

Study of microsatellite sequences in the red fox population



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Red fox

The red fox (*Vulpes vulpes*) is a carnivorous mammal belonging to the dog family. It is one of the five native members of this family in Europe. It is also found in most parts of Asia, northern Africa and North America. It was brought to Australia by humans and is one of the more dangerous invasive species there. Depending on the climate, the red fox is found in a variety of biotopes from forest to open, lowland to mountainous. In Poland, it can be found everywhere, including large cities. The fox is generally a sedentary species, but in extremely harsh conditions it undertakes migrations to areas with a milder climate for the winter. It is characterised by a large variation in colouration but most individuals of the species have the typical more or less red fur. Foxes hunt mainly small rodents, but also feed on hares, invertebrates, young ungulates and occasionally eat plants including fruit and vegetables.



Introduction

Brief characteristics of the study

We obtained data for two populations of red fox. We studied the three sequences REN25E18, REN397J23 and REN75M10. Our task was to analyse the two populations and infer from the calculations whether the populations are in Hardy-Weinberg equilibrium with respect to the given sequences.

Description of the parameters tested

- Expected heterozygosity - the frequency of heterozygotes estimated for the allele frequency of a given locus in a population under Hardy-Weinberg equilibrium conditions.
- Observed heterozygosity - the actual frequency of heterozygotes found in a population.
- Parameter F - characterises the heterozygosity of a population.
- H_I - observed heterozygosity of a given sequence.
- H_S - expected heterozygosity of a given sequence.
- \bar{p}_i - average frequency of a given allele in both populations.
- H_T - expected heterozygosity of a given sequence calculated from the average allele frequency in the population.
- F_{ST} - fixation factor.
- F_{IS} - inbreeding coefficient.

Characterisation of sequences in the population and in subpopulations

Allele frequencies

	REN25E18		REN307J23		REN75M10	
Population I	238	1	356	0,797	184	0,469
			360	0,094	178	0,234
			354	0,109	182	0,109
					180	0,188
Population II	238	0,828	348	0,016	161	0,016
	234	0,172	350	0,266	163	0,016
			352	0,047	167	0,016
			354	0,141	169	0,094
			356	0,078	172	0,063
			358	0,250	174	0,109
			360	0,016	176	0,156
			362	0,063	178	0,109
			364	0,063	180	0,203
			366	0,016	182	0,172
			368	0,047	184	0,016
					186	0,016
					188	0,016

Genotype frequencies

	REN25E18		REN307J23		REN75M10
Population I	238x238	1	354x356	0,219	178x184
			356x360	0,188	184x184
			356x356	0,594	180x184
					0,281
					178/182
					0,094
					182/184
					0,063
					182/182
					0,031
Population II	234×238	0,344	348×358	0,031	161×176
	238×238	0,656	350×350	0,063	163×180
			350×356	0,063	167×178
			350×354	0,125	169×169
			350×362	0,031	169×172
			350×368	0,063	169×182
			352×358	0,031	169×184
			352×362	0,031	169×186
			354×354	0,031	172×174
			354×356	0,031	172×180
			354×358	0,063	172×182
			356×358	0,031	174×174
			356×364	0,031	174×176
			358×358	0,063	174×178
			358×360	0,031	174×180
			358×362	0,031	176×176
			358×366	0,031	176×178
			358×368	0,031	176×180

	REN25E18		REN307J23		REN75M10
		362×364	0,031	176×182	0,031
		364×364	0,031	178×178	0,031
		350×358	0,094	178×180	0,031
		350×352	0,031	180×180	0,094
				180×182	0,031
				182×182	0,094
				182×188	0,031

Observed value of genotypes

	REN25E18		REN307J23		REN75M10
Population I	238x238	1	354x356	0,219	178x184
			356x360	0,188	184x184
			356x356	0,594	180x184
					0,281
					178/182
					0,094
					182/184
					0,063
					182/182
					0,031
Population II	234×238	0,344	348×358	0,031	161×176
	238×238	0,656	350×350	0,063	163×180
			350×356	0,063	167×178
			350×354	0,125	169×169
			350×362	0,031	169×172
			350×368	0,063	169×182
			352×358	0,031	169×184
			352×362	0,031	169×186
			354×354	0,031	172×174
			354×356	0,031	172×180
			354×358	0,063	172×182
			356×358	0,031	174×174
			356×364	0,031	174×176
			358×358	0,063	174×178
			358×360	0,031	174×180
			358×362	0,031	176×176
			358×366	0,031	176×178
			358×368	0,031	176×180

	REN25E18		REN307J23		REN75M10
		362×364	0,031	176×182	0,031
		364×364	0,031	178×178	0,031
		350×358	0,094	178×180	0,031
		350×352	0,031	180×180	0,094
				180×182	0,031
				182×182	0,094
				182×188	0,031

Expected value of genotypes

	REN25E18		REN307J23		REN75M10
Population I	238x238	1	354x356	0,174	178x184
			356x360	0,149	184x184
			356x356	0,635	180x184
					178/182
					182/184
					182/182
					178/180
					180/180
					0,051
					0,103
Population II	234×238	0,285	348×358	0,008	161×176
	238×238	0,686	350×350	0,071	163×180
			350×356	0,042	167×178
			350×354	0,075	169×169
			350×362	0,033	169×172
			350×368	0,025	169×182
			352×358	0,023	169×184
			352×362	0,006	169×186
			354×354	0,020	172×174
			354×356	0,022	172×180
			354×358	0,070	172×182
			356×358	0,039	174×174
			356×364	0,010	174×176
			358×358	0,063	174×178
			358×360	0,008	174×180
			358×362	0,031	176×176
			358×366	0,008	176×178
			358×368	0,023	176×180
					0,063

