

Call Number: Location: ZOOLOGY SECTION LIBRARY

Journal Title : Sociobiology.

Journal Vol: 41

Journal Issue:

Journal Year: 2003

Article Pages: 67-69

Article Author/Title: Vargo, E. L., C. Husseneder, J. K. Grace, G. Hend

Ring

anean termites

Notice: This Material May Be Protected by Copyright Law (Title 17 U.S. Code) 61

**Describing the Spatial and Social Organization of Formosan Subterranean Termite Colonies in Armstrong Park, New Orleans**

by

C. Husseneder<sup>1</sup>, J. K. Grace<sup>1</sup>, M. T. Messenger<sup>2</sup>, E. L. Vargo<sup>3</sup>

& N-Y. Su<sup>4</sup>

**ABSTRACT**

Colonies of the Formosan subterranean termite, *Coptotermes formosanus*, possess a complicated spatial and social organization comprising interconnected foraging sites and nests containing variable numbers of reproductives. This complex colony structure may affect the distribution of bait toxicants through the colony. Due to the cryptic life of subterranean termites, their colony organization cannot be directly observed, but needs to be inferred from the genetic structure. We investigated the genetic structure of *C. formosanus* in Armstrong Park, New Orleans, employing multilocus DNA fingerprinting and microsatellite genotyping. We applied DNA fingerprinting to differentiate colonies according to their genetic profiles. We assigned termites from different sites to colonies through diagnostic bands and genetic similarities. In general, foraging areas of colonies identified by their DNA profiles correlated with results of mark-release-recapture studies. The wide intra- and intercolonial range of genetic similarities indicates a variety of social organizations as well as different proliferation strategies of colonies (budding, swarming). For more detailed analyses of colony organization we are currently using microsatellite genotyping to reveal the numbers of reproductives and degree of inbreeding within colonies. The combined information on genetic structure and social organization of colonies will tell (1) if the majority of colonies is headed by unrelated pairs (colony foundation through swarming) or by multiple related reproductives, and (2) if the presence of multiple reproductives results in a genetic substructure within colonies, which might lead to subsequent colony proliferation through budding. We also intend to apply

<sup>1</sup>Dept. of Plant & Environmental Protection Sciences, University of Hawaii at Manoa, 3050 Maile Way, Room 310, Honolulu, HI 96822, USA

<sup>2</sup>City of New Orleans Mosquito & Termite Control Board, 6601 Stars & Stripes Blvd., New Orleans, LA 70126

<sup>3</sup>Dept. of Entomology, North Carolina State University, Raleigh, NC 27695

<sup>4</sup>Ft Lauderdale Research & Education Center, University of Florida, 3205 College Ave., Ft. Lauderdale, FL 33314

L/2003

SID: 06422

Record 69 of 1

Need Before: 200

Renewal Req:

Next Due Date:

Anderson and D. anean termites

: 67-69

D.H.

.11  
152.1.24.195

SID: 06422

Record 69 of :

r FEIN; ours :

INSURANCE:

:24:25 -05

survival and he Formosan (termitidae).

e on soldier (termitidae) (1).

logue ZR-512 (era). Insectes

a nutritional onies of the Sociobiology.

genetic information to examine how termites invade areas where baiting has eliminated all prior activity.

### INTRODUCTION

There is no need in the Southeastern USA to emphasize the importance of controlling the Formosan subterranean termite, *Coptotermes formosanus* Shiraki (Isoptera: Rhinotermitidae). Especially in the area of New Orleans, Louisiana, *C. formosanus* has had an enormous economic impact during the last decade. Improving management of *C. formosanus* requires a thorough understanding of the biology of this termite species.

Our work is focusing on the identification of colonies and description of their spatial and social structure, because these factors could influence distribution of bait toxicants. Colonies of *C. formosanus* show a complicated spatial and social organization. Colonies consist of widespread interconnected foraging groups and nests containing variable numbers of reproductives. The cryptic life of subterranean termites makes it difficult to affiliate workers collected from different foraging traps to colonies, as well as to estimate the number of reproductives and thus describe colony structure. However, using molecular markers to assess the distribution of genotypes and genetic differentiation among termites from different collection traps allows delimitation of colonies and sheds light on their organization. This paper summarizes preliminary results of work currently in progress in Louis Armstrong Park, New Orleans.

### RESULTS AND DISCUSSION

In order to describe colonies of *C. formosanus* and their organization in Armstrong Park, New Orleans, we have employed multilocus DNA fingerprinting and microsatellite genotyping (Husseneder & Grace 2001a,b; Vargo & Henderson 2000, Husseneder *et al.* 2002). We analyzed termite material from 14 foraging areas previously outlined by mark-release-recapture studies (M. Messenger, unpublished).

