

Research Summary: Genetic population structure in the rare narrow-headed ant *Formica exsecta*

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Background:

This note summarises research undertaken using microsatellite and mitochondrial DNA markers to investigate the genetic and social structure of UK populations of the rare narrow-headed ant, *Formica exsecta*. This is a species of conservation concern both nationally and globally. In Britain, this species has suffered a significant reduction in its abundance over the last 100 years with several local extinctions. Remaining populations are highly fragmented, some containing less than 10 nests.

Genetic diversity enables populations to evolve when faced with changing environmental conditions and without it, populations face an increased risk of extinction. Genetic diversity therefore underpins population adaptation and resilience.

Aim and objectives:

An understanding of the population genetics and social structure of *F. exsecta* will: (i) provide insight into the current genetic status of this species in Britain and (ii) inform the development of conservation management strategies to minimize the risk of extinction. Analyses focussed on identifying inbreeding and genetic bottlenecks, social structure, and population demographics and connectivity.

Research method:

Between 6 and 8 nests were sampled from each of 6 populations. These included samples from the stronghold complex of Abernethy (Tulloch Moor), Glenmore (Badaguish) and Carrbridge (Foregin) in Speyside, two outlying Scottish populations at Rannoch Moor, Perthshire, and Mar Lodge, Deeside, and from the one remaining English site at Chudleigh Knighton, Devon. A small number of samples from mainland Europe were also included for comparison. We analysed mitochondrial DNA sequence data generated from the Cytochrome B and Cytochrome Oxidase I regions and data from eight microsatellite markers.

Findings:

- The Devon population contained genetic markers that were absent from any of the Scottish populations. Taken as a whole, the Scottish population also contained genetic markers absent from the Devon population. Overall, the British population of *F. exsecta* has less genetic diversity than those reported in the literature from mainland Europe.
- Genetic differentiation occurs when there is restricted gene flow between populations. The Devon population is highly differentiated from the Scottish populations. The UK sites were more differentiated than those across a much larger geographic scale in mainland Europe.
- There was a lack of differentiation between Scottish populations. Genetic connectivity is maintained by contemporary migration from Abernethy and Glenmore, Abernethy to Mar Lodge, and to a lesser extent, from Rannoch to Glenmore. There was no evidence of reciprocal migration. It is noteworthy that the small population at Mar Lodge receives a substantial amount of gene flow from Abernethy, a considerable distance away. On a smaller geographic scale there is evidence of recent migration between the nests at the Devon site.
- Of the Scottish sites, Rannoch was the most differentiated. It also had the lowest genetic diversity of any population in Britain.
- For most nests, tests for genetic bottlenecks generated significant results indicative of sharp reductions in population size. Evidence of bottlenecks was severe at Rannoch and Carrbridge, moderate at Glenmore and Mar Lodge, and low/absent at Abernethy and Devon. There was no evidence of inbreeding at any site.
- Nearly all nests showed relatedness values indicative of weak polygyny (~2-4 queens per nest). One nest at Carrbridge and one at Rannoch were clearly monogynous. Relatedness was higher overall at Rannoch and Carrbridge than other sites. Polydomy (>1 nest per colony) was also detected at Mar Lodge and Rannoch despite a protocol designed to avoid sampling more than

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one nest per colony. These polydomous nests were located 25 - 45 m apart.

Discussion:

These results support the general view that in Britain *F. exsecta* is polygynous⁵. However, the genetic evidence of low differentiation and some contemporary migration does not entirely support the contention that the polygynous and polydomous structure is likely to limit long distance geneflow. Many females will have stayed in their natal colonies or formed new nests in the immediate neighbourhood by budding. In contrast, we expect that females from monogynous nests will tend to disperse longer distances by flight to form new colonies elsewhere⁶.

Two of our Devon sequences grouped with a German and a Dutch sample and the rest of the Devon samples grouped with a Finnish sample. Both our findings and those of Goropashnaya et al. (2007)⁷ may indicate that the Devon samples originate from the same lineage as northern European samples. Our sequences are the first for Scottish samples and as they did not group with any of our European samples, we are unable to place them in a lineage.

Species at the edge of their range are often characterised by having lower genetic diversity and this is true when our results are compared with those from mainland Europe. However, the fact that the UK sites were more differentiated than those across a much larger geographic scale in mainland Europe, suggests it is not simply geographic differences in the UK that are causing genetic isolation. Evidence of bottlenecking suggests that most nests may be in decline. Low bottlenecking in the Devon population may be due to conservation efforts which have resulted in a significant increase in the number of nests.



The Scottish and English populations of *F. exsecta* are worthy of consideration as intraspecific units as each contain unique genetic diversity for conservation. **Devon should be considered as a high priority for conservation** as it contains the highest genetic diversity and unique genetic material. Reintroduction to other English sites should be considered in the future if this can be done without endangering the population at Chudleigh Knighton and if other sites now contain suitable habitat.

Maintaining a strong population at Abernethy and Glenmore should also be a priority. These sites hold around 80% of the total UK *F. exsecta* population; an estimated 460 nests. This research has shown that these sites also act as sources of gene flow to other Scottish populations. Migration from Abernethy and Glenmore is unsurprising given their proximity, though perhaps unexpected in only being detected in one direction.

Results indicative of geneflow from Abernethy and Mar Lodge is more surprising given they are separated by c.20 km of mainly mountainous terrain. This indicates that the Deeside site does not appear to be genetically isolated from a large population in a different river catchment. The intervening landscape between the Abernethy and Deeside sites does not therefore seem to act as a significant barrier to geneflow. In this context it is noteworthy that a *F. exsecta* nest was recorded at c.1500 m in the Lairig Ghru in 1952⁸; one of the passes that links the two catchments.

Rannoch bears all the signs of a population in terminal decline. At the last census (2019) there were only nine active nests present. Two of these are part of the same colony and one is monogynous. This means the effective population size is extremely small. No unique genetic markers were found at Rannoch that were not found in other Scottish populations. However, **efforts should be made to maintain and increase the populations at Rannoch, Mar Lodge and Carrbridge** as this spreads the risk across multiple sites with different habitat and environmental conditions.

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