Population structure and genetic diversity of Nathusius' pipistrelle in the Dutch coastal zone

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WOZEP
DUTCH GOVERNMENTAL OFFSHORE
WIND ECOLOGICAL PROGRAMME

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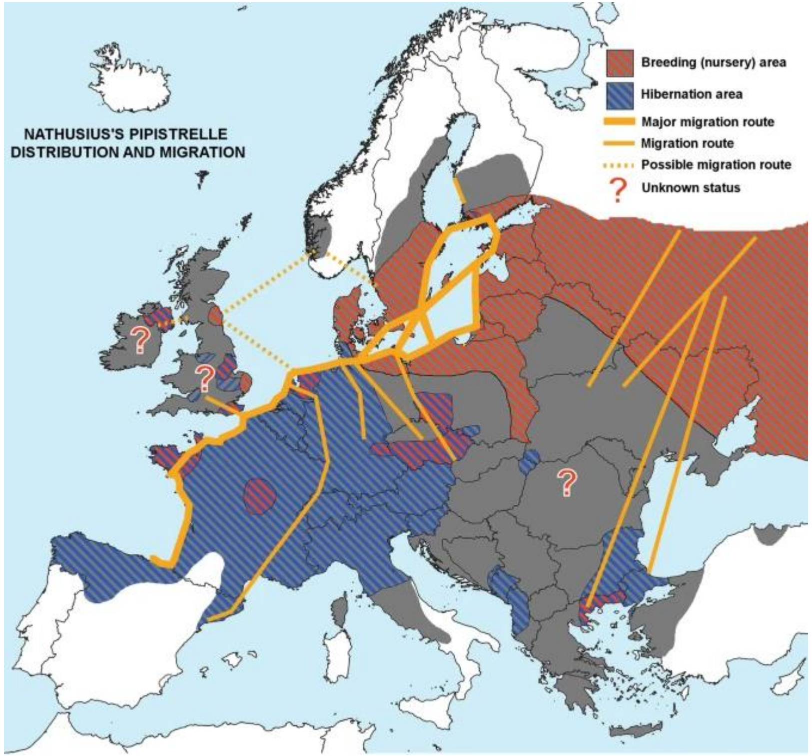
Nathusius’ pipistrelle *Pipistrellus nathusii*

- Main breeding areas in NE Europe. Hibernation in S and W Europe, incl. UK
- Long-distance and partial migrant
- Males establish mating territories along the migration routes in autumn
- 1 - 2 offspring

Photo R Janssen



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Aim of this study is to assess:

- Population structure of the (meta)population of Nathusius' pipistrelle migrating through the Dutch coastal provinces; can subpopulations be identified?
- Genetic diversity baseline and 'effective population size' of the relevant (sub)population(s)?
- Mother-offsping guidance during migration

Fieldwork (WMR)

- Bats were caught during the WOZEP telemetry project (2020-2023), using batboxes, harptraps and mist nets

Photos S Lagerveld / K Stienstra

- Subsequently a wing punch was taken and the bat was tagged

Dataset (438 suitable samples)

Genotypes:

- 77 Ad Male
- 168 Ad Female
- 93 Juv Male
- 100 Juv Female

Per year:

- 2020: 64
- 2021: 106
- 2022: 126
- 2023: 142

Per region:

- South Holland: 103
- North Holland: 248
- Friesland: 87

30 bat boxes
with adult female(s)
and juvenile(s)

Analysis (University of Greifswald)

- Microsatellites (±3% genome)
  - Diverse (‘Alleles’)
  - Pnat: 21 microsatellites
- “genetic fingerprint” of individual identity and relatedness to other individuals
- Diversity metrics
  - Allelic richness
  - Heterozygosity

Photo J van Schaik

Results – recaptures (8)

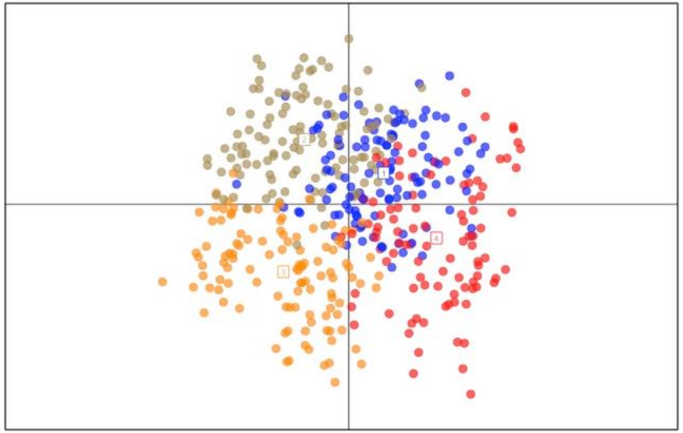
- 5 males, 3 females
- Always same area
- Twice in the same year (6+7)
- Twice in the same bat box (4+5)
- Once after 2 years (8)

