Population size and foraging area of the invasive termite Reticulitermes flavipes (Kollar, 1837) (Blattodea, Rhinotermitidae) in the Canary Islands

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INTRODUCTION

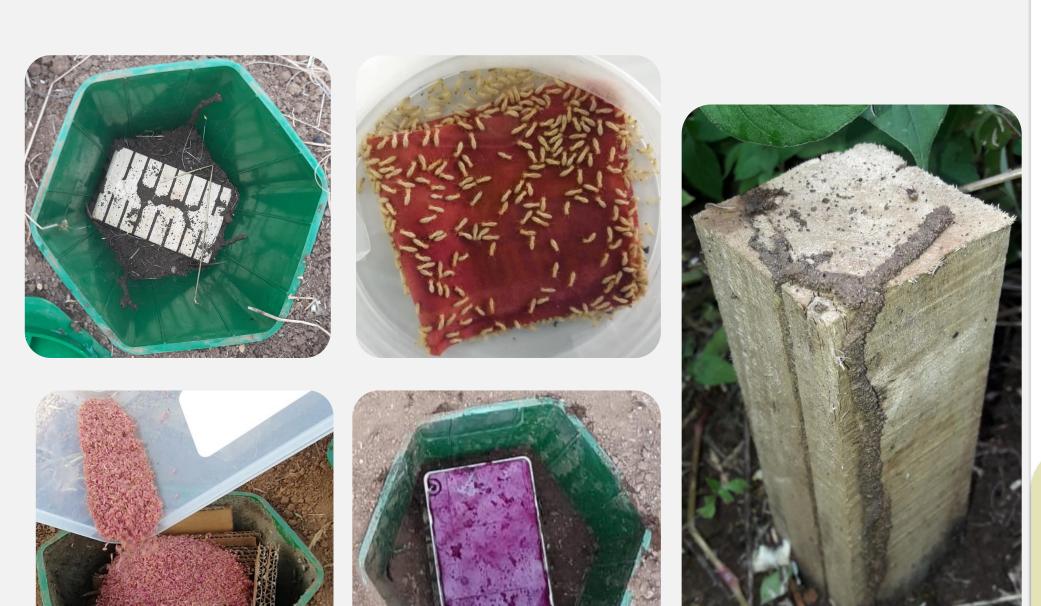
Reticulitermes flavipes is a subterranean termite species native to eastern and central regions of North America. Due to globalization and international trade, this species has been introduced and established in numerous countries, and is considered one of the most harmful subterranean termite pests in the world. It was reported from Tenerife for the first time (Canary Islands, Spain) in 2019. Studies to assess the numbers of individuals and the foraging area size have been conducted at several sites. Given that its foraging behaviour varies depending on whether it is in its native or introduced distribution range, the colonies detected in the Canary Islands have now been characterized.

Primary **Native** Small colonies breeders Neotenic Large colonies breeders



MATERIAL & METHODS

Three mark-release-recapture cycles were conducted in three selected areas. The Lincoln Index and Weighted Mean Model were used to estimate population sizes. Subsequently, the colonies were directly dyed with neutral red in the field to measure their foraging zone during a period of two years (2020-22). This was marked out using wooden stakes (n ≈ 2000) regularly placed ≈ 6 m apart, due to the terrain, to map and quantify the surface area occupied by the dyed termites in a 2-D matrix.



