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Jeffrey Brian Stetz

*The University of Montana*, [jstetz@usgs.gov](mailto:jstetz@usgs.gov)

Katherine Kendall

Christina D. Vojta

Genetic Monitoring (GeM) Working Group

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# Genetic Monitoring for Managers: A New Online Resource

Jeff B. Stetz,\* Katherine C. Kendall, Christina D. Vojta, Genetic Monitoring (GeM) Working Group

**J.B. Stetz**

Wildlife Biology Program, University of Montana, Missoula, Montana 59812

**K.C. Kendall**

U.S. Geological Survey, Northern Rocky Mountain Science Center, West Glacier, Montana 59936

**C.D. Vojta**

U.S. Fish and Wildlife Service, Southwest Region, Flagstaff, Arizona 86001

**GeM Working Group**, chaired by F. W. Allendorf, (University of Montana, USA), and M. K. Schwartz (US Forest Service, USA). Other members are: C. S. Baker (Oregon State University, USA), D. P. Gregovich (University of Alaska, USA), M. M. Hansen (Aarhus University, Denmark), J. A. Jackson (Oregon State University, USA), L. Laikre (Stockholm University, Sweden), K. McKelvey (US Forest Service, USA), M. C. Neel (University of Maryland, USA), I. Olivieri (Université de Montpellier II, France), N. Ryman (Stockholm University, Sweden), R. Short Bull (University of Montana, USA), D. A. Tallmon (University of Alaska, USA), D. M. Waller (University of Wisconsin, USA), and R. S. Waples (National Marine Fisheries Service, USA)

## Abstract

Monitoring our natural resources will increasingly rely on genetic tools in order to understand and respond to invasive species, habitat degradation, fragmentation, disease, or climate-related changes. In recent years, the rapidly evolving field of genetic monitoring has seen explosive growth in sampling methods, genetic markers, and analytical approaches designed to estimate a wide range of parameters from connectivity to population growth rates. Some of these methods have taken root and now dominate particular aspects of population assessment and monitoring, whereas others have seen less success in real-world applications. To aid managers and researchers with limited genetics experience, we developed a web-based resource to help them identify which, if any, molecular genetic methods would be appropriate for population assessments or monitoring. The site was developed in cooperation with a team of experts in fields such as evolutionary biology, demographic parameter estimation, and exotic species detection to provide a broad, dynamic, and easily understood resource with limited jargon. The site also provides distilled examples from the recent literature, along with contact information for experts in various techniques. The website, Genetic Monitoring for Managers, is now available at [http://alaska.fws.gov/gem/mainPage\\_1.htm](http://alaska.fws.gov/gem/mainPage_1.htm).

Keywords: conservation; DNA; genetic monitoring; genetic sampling; molecular ecology

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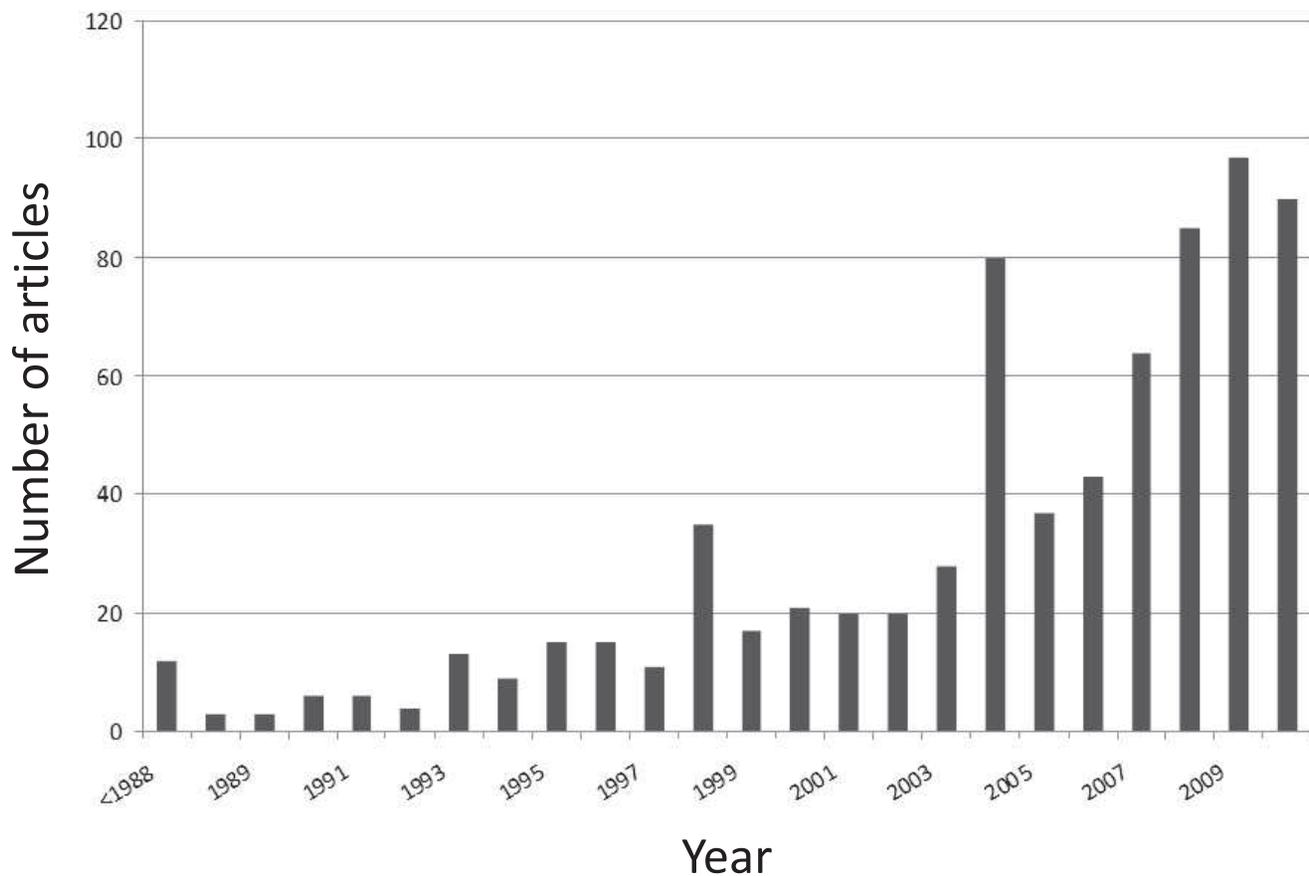
The findings and conclusions in this article are those of the author(s) and do not necessarily represent the views of the U.S. Fish and Wildlife Service.

