

ACKNOWLEDGEMENTS

I thank my committee, Drs. Paul Beier, Bill Block, Laura DeWald, Paul Keim, Tom Sisk, and Tad Theimer. I am especially thankful to Paul Beier for his continued enthusiasm, support, and patience as my research evolved considerably, and to Paul Keim, who welcomed me into his lab.

This research would not have been possible without the help of hunters, taxidermists, and state game management agency personnel who helped to provide tissue samples from hunted pumas. In Arizona, Warner and Wendy Glenn, Steve Favour, Jack Childs, and Matt Colvin were especially helpful in providing samples as well as feedback and suggestions on how to improve my sampling protocol and kits. State game management personnel in the Utah Division of Wildlife Resources, Colorado Division of Wildlife, New Mexico Department of Game and Fish, and Arizona Game and Fish Department either provided samples, helped identify hunters and taxidermists willing to do so, or helped track down location data for samples based on hunter reports. Rich Beausoleil, Jerry Apker, Ron Day, and John Phelps were particularly helpful in these endeavors.

Special thanks are due to the members of the Keim Genetics Laboratory for their help and guidance. Joe Busch was especially generous with his time in helping to get the project started and in providing training. Lynn Huynh helped to genotype pumas before she was drafted to investigate the anthrax attacks in the fall of 2001.

While at NAU I attended the meetings of three lab groups, including the Beier, Keim and Sisk labs. All provided different perspectives on the research questions I pursued, and each was instrumental in the development of this project.

Holly Ernest and Melanie Culver shared protocols for DNA extraction and PCR, reviewed drafts of Chapter 2, and participated in many discussions about puma genetics in general. Thanks to Carlos Driscoll for hints about analyzing microsatellite data in cats, to Marilyn Menotti-Raymond for sharing unpublished primer sequences, and to Phil Hedrick for discussions about gene flow models. Discussions with Harley Shaw about puma ecology were invaluable. Jeff Jenness and Haydee Hampton were always helpful with questions about GIS analyses, projections, and datasets. I had many productive discussions with Brett Dickson about GIS analyses and habitat models as well.

The habitat map shown in Chapter 2 was based on a survey of experts with experience radio tracking pumas, including Paul Beier, Brett Dickson, Lisa Haynes, Ken Logan, Harley Shaw, and Linda Swenor. I thank these researchers for lending their time and expertise in completing the survey.

Others helped with the development of the conductance model described in Chapter 3 and with its testing. I am especially grateful to Paul Flikkema for his guidance on circuit theory and Markov chains, both of which were indispensable in developing the model. I also thank Montgomery Slatkin for productive discussions and for his comments on an early draft of Chapter 3. Tad Theimer and Lutz Tischendorf provided helpful comments on early drafts as well. The wolverine and mahogany datasets reanalyzed in Chapter 4 were kindly shared by Christopher Kyle and Rachel Novick, respectively.

This project was supported by a U.S. Environmental Protection Agency STAR Fellowship and a Merriam-Powell Center for Environmental Research graduate

fellowship. I am also grateful to the Keim Genetics Laboratory at Northern Arizona University for providing additional funding, training, and use of laboratory equipment and reagents. I thank New Mexico Department of Game and Fish for financial support as well.

Finally, I thank my friends for moral support and for feedback on research ideas and practice presentations, especially James Battin, Jessica Girard, Laura Williams, Leslie Reis, Rachel Billowitz, Matthew Loeser and Andrea Redman.