RESULTS & DISCUSSION

Population size

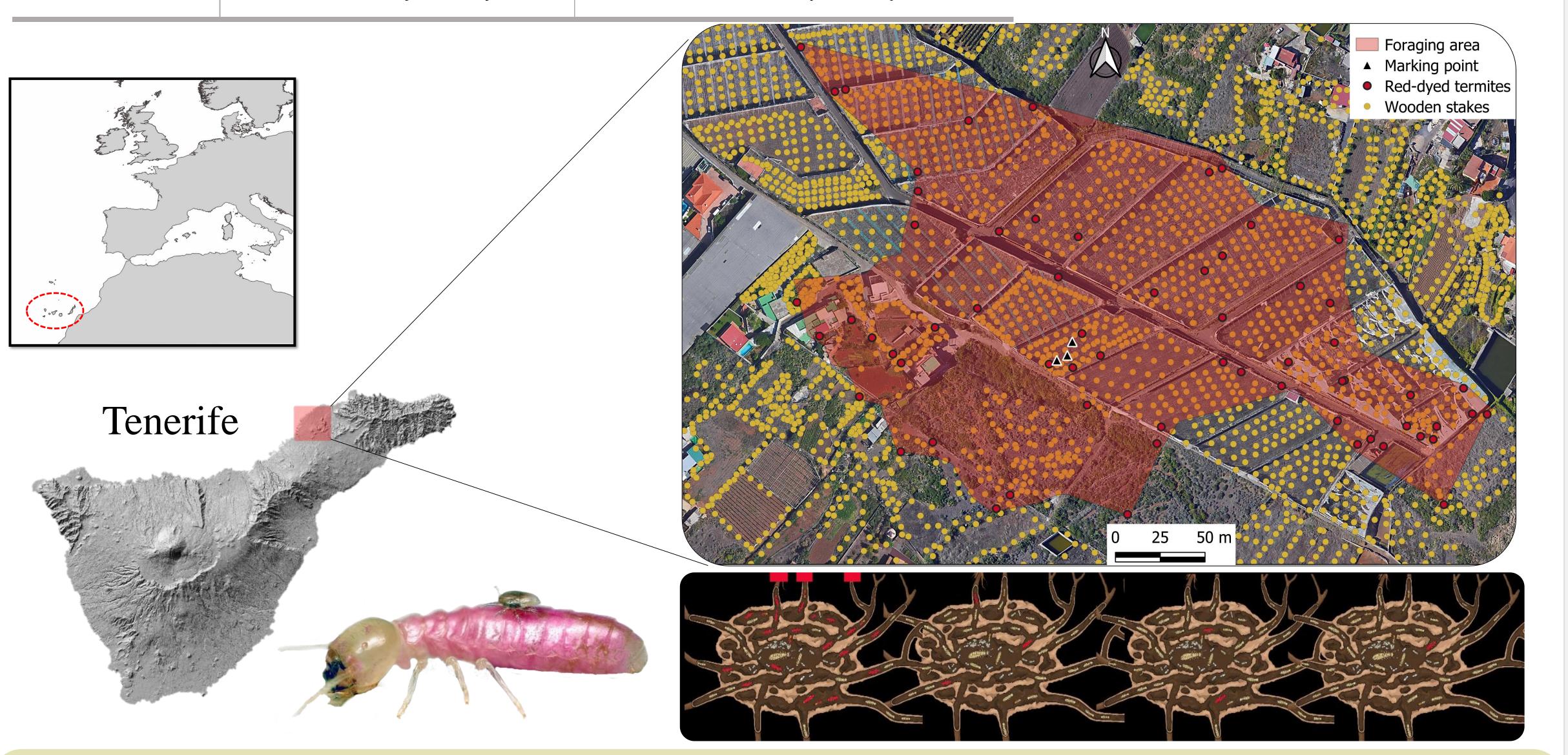
Nº individuals		
Colony	Lincoln Index (SE)	Weighted Mean Model (SE)
1	1,693,696 (60,203)	1,640,917 (21,507)
2	193,817 (11,552)	70,978 (1,568)
3	73,456 (4,312)	111,095 (2,885)

Foraging area (Colony 1)

• 54,200 m²

Maximum linear distance

• 445 m



We calculated the population size of the three colonies studied and the foraging area of one of them (colony 1), since the study is currently in progress. Colonies 2 and 3 had a smaller population size, while colony 1 was more numerous. The large area occupied by colony 1 was probably the result of supercolony expansion. This supercolony may consist of a network of intercommunicated subcolonies, each associated with their respective neotenic reproductives. This extensive colony has been identified as the second largest described for this species in the world.

Baker, P.B., & Haverty, M.I. 2007. Foraging populations and distances of the desert subterranean termite, Heterotermes aureus (Isoptera: Rhinotermitidae), associated with structures in Southern Arizona. Journal of Economic Entomology, 100(4), 1381–1390.

Nobre, T., Nunes, L., & Bignell, D. E. 2007. Estimation of foraging territories of Reticulitermes grassei through mark-release-recapture. Entomologia Experimentalis et Applicata, 123(2), 119–128. Su, N.-Y., Ban, P.M., & Scheffrahn, R.H. 1993. Foraging populations and territories of the Eastern subterranean termite (Isoptera: Rhinotermitidae) in Southeastern Florida. Environmental Entomology, 22(5), 1113–1117.

CONCLUSIONS

Our results confirm the presence of numerically and spatially large colonies of R. flavipes on Tenerife. As expected, this termite shows the same behaviour as where it acts invasively elsewhere, developing supercolonies. In addition, the climatic conditions of the Canary Islands are favourable for this species, allowing it to develop and expand throughout the year. All these factors make it more difficult to combat this invasive insect. Therefore, to gain information about population size and foraging area of the colonies located on the island is definitely useful in planning and optimizing eradication efforts.



FURTHER RESEARCH

The next step in understanding how this supercolony originated and is expanding is to study its breeding system and genetic structure using RADSeq. We expect this powerful and novel genetic technique to determine if the individuals from different parts of the area occupied by the supercolony come from the same type of breeders or not, and their relationships. They could come from a monogamous breeding pair (single family), from neotenic breeders descended from a single monogamous pair (extended family) or from multiple unrelated breeders (mixed family).



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