



Modelling and predicting transport of Acari on the plant import pathway*

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*In: Zhang, Z.-Q., Fan, Q.-H., Heath, A.C.G. & Minor, M.A. (Eds) (2022) *Acarological Frontiers: Proceedings of the XVI International Congress of Acarology (1–5 Dec. 2022, Auckland, New Zealand)*. Magnolia Press, Auckland, 328 pp.

Acari, as with other small arthropods, are most commonly introduced to new areas as contaminants of agricultural trade. The biosecurity risk of such trade is managed by national and regional biosecurity systems, a chief aim of which is to prevent the introduction of agricultural and environmental pests. However, agricultural contaminants are introduced unintentionally, can occur on any product in a wide range of places, and are often very small in size, which makes them inherently difficult to study, understand, and manage.

In a previous review of biosecurity border risk management systems for arthropods, we made three main recommendations for improvement, namely: i) implement appropriate sampling strategies; ii) use inspection methods suitable for detecting small arthropods; and iii) systematically record the methods used, the intercepted organisms, and negative results (Saccaggi *et al.* 2016).

In the current study, we modelled arthropod transport by analysing a dataset of 13,566 plant samples imported to South Africa (2005–2019) that were inspected for arthropods (Saccaggi *et al.* 2021, 2022). All samples in the dataset were inspected under a stereo microscope for the presence of arthropods, and all arthropods found were recorded and identified (although not always to species level). Thus it meets the criteria as set out in the 2016 recommendations regarding biosecurity data analyses. Seven thousand, two hundred and fourteen (7,214) individual interceptions (66% Acari, 31% Insecta, 2% other Arthropods) were recorded on 4,902 “positive” samples (more than one contaminant was often intercepted on the same sample). Eriophyoidea were intercepted twice as frequently as any other group (32% of Acari interceptions), followed by the Tarsonemidae (14%), Tydoidea (11%) and Tetranychoida (8%).

To model the interception data, we employed a machine learning approach based on non-parametric boosted regression trees (BRTs). This approach is insensitive to structure of the data, and thus is suitable for modelling inherently messy interception datasets with missing data. We grouped 31 explanatory variations to generate and test 74 unique non-exclusive models predicting the presence of arthropods on the imported samples. Some patterns could be explained post-hoc by historical events, such as increased sampling or inspector awareness. However, across the whole dataset, only inspected volumes correlated reliably with the detection of arthropods, but this variable could not predict future interceptions. Better predictions were instead correlated to contextual factors such as country, crop or year of import. Using the best-fitting models to target inspections resulted in an increased overall detection rate of 39–43%, especially at lower sample sizes. However, models which predicted well overall were not equally effective at predicting interceptions of specific arthropod taxa, and performed worse at predicting species interceptions. This suggests that certain factors are important for particular crops, commodities, taxa or circumstances, but that there is little general predictive power (Saccaggi *et al.* 2022).

We recommend that biosecurity inspections be tailored to the desired outcome. If interceptions of any foreign arthropod are intended, then general predictive models should be employed to optimise sampling strategy. If, however, a particular taxon or pathway is of concern, then an idiographic approach using details of the pest, pathway and time should be used to create a specific predictive model. We use interceptions of Eriophyoidea to illustrate this. These approaches can be used in conjunction to improve the overall efficiency of live biosecurity systems and thus better protect against accidental introductions.

References

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