

Genetics and Molecular Tools :
Setting the Standard for Biological Science in USGS

Summary of Discussions and Dialogue from the Workshop

**Integration and Collaboration on Emerging Biological Issues and Research
Goals**

(ICEBIRG) I: Genetics and Molecular Tools

held 7-8 December, 1999 at the Leetown Science Center

Steering Committee:

Mary K. Burnham Curtis, Chair

Susan Haig

Tim King

Gael Kurath

Jennifer Nielsen

Gregory Smith, ICEBIRG Advisor

Executive Summary

USGS must make a commitment to developing a nationally-recognized and integrated biological research program to rival its well-respected capabilities in the areas of geology, hydrology, and mapping. The integration of traditional as well as novel technologies is critical to fulfilling our mission to “provide scientific information to...manage biological resources.” Of the available technologies, genetic and molecular tools are the most universal, powerful, and accessible investigative tools available from science today. The application of genetic and molecular tools in USGS science transcends program, species, geographic, and temporal boundaries. Genetic and molecular tools comprise one facet of a diverse research program that is capable of addressing short-term emergent needs as well as long term conservation, restoration, and monitoring programs. Genetic data complement analyses of animal and plant populations by providing information about demographic parameters such as effective population size, migration rate, reproductive success, and family relationships in detail that cannot be obtained with traditional biological tools. Genetic and molecular tools provide robust, irrefutable information that is integral to the USGS national program in: providing the definitions of populations for listing species as threatened or endangered; developing sound responses to invasives; providing appropriate genetic material for restoration and enhancement; monitoring the effects of contaminants; developing effective tools to fight disease in trust organisms. The expertise is available and opportunities exist within USGS to fully integrate all of the accessible and useful tools at our disposal to address resource issues from the local to the ecosystem level. Recent USGS initiatives have not taken full advantage of the power of genetic and molecular tools. USGS leadership should support and encourage consideration of genetics and molecular tools in USGS biological research programs in the interest of producing well-integrated, rigorous research products. Genetic and molecular tools, in combination with other biological and statistical methods, give USGS science a unique suite of tools with which prudent, proactive, and sound science can be used to support the management and conservation of our Nation's natural resources.

Overview

Recent technological advances in genetics and molecular tools have revolutionized our basic understanding of biological and evolutionary processes. These contemporary applications have significantly enhanced our ability to delineate the finest level of biological diversity (i.e., genetic diversity) and provided remarkably sensitive techniques for diagnosing the presence and effects of environmental perturbations on a host of endangered, threatened, or at-risk species. Individual scientists within USGS have kept pace with the advancing technology, but the organization has not fully embraced the utility and capacity of these tools. Simultaneously there has been an exponential growth of critical environmental issues that demand relevant and efficient application of these state-of-the-art technologies.

The USGS/BRD is in a position to benefit from recent technological advances in the areas of genetics and molecular tools and their application to resource identification, conservation, protection, and monitoring. No other federal agency has the staff, skills, or mandate to initiate genetic monitoring of critical biological resources at the national level. If we miss the opportunity to develop and integrate genetics as a standard monitoring tool, USGS/BRD will lose significant support at the federal level as other agencies perceive the need for genetic information on biological resources and proceed to develop their own response.

The USGS has a distinguished scientific reputation, both within and outside of the federal government in vulcanology, hydrology, and geology because a need was recognized at the national level, the appropriate technology and skills base was developed, and the nation was provided with a best-science monitoring service unavailable from other sources. This technological development is an appropriate model for USGS/BRD in genetics and molecular tools. The opportunity is at hand to foster collaborations across USGS in this field as well, particularly in the areas of contaminants and animal health (i.e., water quality and the presence of pathogenic microorganisms such as *E. coli*). The integrated focus available from our current staff and facilities makes this opportunity timely and appropriate for USGS/BRD, but we must act now and set the standard. The ICEBIRG Genetics and Molecular Tools Workshop was organized to develop a framework for addressing these needs within the USGS/BRD.

Critical to providing USGS and our partners with much-needed expertise in Genetics and Molecular Tools is an understanding by USGS leadership and managers of the capabilities that USGS/BRD possesses in the field of genetics and molecular tools. Currently, this expertise is spread across 13 centers from Hawaii to West Virginia (Appendices 1-3). There are over 25 principal investigators whose topical and taxonomic expertise spans the depth and breadth of genetics, ecology, and conservation. Thus, we have a strong base from which to build a 21st century program. However, central to this mission will be to better facilitate communication among these scientists and among scientists and higher level administrators. Most important will be universal integration of this expertise into all facets of USGS/BRD programs.

What are Genetics and Molecular Tools?

