0 135	0 262	0 291	0 238
16_05	16	RL	0 196	0 96	0 124	0 121	0 109	0 182	0 97	0 122	0 78	0 135	0 254	0 291	0 238
16_06	16	RL	0 231	0 96	0 134	0 121	0 125	0 166	0 117	0 122	0 88	0 135	0 262	0 291	0 238
16_07	16	RL	0 196	0 96	0 134	0 125	0 109	0 176	0 109	0 122	0 78	0 135	0 262	0 291	0 206
16_08	16	RL	0 196	0 96	0 134	0 121	0 125	0 184	0 117	0 122	0 88	0 135	0 244	0 291	0 238
16_09	16	RL	0 196	0 96	0 134	0 121	0 125	0 184	0 117	0 122	0 88	0 135	0 244	0 291	0 238
16_10	16	RL	0 196	0 96	0 142	0 121	0 127	0 182	0 97	0 122	0 88	0 155	0 256	0 291	0 206
16_11	16	RL	0 196	0 96	0 138	0 121	0 109	0 182	0 117	0 122	0 78	0 135	0 262	0 291	0 238
16_12	16	RL	0 196	0 96	0 134	0 125	0 109	0 182	0 109	0 122	0 78	0 135	0 246	0 291	0 238
16_13	16	RL	0 196	0 96	0 138	0 123	0 127	0 176	0 111	0 128	0 78	0 135	0 262	0 291	0 206
16_14	16	RL	0 196	0 96	0 142	0 121	0 109	0 182	0 109	0 128	0 78	0 135	0 254	0 291	0 238
16_15	16	RL	0 196	0 96	0 134	0 121	0 125	0 184	0 117	0 122	0 88	0 135	0 244	0 291	0 238
16_16	16	RL	0 231	0 96	0 134	0 121	0 125	0 166	0 117	0 122	0 88	0 135	0 262	0 291	0 238
16_17	16	RL	0 196	0 96	0 134	0 121	0 125	0 166	0 117	0 122	0 88	0 135	0 244	0 291	0 238
16_18	16	RL	0 196	0 96	0 138	0 121	0 109	0 176	0 117	0 122	0 78	0 141	0 246	0 291	0 238

<i>Frogs</i>	<i>Pond</i>	<i>Genotype</i>	<i>Ga1a19re.</i>	<i>Re1Caga10</i>	<i>ReGa1a23</i>	<i>Res16</i>	<i>Res20</i>	<i>RICA18</i>	<i>RICA1a27</i>	<i>RICA1b5</i>	<i>CA1b6</i>	<i>RICA2a34</i>	<i>RICA5</i>	<i>Rrid013A</i>	<i>Rrid135A</i>
16_19	16	RL	0 196	0 96	0 134	0 121	0 125	0 184	0 117	0 122	0 88	0 135	0 244	0 291	0 238
16_20	16	RL	0 196	0 96	0 138	0 125	0 109	0 176	0 109	0 122	0 78	0 135	0 246	0 291	0 206
16_21	16	RL	0 196	0 96	0 124	0 121	0 109	0 182	0 109	0 128	0 88	0 135	0 256	0 291	0 238
16_22	16	RL	0 196	0 96	0 134	0 121	0 109	0 182	0 117	0 122	0 78	0 135	0 246	0 291	0 206
16_23	16	RL	0 196	0 96	0 124	0 121	0 109	0 182	0 109	0 128	0 78	0 155	0 254	0 291	0 206
16_24	16	RL	0 196	0 96	0 124	0 121	0 109	0 182	0 97	0 122	0 78	0 135	0 254	0 291	0 206
16_25	16	RL	0 231	0 96	0 138	0 123	0 109	0 176	0 117	0 122	0 88	0 117	0 256	0 291	0 206
16_26	16	RL	0 196	0 96	0 142	0 121	0 109	0 182	0 109	0 128	0 88	0 135	0 256	0 291	0 238
16_27	16	RL	0 196	0 96	0 134	0 125	0 109	0 182	0 117	0 122	0 78	0 141	0 246	0 291	0 238
16_28	16	RL	0 231	0 96	0 134	0 121	0 125	0 184	0 117	0 122	0 88	0 135	0 262	0 291	0 238
16_29	16	RL	0 231	0 96	0 134	0 121	0 125	0 166	0 117	0 122	0 88	0 135	0 262	0 291	0 238
16_30	16	RL	0 196	0 96	0 142	0 121	0 127	0 182	0 97	0 122	0 78	0 155	0 254	0 291	0 206
