Arthropod vectors in the UK

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UK arthropod vector groups

- Culicoides – biting midges
  Important vectors of several arboviruses affecting animals.

- Ixodidae – ticks
  Transmit Lyme disease bacteria (*Borrelia burgdorferi* sensu lato).

- Culicidae – mosquitoes
  No pathogen transmission to humans in the UK (yet?).
  Concern about invasives, such as *Aedes albopictus* - tiger mosquito.

Vector and VBD surveillance

The Pirbright Institute for Animal Health

Midge and arbovirus monitoring on UK farms
EU reference lab for bluetongue disease diagnosis, increased surveillance since 2006.

Public Health England (governmental agency)

Tick recording scheme – set up in 2005
to monitor UK tick diversity and abundance.

Mosquito monitoring scheme – set up in 2012.
Increased surveillance for invasives since recent outbreaks of MBD in Europe (West Nile and Chikungunya viruses) and elsewhere (Zika).

From surveillance to vector and disease ecology

At CEH, we aim to better understand interactions between vectors, hosts and pathogens:

- Identify what drives the diversity of pathogen and vector populations

- What shapes seasonal and spatial dynamics in vector abundance

- Develop environmental models that predict <u>where and when</u> the risk of vector-borne pathogen transmission risk is high

Host vector pathogen interactions

Molecular ecology of Great Island Virus -
impact of guillemot immune system on virus diversity

Identifying drivers of mosquito population diversity and abundance

At the UK's largest wet grassland: do hydrological management, vegetation and predator abundance shape the distribution, abundance and species composition of the mosquito populations?

Agri-environment schemes provide funding for farmers to maintain water levels at one to three tiers.
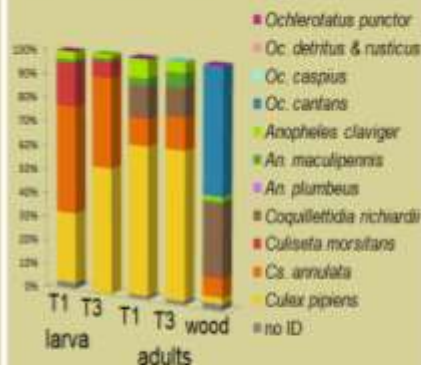
Tier 1 (T1): Highly drained permanent grassland.

Tier 3 (T3): Raised water levels, similar to the natural wetland

The mosquito species composition within T1 and T3 habitats is very similar and distinctly different to that of the local wet woodland.

- Ochlerotatus punctor
- Oc. detritus & rusticus
- Oc. caspius
- Oc. cantans
- Anopheles claviger
- An. maculipennis
- An. plumbeus
- Coquillettidia richiardii
- Culiseta morsitans
- Cs. annulata
- Culex pipiens
- no ID

Both the T1 and T3 areas are dominated by Cx. pipiens and Cs. annulata (38% & 36% at T1, 55% & 33% for T3). Of the other 7 species identified, four showed similar abundances in both grassland types.

Amongst the 10 species of the wet woodland Oc. cantans (54%) and Coq. richiardii (30%) were the most abundant.

Mosquito populations in the highly drained T1 and the natural wetland-like T3 areas follow the same seasonal trends.

Adult abundance peaks in June-July, and larvae numbers are highest in August.
These seasonal differences are highly significant (adults $F_{2,7} = 21.34, P < 0.001$, larvae $F_{2,7} = 6.57, P = 0.001$).
Summing across all species, the difference in mosquito numbers between T1 and T3 grasslands is not significant (adults $F_{1,5} = 0.09, P = 0.77$, larvae $F_{2,7} = 0.21, P = 0.644$).

The overall prevalence of adult and immature mosquitoes at T1 and T3 sites is similar but the proportion of dip points with larva, and the incidence of aquatic predators vary.

- Sites with adults
- Plots with larva in both years
- Dip points with larva
- Plots with predators
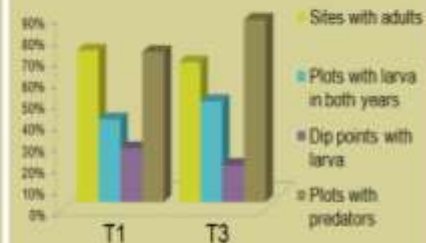
There is no significant difference between the proportion of T1 and T3 ditch plots that had larvae in both sampling years ($X^2_{(1)} = 0.209, P > 0.5$), nor between sites where adults were found ($P = 0.229$).
In T3 areas, a significantly higher proportion ($P = 0.001$) of surveyed dip points contained larvae. The proportion of plots with predators (fish, water boatmen, newts) was also significantly higher ($P < 0.001$) than in the intensely drained T1 grassland areas.