Genetic material provides all living organisms with the blueprint for form (morphology, phenotype), function (physiology), behavior, and reproductive success. The USGS/BRD utilizes genetic information to address issues in:

- Population restoration
- Habitat restoration
- Inventory and monitoring
- Wildlife and fish health
- Contaminants
- Invasive species

Genetic and molecular tools (G&MT) are laboratory and analytical techniques used to assess the critical information available in genetic material such as DNA and RNA. Examples of their use in USGS/BRD include:

- Polymerase chain reaction (PCR)
- DNA sequencing
- Identification and development of genetically-based markers
- Flow cytometry
- Computing software designed to evaluate population structure and viability

How do Genetics and Molecular Tools fit into Biological Sciences in USGS?

□ *Threatened and Endangered Species*

Genetics and molecular tools provide us with the ability to identify, differentiate (at the species, population, and individual levels) and assess threatened, endangered, and at-risk species. This includes identifying evolutionarily significant population segments for listing under the Endangered Species Act and conducting population viability analyses to aid in setting species recovery goals. Genetic methods can also supplement attempts to estimate abundance and distribution of at-risk species by providing estimates of effective population size and gene flow (migration).

The current application of “evolutionarily significant units” (ESUs), “conservation units” (CUs), and “distinct population segments” (DPSs) for the purposes of listing, delisting, and reclassification of vertebrates under the Endangered Species Act speaks volumes on the importance and increasing significance of genetics and molecular tools in the management and recovery of species at risk. The National Marine Fisheries Service (NMFS) has developed a *Policy on the Definition of Species Under the Endangered Species Act* (56 FR 58612-58618; November 20, 1991) which applies to species of salmonids native to the Pacific Ocean. Under this policy, a stock of Pacific salmon is considered a DPS if it represents an ESU by meeting two criteria; 1) it must be substantially reproductively isolated

from other population units of the same species, and 2) it must represent an important component in the evolutionary legacy of the species.

The U.S. Fish and Wildlife Service (USFWS) and NMFS recently published a joint *Policy Regarding the Recognition of Distinct Vertebrate Population Segments Under the Endangered Species Act* (61 FR 4722-4725; February 7, 1996) which endorses the recognition of scientifically-identified evolutionary units for listing, delisting, and reclassification. While NMFS or USFWS do not *require* genetic evidence to be used in determinations under the ESA, the 1996 joint publication in the Federal Record states, "...evidence of genetic distinctness or the presence of genetically determined traits may be important in recognizing some DPSs." To our knowledge, the USGS/BRD has no published or implied guidelines on the development, collection, or application of genetics data for use by management agencies for conservation and recovery of listed or at-risk species. This is a critical deficiency and should be corrected as we further develop the science of evaluating the status of at-risk species, measure the effectiveness of maintenance and recovery efforts for at-risk populations, and identify and enhance scientific understanding of limiting factors for listed and at-risk species.

Goal: Increase awareness of the utility and rigor of G&MT as they are applied to a broad range of species.

Examples of the application of G&MT in the USGS in this area:

- Mitochondrial and nuclear markers are being used to identify "distinct population segments" (DPSs) and evolutionarily significant units (ESUs) in spotted owl, piping plover, snowy plover, Micronesian kingfishers, Snake River steelhead, Atlantic salmon, Atlantic sturgeon, lake trout, brook trout, horseshoe crabs, torrent salamanders, spotted salamanders, wood frogs, bog turtles, and many other species.
- The ability to track progeny, trace parentage, and directly measure the effects of demographic changes makes genetics essential to studies of at-risk species such as lake sturgeon, Atlantic sturgeon, manatee, migratory waterbirds, and some terrestrial vertebrates such as black bear and grizzly bear.
- DNA sequencing of nuclear and mitochondrial DNA regions is being used to determine the molecular systematics of freshwater and marine fish and bivalves, amphibians, and terrestrial and aquatic mammals. One critical limiting factor for some populations is the amount of genetic diversity in the population and the diversity passed on to the next generation through the number of effective breeders. This information can be measured, modeled, and monitored with G&MT.
- G&MT are used to maintain health and control disease in captive propagated populations of at-risk species such as Pacific salmon, Atlantic salmon, and lake trout, and in wild populations of at-risk species such as native Hawaiian birds.
- Restoration and adaptive management strategies are being developed to restore, preserve and maintain "natural" or "native" levels of genetic diversity in populations of Pacific salmon, Atlantic salmon, and lake trout. Levels of genetic diversity are

known to influence long term population viability; a sound scientific basis for restoration and conservation plans for species and communities must incorporate information about population genetics.

- G&MT are used to identify the breeding origin of migratory waterbirds and shorebirds during the winter. This monitoring tool provides substantially greater detail than traditional marking and banding methods.