\* Corresponding author: [jeff.stetz@gmail.com](mailto:jeff.stetz@gmail.com)

The rapid and continuing development of molecular genetic methods has resulted in a powerful, sometimes overwhelming, array of new tools to answer questions relevant to conservation and management of natural resources (Figure 1). Researchers can now assess and monitor most population parameters of

management significance with molecular techniques, alone or in combination with more established methods (DeYoung and Honeycutt 2005; Schwartz et al. 2007). From traditional problems such as estimating abundance, to more contemporary concerns such as identifying adaptive genes to select individuals for population





**Figure 1.** A Google Scholar™ search shows the rapid increase in the number of publications related to genetic monitoring of wildlife populations, pre-1998 through 2010. (Search: all words = genetic monitoring wildlife, plus exact phrase “genetic monitoring”; 22 May 2011; excludes citations and patents).

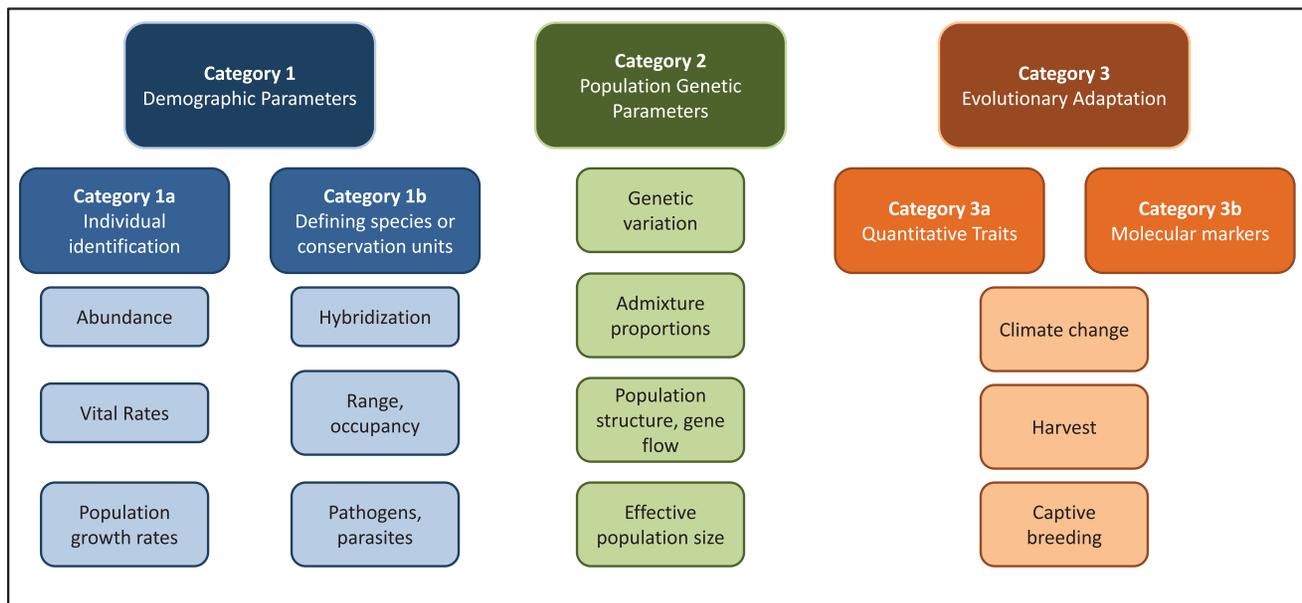
augmentation, molecular genetic methods have changed not only how we answer conservation and management questions, but what questions we ask in the first place.