REN25E18		REN307J23		REN75M10	
		362×364	0,008	176×182	0,054
		364×364	0,004	178×178	0,012
		350×358	0,133	178×180	0,044
		350×352	0,025	180×180	0,041
				180×182	0,070
				182×182	0,030
				182×188	0,005

F statistics

F statistics separately for sequences

	REN25E18		REN307J23		REN75M10	
Population I	Ho	0	Ho	0,406	Ho	0,813
	He	0	He	0,344	He	0,678
	F	1	F	-0,180	F	-0,198
Population II	Ho	0,344	Ho	0,813	Ho	0,656
	He	0,285	He	0,828	He	0,867
	F	-0,208	F	0,019	F	0,243

	REN25E18		REN307J23		REN75M10	
	Hi	0,172	Hi	0,610	Hi	0,735
	Hs	0,358	Hs	0,586	Hs	0,773
	HT	0,157	HT	0,754	HT	0,841
	Fst	-1,276	Fst	0,222	Fst	0,082
	Fis	0,519	Fis	-0,040	Fis	0,049
	Fit	0,095	Fit	0,191	Fit	0,127

F statistics together for sequences

	REN25E18	REN307J23	REN75M10
Hi	0,505		
Hs	0,572		
HT	0,584		
Fst	0,021		
Fis	0,117		
Fit	0,135		

Conclusions

REN25E18 sequence

- Allele most common in population I: 238
- Allele most frequent in population II: 238
- Allele occurring most frequently in both populations: 238
- Inference to F statistics:
 - For this sequence for population one, the F-statistic is 1 which indicates the absence of any heterozygosity. For population two, the F-statistic is -0.208 which indicates a skewing of the F-parameter towards heterozygosity.
- Applications to F_{ST} :
 - The coefficient was -1.276, most likely because only a slice of the population was taken into account. We treat it as zero. It indicates little genetic differentiation between the two subpopulations.
- Applications to F_{IS}
 - The inbreeding coefficient is 0.519 which indicates that the population is not close to Hardy-Weinberg equilibrium. The result indicates an increased number of homozygotes in the population.

REN307J23 sequence

- Allele most common in population I: 356
- Allele most frequent in population II: 350
- Allele most frequent in both populations: 356
- Inference to F statistics:
 - For this sequence for population one, the F-statistic is -0.180 which indicates that the F-parameter is skewed towards heterozygosity. For population two, the F statistic is 0.019 which indicates that the F parameter is slightly skewed towards homozygosity.
- Applications to F_{ST} :
 - The coefficient is 0.222, indicating a large genetic differentiation between the subpopulations. It may be due to the distance of the two populations from each other, selection or genetic drift.
- Applications to F_{IS}
 - The inbreeding coefficient is -0.040, indicating a slight skew towards heterozygosity. However, the population is close to Hardy-Weinberg equilibrium. The observed and expected heterozygosity in both populations are strongly similar.

REN75M10 sequence

- Allele most common in population I: 184
- Allele most frequent in population II: 180
- Allele occurring most frequently in both populations: 184
- Conclusions to F statistics:
 - For this sequence for population one, the F-statistic is -0.198, indicating that the F-parameter skews towards heterozygosity. For population two, the F statistic is 0.243, indicating that the F parameter skews towards homozygosity.
- Applications to F_{ST} :
 - The fixation coefficient is 0.082, indicating a very high genetic differentiation between the two populations. This may be due to the distance of the two populations from each other, selection or genetic drift.
- Applications to F_{IS} :
 - The inbreeding coefficient is strongly close to 0, at 0.049 indicating that the population is close to Hardy-Weinberg equilibrium - expected and observed heterozygosity are almost equal.

Summary

The calculations performed on genotype frequencies and F-statistics aim to investigate among the common fox population the phenomenon of genetic balance and genetic variation among individuals.

The sequence REN25E18 shows low genetic variability and high homozygosity. This sequence is inconsistent with Hardy-Weinberg's law. This may indicate that the population has been segregated in some way, or that the homozygotes reveal traits that are more favourable in the living environment of the individuals studied.

Among the REN307J23 sequences, a large genetic variation between subpopulations can be seen, and there are differences in their structure, with population II showing a significant advantage in the number of genotypes over population I. While the first population is skewed towards heterozygosity, the second population also leans towards homozygosity - so the sequence is close to Hardy-Weinberg equilibrium, but does not reach it.

The REN75M10 sequence tends most strongly towards Hardy-Weinberg equilibrium. Also, the observed and expected value of heterozygosity across the population is most similar.

It should be remembered that the study was conducted on small populations, so the results may be unreliable and not coincide with the actual situation found in the red fox population.



Bibliography

https://www.igib.uw.edu.pl/files/7213/8814/5934/Analizy_populacyjne._Genetyka_w_archeologii_i_kryminalistyce._24-28_maja_2010.pdf

https://upload.wikimedia.org/wikipedia/commons/5/59/Vulpes_vulpes_at_shipwreck.jpg

<https://www.tapeciarnia.pl/tapety/normalne/tapeta-lezacy-rudy-lis.jpg>

https://www.tapetus.pl/obrazki/n/255690_lis-rudy-snieg-galazki.jpg

https://tapety.tja.pl/obrazki/tja_normalne/219961.jpg

https://www.wikiwand.com/pl/Lis_rudy