▣ *Assessment of trends in population structure*

The Nation's biological resources are spread across a vast array of taxa and geographic areas, and the status and condition of these resources is of primary concern to USGS/BRD. The importance of genetic diversity to population fitness is widely accepted, yet assessments of the genetic characteristics of populations are not often incorporated into long term studies. Genetic diversity is a level of biological diversity that should be measured and evaluated, not unlike other measurable parameters such as mortality, fecundity, and abundance which guide management decisions on the basis of sustainability and long-term persistence. Patterns of genetic variability over time can indicate significant risks to populations or species that are otherwise difficult to infer from ecological and demographic analyses alone. A national framework for monitoring biological resources that does not include genetics and molecular tools will lack scientific inference drawn from multiple scales that is critical to adaptive management.

Information on abundance, population structure, recruitment, and survival are crucial to prudent management of populations. Data on these parameters is traditionally obtained through long-term monitoring or physical marking, and extensive repeated efforts to obtain this information must be mounted over time. However, the ability to assess abundance and distribution of a species (aquatic or terrestrial) is not limited to physical methods of marking, tracking, and capturing individuals year after year. Genetic markers contain information coded in the DNA that is inherited across generations, so information gathered in one year can be directly applied to both subsequent and previous generations. Moreover, the same genetic information can be obtained at any lifestage and often by using non-lethal methods. Threats to population integrity from invasive species, interbreeding, and population declines are best analyzed using G&MT. Genetic markers are uniquely effective for measuring relatedness among individuals in a population, estimating effective breeding population size, and comparing family and population structure over time. G&MT are particularly effective for forensic investigations to determine point of origin, illegal harvest, or paternity and parentage.

Genetic markers can provide detailed information about changes in population diversity and population structure that can be modeled and used in a predictive manner in a decision support framework. The cost of obtaining such data is greatly reduced if studies make use of established protocols, but proper study design and efficient data collection depends upon maintaining the appropriate expertise to develop new tools and protocols where needed. Any assessment of status and trends that does not include a genetic component will lead to significant errors in judgement or policy based on a lack of knowledge of the evolutionary history or contemporary reproductive health of the populations or species of interest.

Goal: Fully integrate the collection of genetic characters in population assessments.

Examples of the application of G&MT in the USGS in this area:

- Molecular markers are used to assess cryptic population structure in Arctic mammals and birds.
- Genetic characters are used to identify unique salmonid populations in the Pacific Northwest, the Southwest, the Great Lakes, and the Eastern seaboard. These activities involve numerous international collaborations. Genetic characters are used as the basis for stock identification, especially the identification of hatchery and wild fish, or the assessment of interbreeding and hybridization between native and exotic species.
- Population viability analyses carried out on piping plover help set national and international recovery goals for this species.

✿ *Population restoration*

Populations of wildlife, fish, other aquatic species, and plants are of great importance in every geographic region in the United States. The use of G&MT may seem more immediately applicable to the study of terrestrial animal populations, yet aquatic species are often early indicators of environmental stress or environmental health. Many studies in USGS which could benefit from the use of G&MT have not explored or considered their application (i.e. population viability). Genetic population structure may be the result of long-term processes; therefore, genetic biodiversity has a strong historical component that is unavailable from other ecological biodiversity analyses. Recent human-induced changes such as habitat fragmentation, degradation or elimination of habitat, captive breeding and population supplementation, and invasion of non-native species have led to changes in genetic variation within and between populations in a very short time.

The structure of a population, its relevance to the evolutionary history of the species, and the significance of that structure as an evolutionary legacy we wish to perpetuate are all questions best answered using G&MT. Once a target population is identified for purposes of protection or restoration, the genetic implications to both the target population and the source population must be monitored and evaluated. Without the information available from G&MT, support for long-term recovery of a native organism to pre-critical conditions will be impossible.

Restoration and management programs, particularly interjurisdictional programs, benefit from the use of population genetic information. Material for analysis can often be collected non-lethally or non-invasively. G&MT are especially applicable to animal husbandry and aquacultural projects - the whole basis of animal husbandry is the manipulation of reproduction and development of culture techniques. It is important to note that G&MT also have a very positive use with respect to artificial propagation. Molecular information can be used to augment genetic variation within a population without sacrificing long-term

fitness through excessive inbreeding or outbreeding depression. In addition, population viability analyses and pedigree analyses can model potential strategies for recovery.

Goal: Facilitate a thorough integration of genetic information into the multiple models used to design and evaluate population restoration programs.