The types of information genetic monitoring can provide can be divided into three broad categories (Figure 2). Category 1 includes traditional population parameters such as abundance, survival rates, distribution, and hybridization. Category 2 consists of population genetic parameters such as effective population size, connectivity, and genetic variation. Category 3 addresses questions of evolutionary potential, such as adaptive genes and effects of harvest on population genetics (Allendorf et al. 2008). Schwartz et al. (2007) emphasized the distinction between population monitoring and assessment: the former requires a temporal component, whereas the latter typically provides a snapshot in time. Many of these parameters can be estimated once or in a time series. Monitoring over longer time periods, however, is vastly more powerful in most cases due to inherent variability both within the population (e.g., survival rates) and in our ability to sample populations adequately to detect rare events (e.g., migration events).

As noted by Schwartz et al. (2007), the expansion of molecular genetic techniques, and the coincident explosion of new sampling and statistical methods, has

occurred so rapidly that there has not been enough time to thoroughly assess their rigor or effectiveness under real-world conditions. For example, there has been a spirited debate in the literature, especially in the early years of using noninvasive sampling for estimating abundance, that molecular genetic methods were unreliable due to excessive levels of genotyping error (Taberlet et al. 1999; Mills et al. 2000; Waits and Leberg 2000). Although it has been demonstrated that error rates are typically acceptable for most studies when appropriate protocols are used (Paetkau 2003), there is undoubtedly some latent hesitation by some to use molecular genetic methods even when they are the best tool for the job (Smith et al. 2006). On the other hand, managers and researchers wanting to use the latest and greatest genetic methods may design studies without fully appreciating the limitations, or potential, of those methods. Such studies may then rely on complicated statistical analyses that are difficult to understand for those not immersed in this field. As with all study designs, the selection of sampling and analytical methods should be made in consultation with experts and based on the assessment or monitoring questions, not the desire to use particular methods.

To promote the appropriate use of molecular genetic methods for plant and animal population assessment



**Figure 2.** Categories and examples of specific population parameters of genetic monitoring modified from Schwartz et al. (2007). Categories should be viewed as guidelines to help direct discussions and spur research on genetic monitoring, and are not mutually exclusive.

and monitoring, we developed a web-based resource for managers and researchers with limited genetics experience. The website, Genetic Monitoring for Managers, is now available at [http://alaska.fws.gov/gem/mainPage\\_1.htm](http://alaska.fws.gov/gem/mainPage_1.htm). This site has been developed in cooperation with experts in a range of genetic fields, including demographic parameter estimation, invasive species detection and monitoring, range estimation, evolutionary biology, sample preservation and archiving, and assessing genetic population structure and connectivity. Specifically, our goal was to present a broad, dynamic, and easily understood resource to help researchers and managers identify which, if any, molecular genetic methods will satisfy their informational needs.

The Genetic Monitoring for Managers website provides a synthesis, with minimal jargon, of current technologies including genetic markers and analytical tools, recent examples of genetic research for a wide range of applications, a comprehensive glossary, an extensive literature list, and links to many other resources. Expanding on the categories and specific parameters identified by Schwartz et al. (2007; Figure 2), we have taken examples from the scientific literature and distilled their questions, methods, results, and conclusions into concise summaries.

Our goal was to help users rapidly evaluate the research without getting bogged down in the technical details that can be overwhelming, especially for the more advanced methods such as estimating effective population size. To stay abreast of this rapidly evolving field, the website will be updated periodically to provide the most current information available, such as advancements in analytical methods, novel sampling methods, and recent publications.

The website is not intended to provide users with all of the background and expertise required to design,

execute, analyze, and interpret a genetic study, and we strongly recommend consultation with experts during all phases of developing a research or monitoring program. Instead, the site should serve as an excellent resource for those managers who have conservation, management, or ecological questions, and who are interested in applying genetic techniques to them.

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The use of trade, firm, or product names is for descriptive purposes only and does not imply endorsement by the U.S. Government.

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