Pair	Location	Capture method	Date	Age	Sex
1	Noorderhaven	Box	25.08.20	Ad	Male
1	Noorderhaven	Box	23.09.21	Ad	Male
2	H van Holland	Box	25.08.20	Ad	Male
2	H van Holland	Net	22.09.21	Ad	Male
3	Callantsoog	Box	13.09.20	Ad	Male
3	Callantsoog	Box	17.09.21	Ad	Male
4	Wildrijk	Box*	10.10.21	Juv	Male
4	Wildrijk	Box*	25.09.22	Ad	Male
5	Wildrijk	Box*	09.09.21	Ad	Male
5	Wildrijk	Box*	31.08.22	Ad	Male
6	H van Holland	Box	25.08.20	Ad	Female
6	H van Holland	Net	13.10.20	Ad	Female
7	H van Holland	Box	15.09.21	Ad	Female
7	H van Holland	Box	15.10.21	Ad	Female
8	Noorderhaven	Box	23.09.21	Juv	Female
8	Noorderhaven	Net	02.09.23	Ad	Female

Results – population structure

One genetic population

- dapc – principal component analysis
- STRUCTURE – Bayesian clustering

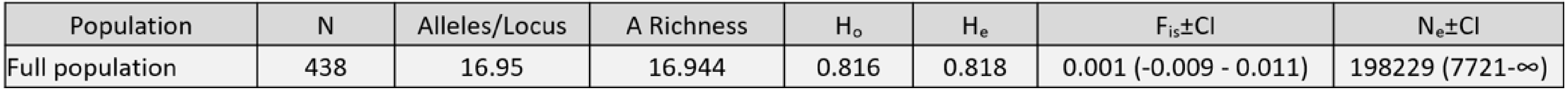


Results – relatedness

- No mother–offspring pairs in the same bat box
- One pair of juveniles related at half-sib level

Results – genetic diversity

- One genetic population

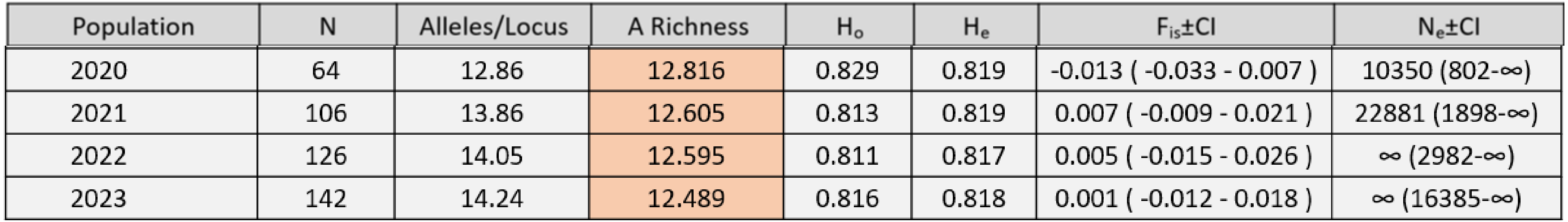


Population	N	Alleles/Locus	A Richness	H_o	H_e	F_{is}±CI	N_e±CI
Full population	438	16.95	16.944	0.816	0.818	0.001 (-0.009 - 0.011)	198229 (7721-∞)

- Effective population size indistuinguable from ‘infinite’ population (>100.000 individuals)

Results – genetic diversity per year

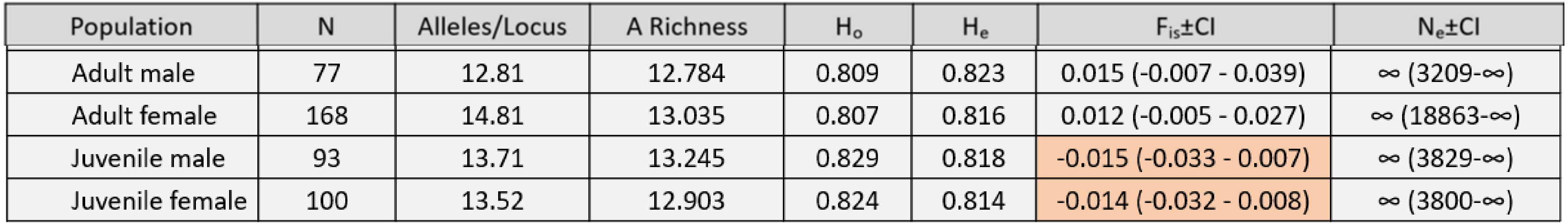
- Allelic richness: every year a slight decrease
- Heterozygosity: no effect



Population	N	Alleles/Locus	A Richness	H_o	H_e	F_{is}±CI	N_e±CI
2020	64	12.86	12.816	0.829	0.819	-0.013 (-0.033 - 0.007)	10350 (802-∞)
2021	106	13.86	12.605	0.813	0.819	0.007 (-0.009 - 0.021)	22881 (1898-∞)
2022	126	14.05	12.595	0.811	0.817	0.005 (-0.015 - 0.026)	∞ (2982-∞)
2023	142	14.24	12.489	0.816	0.818	0.001 (-0.012 - 0.018)	∞ (16385-∞)

Results – genetic diversity per sex/age class

- Juveniles: heterozygote excess, not significant, but still remarkable



Population	N	Alleles/Locus	A Richness	H_o	H_e	F_{is}±CI	N_e±CI
Adult male	77	12.81	12.784	0.809	0.823	0.015 (-0.007 - 0.039)	∞ (3209-∞)
Adult female	168	14.81	13.035	0.807	0.816	0.012 (-0.005 - 0.027)	∞ (18863-∞)
Juvenile male	93	13.71	13.245	0.829	0.818	-0.015 (-0.033 - 0.007)	∞ (3829-∞)
Juvenile female	100	13.52	12.903	0.824	0.814	-0.014 (-0.032 - 0.008)	∞ (3800-∞)

Results

Just published!