Examples of the application of G&MT in the USGS in this area:

- Molecular markers are being used to identify wild stocks and domesticated strains of lake trout in the Great Lakes and to evaluate the contribution of wild and hatchery fish to natural reproduction.
- Molecular markers are being used to study population structure and evaluate restoration of populations of whooping cranes.
- Genetic variation is being surveyed for stands of salt marsh grass and red mangroves.
- Molecular samples are derived from hair and feces of Rocky Mountain forest carnivores as a means of monitoring populations.
- Integrated use of nuclear markers, pedigree analyses, and population viability analyses is being applied to translocation and restoration efforts for red-cockaded woodpeckers. These adaptive management protocols provide information that is complementary to other biological characteristics and can sometimes provide additional insight into the importance of ecological phenomena.

❖ *Ecosystem restoration*

Species interactions, behavior, environmental change, sustainability, and spatial heterogeneity across landscapes are all aspects of ecosystem structure and function that influence and are influenced by patterns of genetic variability. Studies of biogeography and the implications of phylogenetic structure across the landscape must apply G&MT in the effort to identify representative ecosystems throughout the U.S. The USGS/BRD science community has the mandate and skills necessary to integrate genetics and ecosystem science at a national level. Ecosystem restoration planning can be enhanced by applying G&MT to evaluate multiple species in the same ecosystem, and these tools can be used to distinguish between natural and human-induced population fragmentation. G&MT can be used to establish standardized baseline data on the genetic diversity of species and populations that are common across many regions or specific to unique terrestrial or aquatic systems. This type of resource could be particularly useful for species which demonstrate migratory behavior and could be sampled across vast geographic distances.

Decision support systems (population viability analysis, geographic information systems, incidence functions, ranking methods) integrate biological information across ecosystems on different temporal and spatial scales. In many circumstances, collections of data from natural systems are limited by time and funding. The stability of genetic material over time provides a means by which demographic and environmental events and their effect on contemporary

populations may be estimated and included in ecosystem models. Just as the restoration of a species requires knowledge of evolutionary history and genetic population structure, the restoration and adaptive management of impaired ecosystems requires an understanding of the origin and maintenance of genetic biodiversity of species endemic to an ecosystem. This information is only available through the application of G&MT.

The last three decades have witnessed significant growth in the inter-disciplinary approaches of ecological biochemistry, chemical and phytochemical ecology, and studies of the biochemical bases of adaptation to climate and environment. G&MT provide complimentary baseline data for ecosystem modeling activities - patterns of inheritance and rates of mutational changes can be estimated from genetic data regardless of species, location, life stage, or time. Physiological parameters can be measured and used to model predictable physiological responses to environmental variation. The stability of molecular data makes it an ideal candidate for inclusion in ecosystem modeling activities because genetic variation is affected by demographic changes in predictable ways. Using G&MT to describe plant and animal associations, predator/prey interactions, feeding ecology, and co-evolution of defense mechanisms among plants and animals has a long and important scientific history. The use of these tools would contribute significantly to USGS management goals in conservation and sustainability of terrestrial and aquatic ecosystems.

Goal: Apply G&MT in ecosystem research planning efforts.

Examples of the application of G&MT in the USGS in this area:

- Molecular markers are used to assess habitat fragmentation for bird, amphibian, fish, and tree species in Pacific Northwest forest ecosystems.
- G&MT are used to assess status of species at risk and risk of extinction for threatened populations such as spotted salamanders and wood frogs.
- G&MT are used to explore the role of microbes and pathogenic organisms in maintenance of ecosystem balance

◊ *Wildlife and fish health*

Health research is historically one of the earliest fields to embrace the use of genetics and molecular methods due to the global emphasis on human health sciences. Many of the technologies and theories developed in human health research translate easily to studies of health in our mission species. Fish and wildlife health, like human health, requires research into the understanding of disease processes, diagnostic methods, epidemiology, and development of strategies for prevention and control of disease. Studies of host genetics and immunological factors involved in susceptibility and resistance to disease also depend on molecular technologies. Within the mission of USGS/BRD it is important to address disease in 1) wild populations of mission and trust species, 2) cultured animal populations that may impact the health of wild counterparts through shared environmental factors, and 3) captive propagated populations of threatened and endangered hosts. In both wildlife

and fish health research, the interface of disease transmission between wild and cultured host populations is clearly an important aspect of the USGS mission.

Molecular tools are particularly well suited to the study of microbial agents of infectious disease, such as viruses, bacteria, and fungi. Due to the structural simplicity of these organisms, they have been widely used in the development of many of the molecular and genetic technologies available today. The entire complement of genetic material (DNA or RNA) has been cloned for many microbes and provides exquisite tools for development of rapid diagnostic methods and novel control strategies. Molecular epidemiology uses molecular methods to identify the sources of disease outbreaks and defines traffic patterns of disease agents. Where appropriate, the potential impact of wildlife pathogens on human health is also of concern.