17_01	17	RL	0 196	0 96	0 142	0 121	0 125	0 184	0 109	0 128	0 76	0 139	0 256	0 291	0 238
17_02	17	RL	0 196	0 96	0 142	0 121	0 125	0 184	0 109	0 128	0 76	0 139	0 256	0 291	0 206
17_03	17	RL	0 196	0 98	0 142	0 121	0 125	0 178	0 117	0 122	0 76	0 135	0 262	0 291	0 206
17_04	17	RL	0 196	0 96	0 140	0 121	0 103	0 180	0 117	0 122	0 88	0 135	0 262	0 291	0 206
17_05	17	RL	0 196	0 96	0 142	0 121	0 125	0 180	0 117	0 122	0 88	0 141	0 262	0 291	0 206
17_06	17	RL	0 196	0 96	0 142	0 121	0 103	0 184	0 117	0 122	0 76	0 139	0 262	0 291	0 206
18_01	18	RL	0 235	0 98	0 108	0 121	0 121	0 180	0 95	0 148	0 78	0 145	0 233	0 297	0 238
18_03	18	RL	0 196	0 0	0 140	0 121	0 121	0 176	0 117	0 148	0 90	0 155	0 262	0 297	0 238
20_03	20	RL	0 231	0 98	0 108	0 121	0 121	0 186	0 103	0 148	0 88	0 145	0 233	0 297	0 238
20_04	20	RL	0 196	0 98	0 140	0 121	0 121	0 186	0 103	0 148	0 78	0 155	0 252	0 297	0 238
20_11	20	RL	0 196	0 0	0 108	0 121	0 125	0 186	0 103	0 148	0 88	0 145	0 252	0 294	0 206
20_29	20	RL	0 196	0 0	0 140	0 121	0 125	0 180	0 103	0 148	0 78	0 145	0 233	0 297	0 206
20_30	20	RL	0 196	0 98	0 140	0 121	0 125	0 186	0 103	0 148	0 88	0 145	0 233	0 294	0 206
21_01	21	RL	0 196	0 98	0 140	0 121	0 125	0 180	0 117	0 148	0 88	0 145	0 252	0 297	0 206
21_02	21	RL	0 196	0 98	0 140	0 121	0 121	0 186	0 103	0 148	0 78	0 153	0 258	0 297	0 238
21_03	21	RL	0 196	0 0	0 140	0 121	0 121	0 180	0 117	0 148	0 88	0 145	0 252	0 297	0 206
21_04	21	RL	0 196	0 0	0 108	0 121	0 125	0 180	0 103	0 148	0 78	0 145	0 233	0 294	0 238
21_05	21	RL	0 196	0 0	0 140	0 121	0 125	0 180	0 117	0 148	0 78	0 155	0 233	0 297	0 206
23_01	23	RL	0 196	0 0	0 140	0 123	0 121	0 180	0 117	0 122	0 88	0 145	0 233	0 297	0 206
23_02	23	RRRL	0 196	0 96	0 134	0 121	0 121	0 180	0 117	0 122	0 88	0 145	0 256	0 291	0 206
23_03	23	RL	0 196	0 96	0 134	0 121	0 121	0 180	0 117	0 122	0 88	0 145	0 233	0 0	0 206
23_04	23	RL	0 231	0 0	0 134	0 121	0 121	0 180	0 117	0 122	0 88	0 145	0 260	0 297	0 206
23_05	23	RL	0 235	0 96	0 140	0 121	0 125	0 184	0 117	0 148	0 88	0 145	0 233	0 297	0 206
23_06	23	RL	0 196	0 98	0 134	0 123	0 121	0 176	0 117	0 148	0 88	0 153	0 233	0 297	0 206
23_07	23	RL	0 231	0 0	0 134	0 121	0 121	0 180	0 117	0 122	0 88	0 0	0 260	0 297	0 206
23_08	23	RL	0 196	0 96	0 134	0 121	0 121	0 180	0 117	0 122	0 88	0 155	0 256	0 297	0 206
23_09	23	RL	0 196	0 0	0 140	0 121	0 121	0 180	0 117	0 122	0 88	0 155	0 233	0 297	0 206
23_10	23	RL	0 196	0 0	0 134	0 121	0 121	0 180	0 117	0 122	0 88	0 153	0 258	0 297	0 206
23_11	23	RL	0 196	0 96	0 134	0 121	0 121	0 180	0 117	0 122	0 88	0 145	0 233	0 297	0 206