Predictive distribution maps of potential UK vectors

- Testing his models and maps that predict mosquito species distribution, Nick discovered populations of *Culex modestus*, an important vector of West Nile virus. This species had once/last been recorded in the UK in the 1940ies.

Golding, N., Nunn, M.A., Medlock, J.M., Purse, B.V., Vaux, A.G.C., & Schäfer, S.M. (2012). West Nile virus vector Culex modestus established in southern England. *Parasites & Vectors, 5(1), 32. doi:10.1186/1756-3305-5-32*

Re-discovery of *Culex modestus*

- Predictive map and actual observations
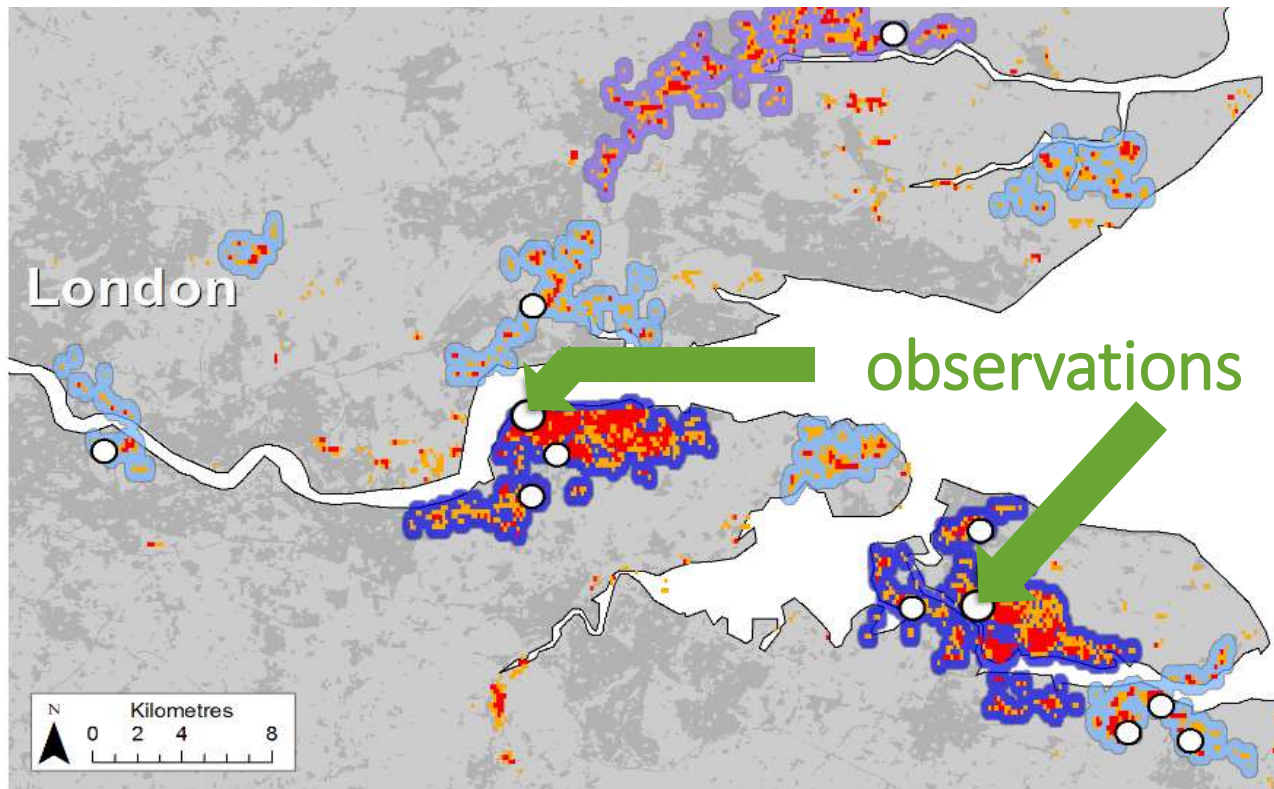
- Principal vector of West Nile virus in Southern France

(Over)reactions to our publication

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West Nile
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News · UK News · Mosquito

By Mike Swain | 3 Comments | 9 Feb 2012 00:00

Deadly mosquito found in the UK for first time since the 1940s

The culex modestus bears the West Nile virus which causes flu-like symptoms and inflammation of the brain and spinal cord

Community ecology important

- Does *Cx. modestus*' presence really dramatically increase the risk of West Nile virus transmission?