A well known feature of disease agents is their capacity to rapidly adapt and evolve due to host or environmental selection pressures, leading to emergence of new diseases. Thus, another important aspect of animal health research in the USGS/BRD is the study of new and emerging diseases that occur in wild and cultured host populations. In many cases novel disease agents are initially unknown or poorly understood, but with the appropriate microbial and molecular expertise, the agent can be identified and tools developed for managing the disease.

Microbial flora exist within all living things and they have co-evolved in the wild with their hosts for centuries. Although they have traditionally been viewed only as undesirable agents of disease, in actuality they are an integral part of all biological systems, and disease is only one element of their impact. The definition of “normative” for pathogens in the wild is only beginning to be investigated, but it is clear that normal levels of microbial flora may contribute in a positive way to controlling host population levels, and thus to overall ecosystem balance. Therefore, disease control is not universally desirable and should only be considered where the impact of disease is out of balance due to unnatural causes. Typically this occurs whenever humans culture plants or animals at high density, facilitating disease transmission and amplification of pathogens to unbalanced levels. Additionally, human impacts such as pollution can render wild hosts more susceptible to disease. Research into defining the normative role of pathogens in maintaining ecosystem balance will lead to an integration of disease aspects into our understanding of ecosystem function.

Goal: Gain a deeper understanding of disease agents and processes and facilitate design of more effective control strategies that minimize the effects of disease in wild and cultured host populations where appropriate. Additionally, we need to maintain the expertise and flexibility to respond to new and emerging diseases as they occur.

Examples of the application of G&MT in the USGS in this area:

- Ongoing research on avian malaria in endangered Hawaiian birds is providing the only hope for conservation of this species. Development of new diagnostic tools and studies of host and parasite diversity relies on molecular tools.

- Researchers are using G&MT to address duck plague virus and the organisms that cause avian cholera and avian botulism. This involves development of novel PCR diagnostic methods for these pathogens.
- Molecular epidemiology of IHN virus disease outbreaks in Pacific salmon is revealing complex virus traffic patterns throughout large geographic regions.
- Transmission of virus between wild and cultured fish populations has been documented. Development of an effective DNA vaccine to prevent viral disease in cultured salmon populations has potential to greatly reduce the possibility of disease transmission to wild fish populations.
- Studies of the whirling disease parasite that has recently spread into wild trout of the intermountain west illustrate response to emerging new diseases.
- Recent studies involving brucellosis in bison and West Nile Virus in birds illustrate realizations of the potential threat of animal diseases to human health.
- Ongoing research on avian malaria in endangered Hawaiian birds is providing the only hope for conservation of this species. Development of new diagnostic tools and studies of host and parasite diversity relies on molecular tools.

◆ *Contaminants*

Effects of environmental pollutants on the health of fish and wildlife populations was thrust into the spotlight in the 1960's by the work of Rachel Carson, a research scientist with the U.S. Bureau of Fisheries. Today, the impact of contaminants on the environment continues to be a significant area of research that encompasses not only their detection in the environment, but the effects of passage and accumulation of contaminants in flora and fauna. The ability to detect fine-scale adverse impacts of contaminants on living things can only be accomplished with the use of molecular tools such as flow cytometry, cytological assays, and molecular tagging. Discovery of endocrine disruptors, DNA damage from petroleum and metal contamination and bioaccumulation, and the manifestation of heavy metal contamination in behavioral and physical anomalies serves to underscore the essential role that G&MT have in USGS/BRD research. Results derived from the use of these molecular tools provide important information on multiple scales to our assessment of metabolic, nutritional, and biochemical effects of stress in key ecosystems before and after contamination events.

Development of molecular and biochemical indicators of stress over the last decade underscores the utility of measuring molecular effects from both specific and non-specific environmental stressors. Nucleic acid (DNA and RNA) analyses are critical to the USGS/BRD's characterization and monitoring of sites which are naturally at risk of accumulating compounds harmful to short or long-term survival of animal and plant populations. Knowledge of DNA/RNA dynamics in bacterial populations and processes will aid in evaluating contaminated sites that have different contaminant loads or

remediation strategies. Biodegradation modeling requires the application of G&MT to determine the spatial and temporal dynamics of microbial communities and examine changes in population structure and contaminant sensitivities. Recent investigations into the heat shock response and the molecular actions of fish hormones under the influence of natural and artificial estrogenic compounds demonstrate the value of monitoring molecular indicators to improve our understanding of environmental stressors.

Goal: Develop cost-effective contaminant screening tools.