23_12	23	RL	0 196	0 96	0 134	0 121	0 121	0 180	0 117	0 122	0 88	0 145	0 256	0 291	0 206
23_13	23	RL	0 196	0 98	0 134	0 121	0 121	0 176	0 117	0 122	0 88	0 155	0 256	0 297	0 206
23_14	23	RL	0 196	0 98	0 134	0 121	0 121	0 176	0 117	0 148	0 88	0 155	0 233	0 297	0 206

Frogs	Pond	Genotype	Ga1a19re.	Re1Caga10	ReGa1a23	Res16	Res20	RICA18	RICA1a27	RICA1b5	CA1b6	RICA2a34	RICA5	Rrid013A	Rrid135A
23_15	23	RL	0 196	0 98	0 134	0 123	0 121	0 176	0 117	0 122	0 88	0 153	0 233	0 297	0 206
23_16	23	RL	0 196	0 96	0 138	0 121	0 125	0 180	0 117	0 148	0 88	0 153	0 256	0 297	0 206
23_17	23	RL	0 196	0 96	0 138	0 123	0 121	0 176	0 117	0 122	0 88	0 155	0 258	0 297	0 206
23_18	23	RL	0 196	0 98	0 138	0 121	0 125	0 180	0 117	0 148	0 78	0 153	0 256	0 297	0 238
23_19	23	RL	0 231	0 98	0 140	0 121	0 125	0 176	0 117	0 122	0 88	0 145	0 233	0 297	0 206
23_20	23	RL	231 231	96 96	134 134	121 121	121 121	184 184	117 117	148 148	88 0	155 145	260 260	297 297	206 206
23_21	23	RL	0 0	0 0	0 134	0 121	0 121	0 180	0 117	0 0	0 0	0 145	0 0	0 297	0 206
23_22	23	RLL	0 231	0 0	0 134	0 123	0 121	0 180	0 117	0 148	0 88	0 145	0 260	0 297	0 206
23_23	23	RL	0 231	0 96	0 138	0 123	0 121	0 176	0 117	0 122	0 88	0 155	0 258	0 297	0 206
23_24	23	RL	0 196	0 96	0 140	0 121	0 121	0 184	0 117	0 148	0 88	0 155	0 233	0 297	0 206
23_26	23	RL	0 196	0 0	0 134	0 121	0 121	0 180	0 117	0 148	0 88	0 145	0 233	0 297	0 206
23_27	23	RL	0 196	0 98	0 140	0 121	0 125	0 176	0 117	0 122	0 88	0 145	0 233	0 297	0 206
23_28	23	RL	0 235	0 96	0 140	0 123	0 125	0 180	0 117	0 148	0 88	0 145	0 262	0 291	0 206
23_29	23	RL	0 231	0 0	0 134	0 123	0 121	0 180	0 117	0 122	0 88	0 155	0 260	0 297	0 206
23_30	23	RL	231 231	98 98	138 138	121 121	125 121	184 184	117 117	122 122	88 0	153 153	258 258	297 297	206 206
32_01	32	RL	0 196	0 96	0 124	0 121	0 125	0 176	0 117	0 122	0 78	0 109	0 262	0 297	0 238
32_02	32	RLL	0 235	0 0	0 124	0 121	0 125	0 176	0 97	0 124	0 88	0 145	0 262	0 291	0 206
32_03	32	RL	0 231	0 96	0 138	0 121	0 125	0 176	0 117	0 122	0 78	0 109	0 256	0 291	0 238
32_04	32	RL	0 196	0 96	0 124	0 125	0 109	0 182	0 103	0 122	0 78	0 145	0 256	0 297	0 238
32_05	32	RL	0 235	0 96	0 138	0 121	0 109	0 176	0 117	0 122	0 88	0 155	0 262	0 291	0 206
32_06	32	RL	0 196	0 96	0 138	0 121	0 125	0 180	0 97	0 148	0 88	0 145	0 246	0 297	0 206
32_07	32	RL	0 196	0 96	0 138	0 121	0 109	0 180	0 103	0 148	0 78	0 139	0 256	0 297	0 206
32_08	32	RL	0 235	0 96	0 138	0 123	0 125	0 180	0 103	0 124	0 78	0 109	0 246	0 291	0 206
32_09	32	RL	0 235	0 96	0 144	0 121	0 125	0 180	0 117	0 122	0 88	0 155	0 246	0 291	0 238