- Not if WNV is not in the wildfowl population.

- Twelve other native UK species are considered potential WNV bridge vectors.

- To assess and mitigate disease transmission risk, detailed knowledge on ecology, behaviour and spatial distribution of UK mosquito species and wild WNV reservoirs hosts, in brief, a community ecology approach is needed.

Culicoides, livestock and wild deer – community ecology to understand midge-borne disease transmission risk in the UK

Centre for Ecology & Hydrology

NATURAL ENVIRONMENT RESEARCH COUNCIL

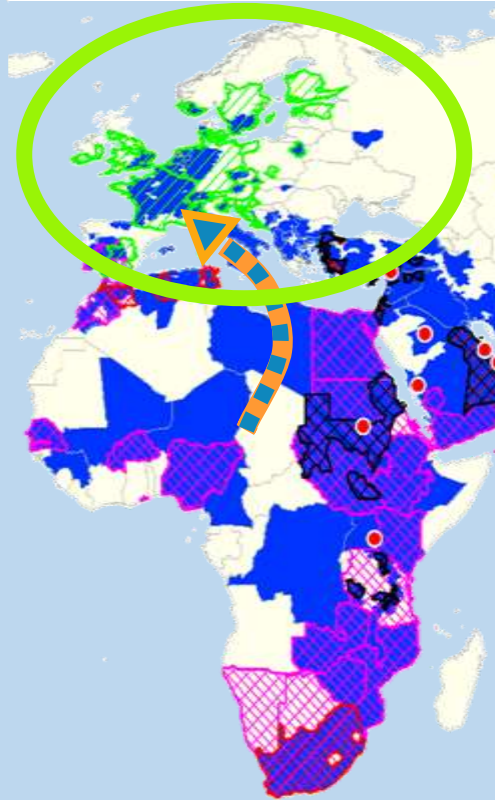# *Culicoides* biting midges

1mm

- diverse genus, 1300 species worldwide

- vectors of viruses and pathogens mainly of animals

Culicoides-borne viruses affecting livestock and humans

see *Purse et al.* 2015 Ann.Rev.Ent.

In 2006-2008:
first incursion of
exotic Bluetongue
Virus (BTV).
Caused disease
epidemics in livestock.

Economic loss >1000
million €.

In 2011:
emergence of novel
Schmallenberg Virus
(SBV), causing wide-
spread disease.

In March 2017,
renewed outbreaks
in Scotland.

Two examples of **unexpected** midge-borne viruses
that emerged in northern Europe.

Midge-borne disease systems are dynamic and complex

High infection prevalence of BTV and sustained viraemia in **red deer** suggest they act as **reservoirs** for bluetongue disease in southern Europe.

Knowledge gaps

Aspects of the **vectorial capacity** of some *Culicoides* are not fully understood:

- Some key vector midge species are **difficult to identify**, hampering assessment of their **seasonal abundance dynamics**.

- **The feeding behaviour** of potential midge vectors is not fully understood for all landscape contexts, especially with regards to wildlife.

Seasonal **movement patterns** and density of **wild deer** populations in **agricultural landscapes** are understudied.

CEH's Community Ecology Approach

Empirical field studies to

- assess **midge community composition** in areas used by domestic and wild ruminants.

- **quantify** relative host preferences and **biting rates** of *Culicoides* species for **sheep** and **red deer**.

Aim: to identify indigenous bridge vectors and hosts.

Modelling of the dynamics of **midge populations** and **landscape use by hosts** to identify **where and when** wild and domestic ruminants and key vectors overlap.

Aim: to assess midge-borne disease transmission risk.