Mammalian Biology
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ORIGINAL ARTICLE

Diverse but declining? Population genetic structure and genetic diversity of Nathusius' pipistrelle along the Dutch coastline during the autumn migration period

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Abstract

Migratory bats are experiencing substantial increases in mortality risk from wind energy developments, but data on their migratory behavior and population dynamics are often lacking. Here, we develop a novel microsatellite panel for one such migratory bat species, the Nathusius' pipistrelle (*Pipistrellus nathusii*), and apply it to 448 samples collected at stopover sites along the Dutch coast during autumn migration over four consecutive years. With this dataset, we assessed whether the population is genetically sub-structured, characterize its current genetic diversity, and evaluate whether mothers guide their offspring during migration. We found that the population is panmictic and diverse, with an effective population size estimate that cannot be distinguished from infinite. However, we also observed a consistent decline in allelic richness across the sampling period, as well as a heterozygote excess in individuals sampled as juveniles, both suggesting an ongoing population decline. We did not find any parent-offspring pairs in our dataset, which included 30 box captures where adult female and juvenile bats were found roosting together, suggesting that juvenile bats do not follow their mothers during their first migration. Our findings provide an initial characterization and baseline measure of genetic diversity for the Nathusius' pipistrelle that can be used as a reference for subsequent studies and systematic efforts to monitor the genetic diversity of the species. Given that monitoring population trends of migratory bat species with traditional methods remains challenging, such tracking of genetic diversity may offer a valuable proxy by which to observe substantial population declines if they occur.

Keywords Bat conservation · Chiroptera · *Pipistrellus nathusii* · Wind energy · Microsatellite · Genetic monitoring

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Conclusions + implications (1)

Nathusius' pipistrelles residing or migrating through the Dutch coastal zone belong to a single panmictic population.

Implications:

- There is no need to consider various sub-populations as independent management units
- Mortality in the Netherlands will affect the species throughout the entire catchment area of the migratory pathway, and vice versa.

Conclusions + implications (2)

Indications of negative population trend:

- Allelic richness gradually decreases between 2020 - 2023
- Heterozygote excess in first year bats may refer to a bottleneck

Implications

- A potential risk for the roll-out of wind energy and other spatial developments

Recommendation:

- Monitor the genetic population trend regularly, using the current allelic richness as baseline reference

Conclusions + implications (3)

No mother-offspring pairs → no guidance:

Implications

- Migration seems to be innate (e.g. compass direction)
- Unlikely that first year bats learn from adults where wind farms are located
- No additional mortality when mother dies

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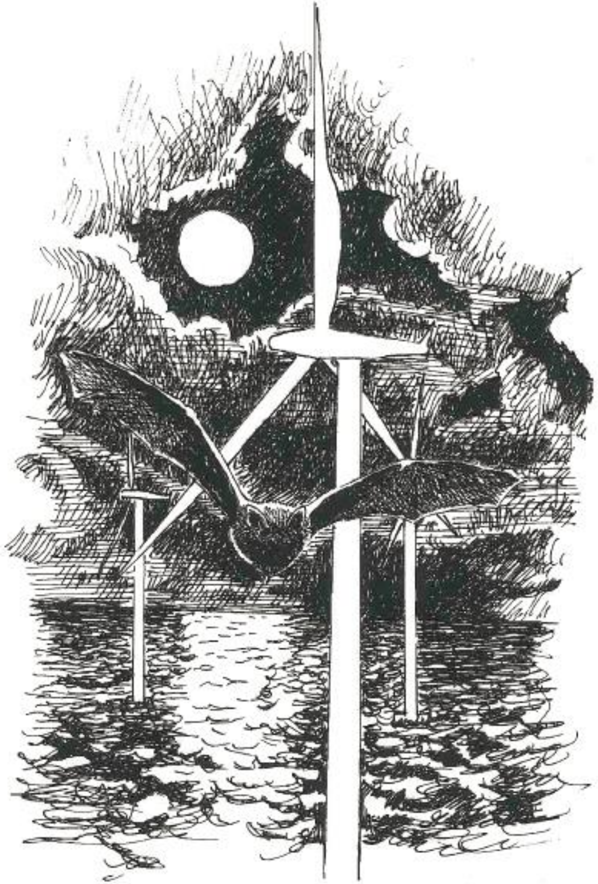
Thanks for your attention!



For more information:

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