First, we applied DNA fingerprinting to test if termites from collection traps within the foraging areas delimited by mark-release-recapture belonged to single colonies, and if these colonies could be differentiated using genetic markers. Pairwise genetic similarities (Lynch 1990) between individuals from the same collection trap were approximately normally distributed and did not show any evidence for mixing of genetically distinct groups. Genetic similarities within single collection traps lay in the same magnitude as genetic similarities between termites from different collection traps within the same foraging area

(0.63, SD=0.08, genetic similarity) (0.35, SD=0.14, genetic profiles) approaches identical 3 foraging areas clearly different confirm that for correspond to c individuals as well traps. Different

Secondly, ha colonies whether traps to their co termites from o colony if their p to different colo individuals can tic bands for col known colonies colonies contain each colony fro bands can be a the termites co bands. Individ 100% because 63% of the ba distinguished of the colony cannot be ass overcome by g

We determin als and subje from the sam genetic simila described in t nearest group than that cas to be equal assigned to successful as Thus, using

Journal Title : Sociobiology.

Journal Vol: 41

Journal Issue:

Journal Year: 2003

Article Pages: 67-69

Article Author/Title: . Vargo, E. L., C. Husseneder, J. K. Grace, G. Henderson and D.

Ring

(Colony and ...)

ranean termites from

Husseneder, C. et al. - Termite Colonies in Armstrong Park

63

(0.63, SD=0.08, 22 traps). These values are significantly higher than genetic similarities between termites from different foraging areas (0.35, SD=0.14, 43 pairs of traps). Similarly, bandsharing between genetic profiles derived from pools of 10 termites per collection trap approaches identity within foraging areas (0.95, SD=0.03, 2-7 traps in 3 foraging areas). Among foraging areas, however, genetic profiles are clearly different (0.50, SD=0.08, 91 pairs of traps). These results confirm that foraging areas outlined by mark-release-recapture studies correspond to colonies identified by genetic similarities between individuals as well as between genetic profiles representative of collection traps. Different foraging areas represent genetically distinct colonies.

Secondly, having outlined colonies, we then tested on a subset of six colonies whether we could assign termites from different collection traps to their colony of origin. Based on the results above, pools of ten termites from different collection traps can be assigned to the same colony if their pooled genetic profiles are identical (95% bandsharing) or to different colonies if their genetic profiles are different. Furthermore, individuals can be assigned to colonies based on two methods: diagnostic bands for colony membership, and genetic similarity to termites from known colonies. The genetic profile of each of the six investigated colonies contains on the average 3-4 diagnostic bands distinguishing each colony from the others. On average termites that possess these bands can be assigned to one of these colonies. On the average, 77% of the termites could be assigned to their colony on the basis of diagnostic bands. Individual assignment by diagnostic bands, however, is not 100% because individuals of a colony share on the average only around 63% of the bands (see above). In cases where a colony's profile is distinguished from other colonies by only a few diagnostic bands, some of the colony members might lack those particular bands and thus cannot be assigned to a single colony. However, this drawback can be overcome by grouping individuals according to their genetic similarity.

We determined the pairwise genetic similarities between all individuals and subjected the data matrix to discriminant analysis. Termites from the same colony consistently grouped together due to higher genetic similarity within colonies compared to between colonies, as described in the previous paragraph. Each termite was classified to the nearest group by the discriminant functions derived from all cases other than that case. Prior probabilities of group membership were assumed to be equal (Husseneder & Grace 2000). When each termite was assigned to the genetically most similar group of termites, 100% successful assignment to the actual colony of origin was achieved. Thus, using multilocus DNA fingerprinting, termite colonies can be

1/2003

SID: 06422

IL

Record 69 of 112

NeedBefore: 20031221

RenewalReq:

NewDueDate:

Henderson and D. Ring  
ranean termites from

: 67-69

D.H. Hill  
11 Raleigh  
152.1.24.195 / Library

SID: 06422

IL

Record 69 of 112

: FEIN; ours is 56-

INSURANCE:

24:25 -0500

outlined by assigning collection traps and in most cases even single individuals to colonies. The power of this method is the greater when the number of potential colonies of origin is small and genetic differentiation between them is high.

In addition to assigning termites to colonies, we also intend to apply genetic information to examine how termites invade areas where baiting has eliminated all prior activity. Genetic profiles can be used to "fingerprint" colonies prior to elimination for re-invasion studies. When termites reappear in the same location after elimination, comparison of genetic profiles can tell us if they are remnants of the same colony (profiles identical to previous colony), invaders from neighboring colonies (profiles identical to another colony), or new infestations from outside the immediate area (profiles do not match any known colony).

