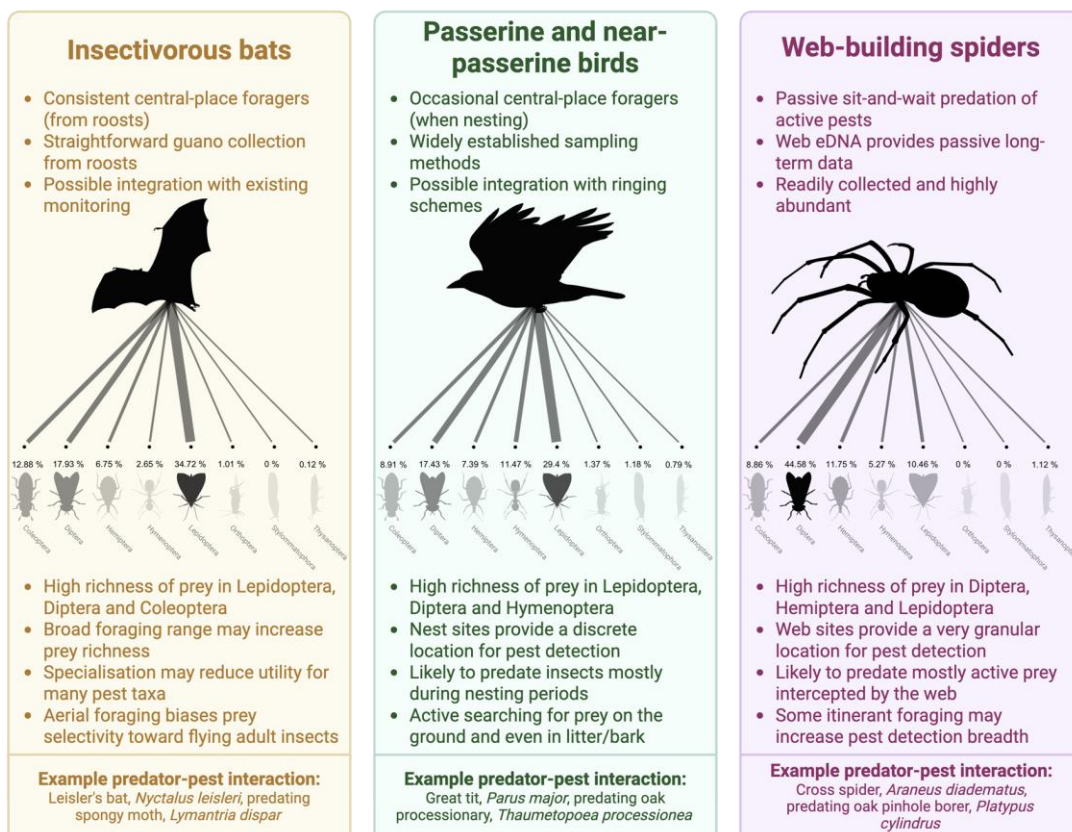


Evaluating the potential of predator diet analysis as a monitoring tool for plant pests of concern

Policy Summary



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Policy Summary

Background

This review assesses the feasibility of using DNA-based analysis of wild predator diets to monitor the spread and emergence of plant pests. Traditional monitoring methods for plant pests scale poorly and introduce latency to detections and responses. By analysing the DNA in the guts of wild predators, it is possible to detect and identify pests eaten by those predators. This offers a relatively targeted and cost-effective solution compared to bulk sample collection, which often includes non-target species and occasionally very few target pests. To understand whether this approach could be effective in the context of monitoring pests that are not readily caught in existing bulk traps in Scottish forests, we have conducted a systematic review of the existing literature.

Key Research Questions

This review had the following objectives: 1) Systematically review current applications of predator molecular dietary analysis for the detection of pests. 2) Develop guidance for both targeted and generalised pest detection. 3) Establish broadly applicable case studies to exemplify potential deployment. 4) Evaluate alignment of this approach with existing policy and regulations.

Main Findings

DNA-based monitoring of plant pests in predator diets is effective, but evidence remains limited

The studies reviewed demonstrate that dietary DNA analysis can be highly effective for detecting and identifying plant pests, though it has only been tested with a limited range of wild predator species. Bats, birds and spiders were the focus of most studies. Although the UK was well represented, the limited overall evidence base requires more UK and Scottish studies to validate this approach locally and identify other appropriate predator species to monitor.

Bats, birds and spiders offer the most promise for pest monitoring

Several UK Plant Health Risk Register pests were identified in predator diets within reviewed literature, including from UK native predators (though not in UK-based studies). The reviewed studies provide some generalisable findings that can guide the design of monitoring programmes. This has guided the development of three case studies exploring the use of bats, birds and spiders for monitoring pests in a Scottish forestry context.

Implementation can work within existing regulatory frameworks

Sample collection from protected predator species (bats, birds) requires licensing and trained personnel. While this may constrain rapid scaling, it can be facilitated through coordination with existing wildlife licensing systems and established stakeholder groups such as bird ringing schemes, bat survey networks and university partnerships.

Methodological standardisation is needed for reliable implementation

Reviewed studies varied greatly in their methodological approaches. Standardisation is important for ensuring data are comparable across studies and that work is conducted according to best practice, though this is challenging as different predator study systems

require different sampling processing and analysis processes. Many reviewed studies used did not optimise their methods to their specific system, which may have biased the data and outcomes - for example, using PCR primers that amplified predator DNA alongside prey DNA, or lacking appropriate controls. Standardising key workflow steps will be crucial for wider implementation, requiring development of best practice standards, documentation and protocols for uniform adoption of this monitoring approach - particularly where detections could inform policy or management responses, since the risk of misidentification or false positive detections introduces sensitivities with real-world consequences.

Recommendations

Build scalable monitoring systems

This review concludes that detecting plant pests via DNA analysis of predator diets is feasible, effective and ready for wider implementation. To reach a fully realised monitoring system, several key requirements need to be addressed:

- Refine operational and logistical implementation: Integrate sample collection with existing predator monitoring programmes for streamlined and cost-effective delivery
- Mitigate methodological pitfalls: Trial and develop best practice protocols through pilot studies for validation
- Streamline workflows: Build laboratory and computational capacity to generate accurate results with sufficient speed to facilitate rapid intervention

Pilot and validate locally

Investment in pilot projects will be key to successful delivery at larger scales. We recommend:

- Validate the approach: Conduct pilot studies to detect priority plant pests in the diets of bats, birds and spiders, comparing results against parallel conventional monitoring programmes to confirm validity in Scottish contexts
- Identify optimal systems: Use pilot studies to identify which predator-pest interactions are most suitable for operational monitoring, focusing on established and spreading pests

This would enable follow-on studies determining pest distribution and spread solely through predator dietary analysis.

Standardise and streamline by building collaborative and stakeholder networks

Effective implementation requires standardisation and best practice development in line with Scotland's route-map for use of DNA for monitoring of biodiversity (in development). This should draw on wider national and international efforts towards harmonisation of DNA-based methods (e.g., Defra DNA Centre of Excellence, UK DNA Working Group). The proposed monitoring scheme would require collaboration between regulatory bodies, landowners, wildlife monitoring bodies, molecular ecologists and bioinformaticians. We recommend consultation amongst these groups to identify where capacity for collaboration exists and where it will be required. Future work should also consider data sharing, governance and public-facing communications arrangements. Aligning these with wider national discussions on Next-Generation/High-Throughput Sequencing capability would support interoperability, transparency and public understanding should dietary DNA approaches inform operational surveillance.

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