32_10	32	RL	0 235	0 96	0 130	0 121	0 123	0 180	0 97	0 124	0 90	0 155	0 262	0 297	0 206
32_11	32	RL	0 196	0 96	0 124	0 121	0 123	0 180	0 103	0 122	0 88	0 145	0 262	0 291	0 206
32_12	32	RL	0 196	0 96	0 124	0 121	0 125	0 180	0 117	0 122	0 78	0 155	0 246	0 297	0 206
32_13	32	RL	0 235	0 96	0 130	0 121	0 123	0 182	0 97	0 124	0 90	0 155	0 262	0 291	0 206
32_14	32	RL	0 231	0 96	0 124	0 121	0 125	0 180	0 103	0 148	0 90	0 145	0 262	0 297	0 206
32_15	32	RL	0 196	0 96	0 130	0 123	0 125	0 176	0 97	0 122	0 88	0 145	0 246	0 291	0 206
32_16	32	RL	0 196	0 96	0 138	0 121	0 125	0 180	0 103	0 148	0 90	0 145	0 262	0 291	0 206
32_17	32	RL	0 235	0 96	0 138	0 121	0 123	0 176	0 103	0 148	0 78	0 145	0 246	0 291	0 206
32_18	32	RL	0 231	0 96	0 130	0 121	0 123	0 182	0 95	0 122	0 90	0 145	0 233	0 291	0 206
33_01	33	RL	0 196	0 96	0 130	0 125	0 125	0 176	0 0	0 0	0 78	0 117	0 246	0 294	0 238
33_02	33	RL	0 196	0 96	0 138	0 121	0 109	0 176	0 117	0 122	0 78	0 117	0 252	0 291	0 238
33_03	33	RL	0 196	0 96	0 138	0 123	0 125	0 182	0 103	0 124	0 78	0 155	0 262	0 291	0 206
33_04	33	RL	0 231	0 96	0 140	0 121	0 109	0 182	0 97	0 124	0 90	0 155	0 262	0 291	0 206
33_05	33	RL	0 196	0 96	0 124	0 121	0 125	0 180	0 117	0 122	0 88	0 145	0 262	0 297	0 206
33_06	33	RL	235 196	96 96	144 138	121 121	123 123	180 176	95 95	122 122	88 88	155 155	262 262	291 291	0 0
33_07	33	RL	0 196	0 96	0 140	0 121	0 109	0 176	0 117	0 122	0 78	0 145	0 262	0 294	0 206
33_08	33	LL	0 196	0 96	0 138	0 0	0 0	0 182	0 103	0 124	0 78	0 0	0 262	0 291	0 206
33_09	33	RL	0 196	0 96	0 138	0 123	0 125	0 182	0 97	0 124	0 78	0 155	0 262	0 291	0 206
33_10	33	RL	0 196	0 96	0 138	0 121	0 125	0 182	0 103	0 122	0 78	0 145	0 262	0 291	0 206
34_01	34	RL	0 196	0 96	0 138	0 123	0 121	0 166	0 97	0 128	0 78	0 135	0 246	0 291	0 238

<i>Frogs</i>	<i>Pond</i>	<i>Genotype</i>	<i>Ga1a19re.</i>	<i>Re1Caga10</i>	<i>ReGa1a23</i>	<i>Res16</i>	<i>Res20</i>	<i>RICA18</i>	<i>RICA1a27</i>	<i>RICA1b5</i>	<i>CA1b6</i>	<i>RICA2a34</i>	<i>RICA5</i>	<i>Rrid013A</i>	<i>Rrid135A</i>
34_03	34	RL	0 196	0 96	0 134	0 121	0 127	0 166	0 117	0 122	0 78	0 155	0 256	0 291	0 206
34_04	34	RL	0 196	0 96	0 124	0 123	0 121	0 166	0 111	0 122	0 78	0 109	0 256	0 291	0 238
34_05	34	RL	0 196	0 96	0 124	0 121	0 121	0 166	0 117	0 122	0 78	0 155	0 246	0 291	0 206
34_06	34	RL	0 196	0 96	0 138	0 123	0 121	0 166	0 117	0 122	0 78	0 155	0 262	0 291	0 206
34_08	34	RL	0 196	0 96	0 138	0 123	0 121	0 166	0 117	0 122	0 78	0 135	0 246	0 291	0 238
34_09	34	RL	0 196	0 96	0 138	0 123	0 109	0 166	0 117	0 122	0 78	0 155	0 246	0 291	0 206