Thirdly, we investigated the possibility of genetic differentiation occurring within colonies due to the presence of multiple reproductives. We employed microsatellite genotyping to test the genotypic distribution among 15-24 workers of the 14 colonies at 8 loci for deviation from the ratios expected for a single pair of reproductives (Mendelian ratios). Results show that about a third of the colonies are headed by multiple reproductives. These colonies showed either genotype combinations that are not possible with only a single pair of reproductives or genotypic ratios that deviated from the expectations for a single pair (Chi-square test).

The presence of multiple kings and queens may lead to asymmetries in spatial distribution within a colony, if reproductives are located in different nests or if the offspring are otherwise separated (Kaib *et al.* 1996). Preliminary data derived from multilocus DNA fingerprinting and confirmed by microsatellite genotyping suggests a slight genetic differentiation between six collection traps belonging to one colony. However, this genetic differentiation is much smaller than the differentiation between colonies. This is the pattern we would expect in a colony with multiple interconnected satellite nests. Future research is required since such a spatial structures could influence distribution of bait toxins within colonies.

In conclusion, using multilocus DNA fingerprinting, we were able to establish that foraging areas represented individual colonies and assign termites to their colony of origin. We now intend to apply this information to re-invasion studies in Armstrong Park. Using microsatellite genotyping, we found multiple reproductives within a third of the *C. formosanus* colonies. The presence of multiple reproductives resulted in a small degree of genetic differentiation between collection traps within

at least one colony  
on colony social o

This paper was  
*Coptotermes form*  
Funding was prov  
58-6435-8-107. 1  
Tropical Agricultu

- Husseneder, C. & J.  
tests and morp  
Formosan subt  
Husseneder, C. & J.  
genetic similar  
Rhinotermitida  
Husseneder, C. &  
aggression test  
Formosan subt  
Husseneder, C., Va  
and microsat  
investigating c  
termites. Soci  
Kaib, M., Hussene  
biased foragin  
263: 1527-15  
Lynch, M. 1990. T  
7: 478-484.  
Vargo, E. L. & G. H  
loci in the F  
Shiraki. Mole

at least one colony in the park, suggesting a need for additional research on colony social organization.

#### ACKNOWLEDGMENTS

This paper was presented in the 2<sup>nd</sup> International Symposium on *Coptotermes formosanus*, New Orleans, Louisiana, 13-15 May 2001. Funding was provided by USDA-ARS Specific Cooperative Agreement 58-6435-8-107. This is Journal Series No. 4612 of the College of Tropical Agriculture and Human Resources.

#### REFERENCES

- Husseneder, C. & J. K. Grace. 2000. What can DNA fingerprinting, aggression tests and morphometry contribute to the identification of colonies of the Formosan subterranean termite? IRG/WP 00-10371, 8pp.
- Husseneder, C. & J. K. Grace. 2001a. Similarity is relative: The hierarchy of genetic similarities in the Formosan subterranean termite (Isoptera: Rhinotermitidae) in Hawaii. *Environmental Entomology* 30: 262-266.
- Husseneder, C. & J. K. Grace. 2001b. Evaluation of DNA fingerprinting, aggression tests and morphometry as tools for colony identification of the Formosan subterranean termite. *Journal of Insect Behavior* 14: 173-186.
- Husseneder, C., Vargo E. L. & J. K. Grace. 2002. Multilocus DNA fingerprinting and microsatellite genotyping: complementary molecular approaches to investigating colony and population genetic structure in subterranean termites. *Sociobiology* 40: 217-226.
- Kaib, M., Husseneder, C., Epplen, C., Epplen, J. T. & R. Brandl. 1996. Kin-biased foraging in a termite. *Proceedings of the Royal Society of London B* 263: 1527-1532.
- Lynch, M. 1990. The similarity index and DNA fingerprinting. *Mol. Biol. Evol.* 7: 478-484.
- Vargo, E. L. & G. Henderson. 2000. Identification of polymorphic microsatellite loci in the Formosan subterranean termite *Coptotermes formosanus* Shiraki. *Molecular Ecology* 9: 1935-1938.



cases even single  
e greater when the  
genetic differentia-

also intend to apply  
reas where baiting  
can be used to  
ion studies. When  
ion, comparison of  
the same colony  
neighboring colo-  
infestations from  
ny known colony).  
tic differentiation  
ple reproductives.  
enotypic distribu-  
for deviation from  
Mendelian ratios).  
eaded by multiple  
ype combinations  
ctives or genotypic  
e pair (Chi-square

ad to asymmetries  
ves are located in  
rated (Kaib *et al.*  
NA fingerprinting  
is a slight genetic  
ng to one colony.  
than the differen-  
expect in a colony  
e research is re-  
ce distribution of

g, we were able to  
lonies and assign  
ply this informa-  
ng microsatellite  
a third of the C.  
ctives resulted in  
ction traps within