Examples of the application of G&MT in the USGS in this area:

- Flow cytometry was used to demonstrate a relationship between DNA damage and concentration of contaminants in lesser scaup in the Indiana Harbor Canal. If the reproductive potential of individuals is compromised by DNA damage or reduced by lower fertility, then the long term fitness of the population could be at risk due to genetic bottlenecking.
- Contaminant sensitivity analysis of DOI trust species highlights the effects of environmental contamination which may be covert in one generation if the effect is occurring at the level of germ cell formation or gamete development. Thus, G&MT can provide methods by which fine-scale physiological effects may be detected prior to catastrophic impacts on populations of trust species.
- White-faced ibis are used as an indicator species to track bioaccumulation and movement of heavy metals from mines in Nevada. This work illustrates that molecular and biochemical indicators can be more sensitive and show a more rapid response to stressors than most other biological measurements.

◆ *Invasive Species*

Genetics and molecular tools are critical to our understanding of the introduction of invasives. DNA-based point-of-origin studies can be used to locate the source population of intentionally or inadvertently introduced organisms. Comparisons of genetic diversity and patterns of variation can rigorously predict country of origin for novel or cryptic species. Studies of the origins and patterns of colonization and effects of both nonindigenous plant and animal species have been carried out with G&MT as an integral component of the work.

In addition to discovering point of origin for invasives, G&MT are useful for tracking the spread of invasives in new systems. Many colonizing species go through a period of rapid adaptation to their new environments. Genetics and molecular tools can be useful for investigating the mechanisms of rapid adaptation. Some invasive species are cryptic in their adopted environments and appear to mimic local species. DNA profiling and monitoring in potential impact areas will provide critical information for the recognition and management of such species.

The term “biocontrol” refers to the use of biological agents, such as pathogens, to control undesirable and invasive species. Although the use of biological control is to be approached with caution, in some cases these agents are extremely successful where other control strategies fail. Investigation of both the benefits and risks of potential biocontrol strategies are clearly within the USGS mission regarding invasive species. G&MT are important tools in both development of candidate biocontrol agents and in sensitive methods for tracking the agents and monitoring success and possible risks.

Goal: Take advantage of the sensitivity of genetic and molecular tools for evaluation and remediation of invasive species, and for the protection of native species by utilizing the ability to predict genetic effects of environmental and demographic changes caused by non-indigenous species.

Examples of the application of G&MT in the USGS in this area:

- Genetic characters are used to trace a species or population to a point of origin. This information is subsequently used to define potential impacts of the invader in the new environment based on its ecology in its location of origin as well as develop remediation and control measures needed to protect native species.
- The use of G&MT led to the testing of sterile males as a control measure for parasitic sea lamprey populations in the Great Lakes. Molecular tools are widely used for development and evaluation of biocontrol and physiological control measures for invasives.
- DNA studies of crab larvae from point source collections of ballast water contributions to U.S. ports showed direct lineage effects, dispersal patterns, and potential impacts for the invasion of European Green crabs (*Carcinus meanas*) into Pacific ports of the U.S. from Europe. Interestingly, green crabs collected in Woods Hole (not a commercial port) did not fit into the same lineage as green crabs found in San Francisco Bay. The Woods Hole crabs are speculated to be the result of releases from another source population as opposed to an invasion facilitated by ballast discharge from commercial vessels.
- Spread of aquatic invaders throughout the Great Lakes is facilitated by a network of commercial shipping operations which can carry organisms in ballast water. Identification of colonization pathways by natural or facilitated means would provide additional insight into the potential impacts of nonindigenous species and into strategies for prevention of future invasions.

◆ *Application of Science Information to Management*

Genetics and molecular tools are used to enhance our understanding of natural processes by providing a greater understanding of historical and contemporary population structures, community interactions, effects of exotics, and unique identities of endemic species. All of this information is applicable to development of decision support systems that assist with management and conservation of species, habitats, communities, and ecosystems. The

National Biological Information Infrastructure is an appropriate vehicle by which USGS/BRD can take a leadership role in maintaining baseline genetic databases for trust species. USGS/BRD is uniquely poised to take advantage of the opportunity to incorporate a truly multidisciplinary approach to natural resource stewardship. By incorporating all aspects of population biology, including genetic and molecular processes, into a framework of sound scientific investigations, USGS/BRD can produce relevant and useful information for DOI and other resource managers. A network of capable scientists in the field and at the lab bench with appropriate available resources and tools is essential for the development, application, and improvement of technologies critical to sound stewardship of our Nation's biological resources.

