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Population genetic inference of demographic processes in the African Wild Silk Moth, *Gonometa postica* (Lasiocampidae)

by

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Declaration

I declare that this dissertation, which I hereby submit for the degree Philosophiae Doctor at the University of Pretoria, is my own work and has not previously been submitted by me for a degree at this or any other tertiary institution.

13 December 2005

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For Linda

Gonometa postica

female

male

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Summary

The African Wild Silk moths (*Gonometa* spp., Lasiocampidae) are species that are presently of particular economic interest in southern Africa. Both *Gonometa postica* and *G. rufobrunnea*, two species of African Wild Silk moth native to southern Africa, have been shown to possess a silk fibre of exceptional quality. A small-scale cottage industry utilizing the silk of *Gonometa* species currently exists in southern Africa, yet a consistent complaint is the lack of supply of cocoons. The *Gonometa* species in southern Africa have been shown to exhibit large inter-annual population fluctuations. However, it is uncertain whether eruptions are only the result of local populations experiencing ideal conditions or whether current eruptions are initiated by dispersal of individuals from eruptive populations in previous generations. A second observation, regarding eruptions, is that they are patchily distributed at both the local (within outbreaks) and regional scale (across southern Africa).

In this thesis I have studied population eruptions through distribution analysis of three years of presence/absence data, and through spatial and temporal population genetic analysis. The analysis of population genetic data allows the inference of population demographic parameters such as population size fluctuations and migrations. In particular, the use of microsatellite markers allows a high-resolution analysis of the connectivity of populations, and provides signal of population size fluctuations. I utilise both mitochondrial DNA control region sequences and polymorphic microsatellite loci to make inferences of population processes in *G. postica,* using a combination of both analytical and simulation model analysis approaches. The results, in general, indicate that dispersal of moths across South Africa is extensive. These results are further considered in light of the effects of population size fluctuations on spatial genetic pattern, where the potential exists for unstable population demography to influence the inference of dispersal from population genetic data. The population genetic analyses presented here allow the inference of the extent of a local population/outbreak, and the degree of movement between local populations. Given that a large-scale population dynamics project based on *G. postica* is currently under development, the results determine the geographical extent at which the population dynamics study should be conducted. Furthermore, the population genetics data

University of Pretoria etd – Delport, W (2006)

generated will contribute to the construction of a population dynamics model, including abiotic and biotic variables, which will allow a better understanding of eruptions in this species.

University of Pretoria etd – Delport, W (2006)

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"But thanks for your time
Then you can thank me for mine
And after that's said
Forget it"

Rodriguez

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University of Pretoria etd – Delport, W (2006)

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University of Pretoria etd – Delport, W (2006)

Table of Contents

Chapter 1	Introduction	1
Chapter 2	Temporal and spatial distribution of African Wild Silk Moth, *Gonometa postica*, eruptions in southern Africa	22
Chapter 3	Characterisation of six microsatellite loci in the African Wild Silk Moth (*Gonometa postica*, Lasiocampidae)	41
Chapter 4	The effect of large annual population size fluctuations on spatial genetic pattern in the continuously distributed African Wild Silk Moth (*Gonometa postica*)	48
Chapter 5	Temporal and spatial genetic patterns in the African Wild Silk Moth (*Gonometa postica*) and implications for cyclical population dynamics	89
Chapter 6	CoalFace: a graphical user interface program for the simulation of coalescence	114
Chapter 7	Conclusions	124
Appendix I	A population genetics pedigree perspective on the transmission of *Helicobacter pylori*	130
Appendix II	LatticeFlucIII C Source code	160
Appendix III	CoalFace Kylix/Delphi Source Code	207

University of Pretoria etd – Delport, W (2006)