Midge fauna near different vertebrate hosts
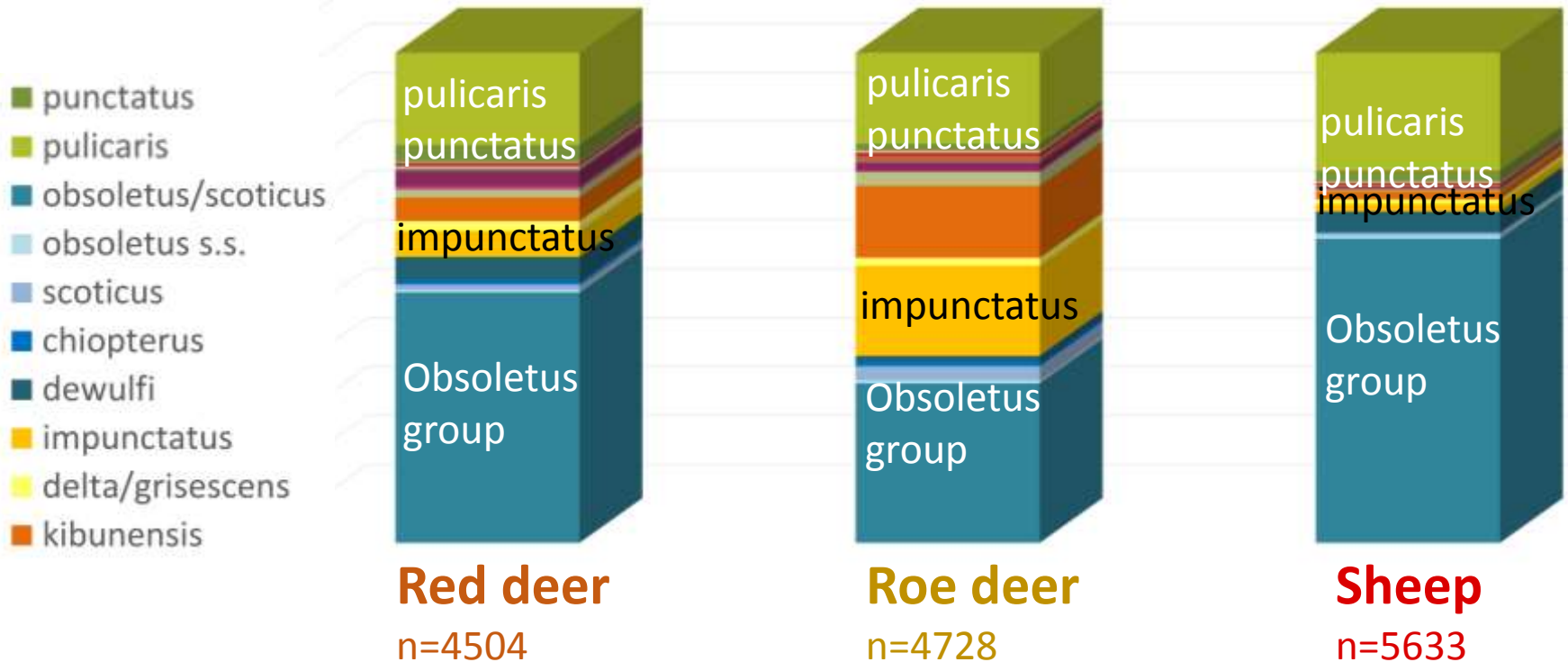## Hopetoun House southern Scotland

red deer

roe deer

sheep

sheep

Light trapping 2 seasonal snapshots 2013 & 2014

Diversity of midge communities

Legend:
- punctatus
- pulicaris
- obsoletus/scoticus
- obsoletus s.s.
- scoticus
- chiopterus
- dewulfi
- impunctatus
- delta/grisescens
- kibunensis

Red deer n=4504
Roe deer n=4728
Sheep n=5633

All 7 potential vectors of BTV in northern clines were present in all habitat types.

Potential bridge vector species?

- *C. obsoletus/scoticus* and *C. pulicaris* are **highly abundant** all three habitats.

- All 3 species have a broad host range and **feed** on different **livestock** species as well as **deer**.

- This **host range overlap** suggests there is potential for these midges to act as **bridge vectors** and transmit pathogens between domestic and wild ruminants.

Assessing midge feeding behaviour

- Summer 2016: field experiment to quantify relative host preferences of *Culicoides* species for sheep *versus* **red deer**.

- Not previously been assessed in an European agricultural habitat.

Drop tents to quantify relative attack and engorgement rates

15 min exposure

20 min biting/engorgement

15 min aspiration

- 4 observation cycles/night
- 9 nights of deer *vs* sheep comparisons
- 5 nights of sheep only

Conclusions

- Our light trap surveys suggest that habitat dominated by sheep, roe and red deer all support populations of several putative *Culicoides* vector species.

- Host preference parameters from the midge biting rate experiment will inform disease transmission models.

- Combined with environmental models of seasonal landscape use by deer and midge vectors, these will help to identify spatial and seasonal hotspots of midge-borne pathogen transmission risk.

Many thanks to

CEH

Vmerge
Emerging viral
vector-borne diseases