Recommendations to enhance USGS/BRD Science

1. G&MT should be an integral part of all strategic planning performed in USGS/BRD.
2. USGS should address G&MT directly at the Program Element level. Genetics is indispensable in the planning process to achieve many of the current USGS/BRD Program Element goals.
3. G&MT should be considered at the beginning of the project planning process rather than as an afterthought.
4. USGS leadership and managers should facilitate continued communication and interaction among USGS geneticists and molecular biologists.
5. Scientists and science managers should effectively communicate the capabilities and significance of G&MT to our leadership, colleagues, partners, and the scientific community.
6. Use of G&MT in USGS/BRD science is essential to the development of a truly integrated program. Genetics provides a suite of diverse and sophisticated tools that are complementary to many other approaches in biological research. In funding areas such as Species at Risk, an important part of the review process should include an evaluation of the potential application of G&MT for more effective science.
7. G&MT should be used in long term monitoring and assessment of fish, wildlife, and plant populations as well as in emergent studies.
8. Recognizing that there is currently no independent budget initiative for genetics, managers need to implement innovative solutions to provide the necessary funding for the genetics components of research.
9. In the budgeting process for new initiatives, adequate funding should be provided to meet genetic goals.
10. The USGS/BRD commitment to resolving complex biological issues/problems requires that the necessary genetics expertise be considered in center staffing plans.

APPENDIX 1. Areas of topical interest and expertise among USGS/BRD scientists using Genetics and Molecular Tools.

<i>USGS CENTER</i>	<i>Systematics & Conservation Units</i>	<i>Population Structure & Viability</i>	<i>Stock & Population Assessment</i>	<i>Disease</i>	<i>Contaminants</i>
Alaska Biological Science Center	X	X	X		
Forest and Rangeland Ecosystem Science Center	X	X	X		
Great Lakes Science Center	X	X	X		
Leetown Science Center	X	X	X	X	
Midcontinent Ecological Sciences Center	X	X			
National Wetlands Research Center		X			
National Wildlife Health Center				X	
Northern Prairie Wildlife Research Center		X			
Northern Rocky Mountain Science Center		X	X		
Pacific Islands Ecosystems Research Center	X	X		X	
Patuxent Wildlife Research Center		X			X
Upper Midwest Environmental Sciences Center					X
Western Fisheries Research Center	X		X	X	

APPENDIX 2: Areas of taxonomic expertise among USGS/BRD scientists using Genetics and Molecular Tools.

<i>USGS CENTER</i>	<i>Birds</i>	<i>Mammals</i>	<i>Herps</i>	<i>Fish & Aquatics</i>	<i>Plants</i>
Alaska Biological Science Center	X	X		X	X
Forest and Rangeland Ecosystem Science Center	X	X	X		
Great Lakes Science Center				X	
Leetown Science Center		X	X	X	
Midcontinent Ecological Sciences Center	X				X
National Wetlands Research Center					X
National Wildlife Health Center	X	X	X		
Northern Prairie Wildlife Research Center					X
Northern Rocky Mountain Science Center		X			
Pacific Islands Ecosystems Research Center	X				
Patuxent Wildlife Research Center	X				
Upper Midwest Environmental Sciences Center	X				
Western Fisheries Research Center		X		X	

APPENDIX 3: USGS/BRD Expertise in Genetic and Molecular Tools

Alaska Biological Science Center

1011 E. Tudor Road
Anchorage, AK 99516

Contacts: Jennifer Nielsen; 907-786-3670 (O), 907-786-3636 (F), jennifer_nielsen@usgs.gov
Sandra Talbot; 907-786-3683 (O), 907-786-3582 (Lab), 907-786-3636 (F), sandy_talbot@usgs.gov

Focus Areas: Phylogeography and population genetics structure of vertebrates and plants.
Genetic status of threatened and endangered species.
Delineation of conservation units.
Genetic composition of admixed vertebrate assemblages.

Forest and Rangeland Ecosystem Science Center

3200 SW Jefferson Way
Corvallis, OR 97331

Contact: Susan Haig; 541-750-7482 (O), 541-758-7761 (F), 541-750-7433 (L), susan_haig@usgs.gov

Focus Areas: Population structure in birds, mammals, and amphibians.
Definition of conservation units using molecular markers.
Pedigree analyses of wild and captive species.
Population viability analyses.

Great Lakes Science Center

1451 Green Road
Ann Arbor, Michigan 48105

Contact: Mary Burnham Curtis; 734-214-7242 (O), 734-994-8780 (F), mary_curtis@usgs.gov

Focus Areas: Population genetics and systematics: particularly with native Great Lakes fish.
Genetic stock identification: hatchery vs. wild fish, forensic analysis.
Evaluation of population structure of managed fish for use in pedigree analyses.

Leetown Science Center

1700 Leetown Road
Kearneysville, WV 25430

Contacts: Tim L. King; 304-724-4450 (O), 304-724-4451 (L), 304-724-4435 (F), tim_king@usgs.gov
Bane Schills; 304-724-4438 (O), 304-724-4435 (F), bane_schills@usgs.gov

Focus Areas: Population genetics, molecular systematics, definition of conservation units for at-risk fish and wildlife.
Gene marking to assess stocking programs and mark and recapture studies.
Study of pathogens and pathogenicity.
Ecology of bacterial assemblages.