List of Tables

Chapter 2	**1**	Climatic predictors and response variables used to model the distribution of *Gonometa postica* eruptions	29
	2	Total number of sampled sites and proportion of presence sites of all sites sampled during 2002, 2003 and 2004.	32
Chapter 3	**1**	Microsatellite loci isolated and optimized for *Gonometa postica*.	45
Chapter 4	**1**	Statistics for the optimal distance classes chosen for spatial correlogram analysis.	57
	2	Sampling variance in the calculation of neighbourhood size.	61
	3	Indirect morphological estimates of dispersal ability in *Gonometa postica*.	62
	4	Calculation of mtDNA pairwise-population F_{ST} values using Arlequin (Schneider *et al.* 2000) for subpopulations/demes defined in Figure 1.	64
	5	Tests of the deviation from Hardy-Weinberg, the random-association of alleles within diploid individuals as calculated using Arlequin v2.0 (Schneider *et al.* 2000).	67
	6	Results of permutation tests for the regression of spatial autocorrelation statistics against ln (distance).	69
	7	Relationship between dispersal parameter, *d*, and the equilibrium neighbourhood size for a continuous population of constant size.	75
Chapter 5	**1**	Custom migration model enforced in migrate-n such that only migration between populations in successive years is estimated.	96
	2	The spatial distribution of alleles for each of the six microsatellite loci.	99
	3	Maximum likelihood estimates of migration between	101

University of Pretoria etd – Delport, W (2006)

2002 demes (Figure 1) and θ ($4N\mu$, N = population size, μ = mutation rate) for each deme, as estimated with migrate-n (Beerli & Felsenstein 1999, 2001).

4 Maximum likelihood estimates of temporal migration and θ (boxed), as estimated with migrate-n (Beerli & Felsenstein 1999, 2001). 104

University of Pretoria etd – Delport, W (2006)

List of Figures

Chapter 2	**1**	Distribution of rainfall and temperature weather stations used for the calculation of interpolated climate surfaces. The extent of the eruptive zone and distribution of the Kalahari biome in southern Africa is also shown.	27
	2	Temporal change in presence and absence of *G. postica* eruptions as determined with annual surveys from 2002-2004.	31
	3	Distribution of environmental predictors and the occurrence of presence/absence samples.	33
	4	Statistical correlations between pairs of climate predictor variables used in the GAM model.	34
	5	Response curves of predictor variables in selected generalized additive model (GAM).	35
Chapter 3	**1**	Sequenced alleles for each of the microsatellite loci isolated.	46
Chapter 4	**1**	Distribution of Gonometa postica in southern Africa and sampling localities for mtDNA and microsatellite samples.	53
	2	Mitochondrial DNA allele network constructed in TCS (Clement *et al.* 2000).	63
	3	Distribution of microsatellite allele frequencies for each of the six loci analysed for 137 G. postica samples collected across the distribution of the species.	66
	4	Correlograms of spatial autocorrelation statistics plotted against geographic distance classes.	68
	5	Genetic differentiation in the African Wild Silk Moth, *Gonometa postica*, represented as the regression of pairwise genetic distance against the natural logarithm of distance (km).	70
	6	Changes in F_{ST} and F_{IS} calculated over six polymorphic microsatellite loci for each subsequent pooling level in the hierarchical F_{ST} analysis.	72

University of Pretoria etd – Delport, W (2006)

	7	Examples of population size fluctuations achieved with the Ricker logistic growth model (Ricker 1954).	73
	8	Changes in neighbourhood size over time under constant population size and fluctuating population size for three levels of dispersal, and three starting population neighbourhood sizes.	76
	9	Changes in heterozygosity over time under constant population size and fluctuating population size for three levels of dispersal, and three starting population neighbourhood sizes.	77
Chapter 5	**1**	Temporal and spatial distribution of microsatellite allele frequencies.	94
	2	Maximum likelihood estimates of migration (from 2002 samples) using migrate-n (Beerli & Felsenstein 1999, 2001).	102
	3	Temporal estimates of migration, $M = m/\mu$ (m = immigration rate, μ = mutation rate), between demes sampled in successive years.	103
	4	Likelihood surfaces of change in effective population size over the sampling period.	105
Chapter 6	**1**	Screenshot of CoalFace showing the visually orientated representation of coalescent genealogies.	117
	2	Distributions of (a) time to the most recent common ancestor, and (b) nucleotide diversity derived from 1000 simulations of the coalescent process (k = 50, N = 10000).	119
Chapter 7	**1**	Per generation changes in a) allelic diversity and b) ADI in a population of constant size (N = 125000) over 5000 generations with a microsatellite mutation rate of 2.5×10^{-4}.	121