Midcontinent Ecological Sciences Center

Department of Biological Sciences
University of Denver
Denver, CO 80208

Contact: Sara Oyler-McCance; (303) 871-7532 (O), (303) 871-3535 (L), email: soyler@du.edu

Focus Areas: Population genetics of vertebrates
Plant molecular systematics
Avian sexing techniques

National Wetlands Research Center

700 Cajundome Blvd.
Lafayette, LA 70506

Contacts: Ed Proffitt; 337-266-8509 (O), 337-266-8962 (F), ed_proffitt@usgs.gov
Sue Grace; 337-266-8518 (O), 337-266-8962 (F), sue_grace @usgs.gov

Focus Areas: Restoration and conservation genetics of plants.
Allozyme, DNA-AFLP, and DNA-RAPD analyses of populations.

National Wildlife Health Center

6006 Schroeder Road
Madison, WI 53711-6223

Contacts: Mark Wolcott; 608-270-2466 (O), 608-270-2415 (F), mark_wolcott@usgs.gov
Wallace Hansen; 608-270-2474 (O), 608-270-2415 (F), wallace_hansen@usgs.gov
Douglas Docherty; 608-270-2464 (O), 608-270-2415 (F), doug_docherty@usgs.gov
Tonie E. Rocke; 608-270-2451 (O), 608-270-2415 (F), tonie_rocke@usgs.gov

Focus Areas: Wildlife disease pathogen detection, identification, and characterization.
Detection, identification, and quantification of microbial pathogens in environmental samples.
Molecular epizootiology to understand ecology and distribution of wildlife diseases.
Endocrine growth factor patterns in amphibians.

Northern Prairie Wildlife Research Center

303 Gentry Hall
University of Missouri
Columbia, MO 65211

Contact: Esther Stroh; 573-882-2842 (O), 573-884-5133 (F), esther_schneider@usgs.gov

Focus Areas: Gene flow between native plant populations.
Genetic similarity/distance of native plant populations.

Northern Rocky Mountain Science Center

Glacier National Park
West Glacier, MT 59936

Contact: Kate Kendall; 406-888-7994 (O), 406-888-7990 (F), katherine_kendall@usgs.gov

Focus Areas: Non-invasive genetic sampling and microsatellite genotyping to estimate forest carnivore population density via mark-recapture techniques.
Use of sign surveys to monitor forest carnivore population trends from barbed wire hair traps, surveys for feces, and hair on rub trees.

Pacific Islands Ecosystems Research Center

Hawaii Volcanoes National Park, HI 96718

Contact: Susan Jarvi; 808-967-8119 x269 (O), 808-967-8545 (F), sue_jarvi@usgs.gov

Focus Areas: Avian major histocompatibility complex
Diversity of Pathogens
Molecular Diagnostics
Avian Population Genetics

Patuxent Wildlife Research Center

12100 Beech Forest Road
Laurel, MD 20708-4039

Contacts: George F. Gee; 301-497-5750 (O), 301-497-5675 (F), George_Gee@usgs.gov
Caldwell Hahn; 301-497-5653 (O), 301-497-5624 (F), caldwell_hahn@usgs.gov
Mark J. Melancon; 301-497-5710 (O), 301-497-5675 (F), mark_melancon@usgs.gov
Peter Albers; 301-497-5700 (O), 301-497-5675 (F), pete_albers@usgs.gov

Focus Areas: Effects of bottlenecks on diversity in small populations
Kinship and pedigree analysis in small populations.
Reproductive strategies to preserve and expand genetic diversity
Application of genetics techniques to brood parasites

Upper Midwest Environmental Sciences Center

2630 Fanta Reed Road
La Crosse, WI 54603

Contacts: Thomas W. Custer; 608-781-6375 (O), tom_w_custer@usgs.gov
Christine M. Custer; 608-781-6247 (O), christine_custer@usgs.gov

Focus Area: Flow cytometry as an indicator of genetic damage in wildlife.

Western Fisheries Research Center

6505 NE 65th St.
Seattle, WA 98115

Contacts: Gael Kurath; 206-526-6583 (O), 206-526-6654 (F), gael_kurath@usgs.gov
Aldo Palmisano; 206-526-6282 x278 (O), 206-526-6654 (F), aldo_palmisano@usgs.gov
Rusty Rodriguez; 206-526-6282 x335 (O), 206-526-6654 (F), rusty_rodriguez@usgs.gov
Jim Winton; 206-526-6282 x328 (O), 206-526-6654 (F), jim_winton@usgs.gov

Focus Areas: Diagnosis, epidemiology, pathogenesis and evolution of fish pathogens.
Control strategies including DNA vaccines for salmon pathogens.
Genetic markers for determination of sex, stock, and hybridization in salmon.
Biocontrol agents for reducing agrichemical use.