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Sense and Nonsense of genetic Studies on endangered Species (*)

by

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SUMMARY

Genetic diversity represents biodiversity at the population level and thus it is the basis for stability and adaptability of populations. Regarding endangered species, this factor, naturally, bears particular importance.

Anthropogenic influences on the biocoenoses often result in uncontrolled changes of genetic structures. To minimise or control, respectively, these uncontrolled influences is an essential task of genetics in view of management efforts for species protection.

The development of genetic indicator and monitoring systems as estimators of the ability to adaptation and thus to evolutionary progress seems to be an indispensable prerequesite of any future conservation efforts.

These systems will have to function as analytical and controlling tools in the scope of species protection. They are to facilitate the survey and supervision of genetic structures as a mirror image of long-term adaptability and thus survivability of endangered populations, hence enhancing the prospects for success of various management measures.

To identify appropriate marker systems, it requires some preconditions : first, we need biochemical or molecular traits. It would be an advantage if these traits can be observed even in non-invasive ways such as from e.g. hair or feathers. Moreover, a formal genetic analysis of complete families is an indispensable precondition to identify these traits as genetic markers. When the mode of inheritance has been made clear by genetic analysis, we should combine a set of markers beeing inherited biparenal as well as monoparental, allowing to study particular problems of species conservation. In addition, it would be helpful that several groups dealing with one and the same species should apply identical marker systems to make their results comparable.

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Introduction

Genes are the basic material of evolutionary development and also they serve as records of events occurred in the past. Conservation of species can be seen as conservation of the results of an evolutionary process manifested in the genetic structure of a population (LOESCHKE *et al.* 1994). In addition to that, conservation biology has not only to focus on the results of a previous development but also on the future aspect of evolutionary change under changing environmental conditions.

Genetics contributes to conservation biology in numerous ways. It provides the theory to understand and different tools to describe and evaluate genetic structures of populations. On this basis, genetic studies are an indispensable basis for studies on conservation of genetic ressources, but also on different components of physiology and ethology of an animal species. For endangered species, primarily the conservation of genetic ressources may stay in the focus of scientific interest.

Conservation of genetic resources serves various motives and objectives. Depending upon the selected goal and the available external conditions there is a huge number of methodical options. These have been explained and discussed in detail by various authors such as ZIEHE *et al.* (1989).

Genetic diversity is representative of the biodiversity at population level. It forms the basis for stability and adaptability of populations to recent as well as to future environmental conditions. Regarding endangered species, this factor, naturally, bears particular importance. As the basis of any evolutionary progress the preservation of genetic diversity does not only play a decisive role within the framework of species protection, but also within the framework of any anthropogenic impacts in natural populations and life communities (biocoenoses, see e.g. RISSER 1995).

Anthropogenic influences on the biocoenoses often result in uncontrolled changes of genetic diversity parameters. To minimise or control, respectively, these uncontrolled influences is an essential task of genetics in view of management measures for species protection. In this connection, a genetic monitoring is becoming compulsory, so that in the present project, based on molecular markers, a system of monitoring and indicators for quantification of genetic variation and differentiation, and thus for the assessment of genetic adaptability in populations of endangered species is to be developed, which both can serve as an estimation of the danger potential in wild populations and as a means of valuation of the success of management efforts.

Conceptual basis

We encounter biodiversity at various hierarchical levels. Such levels are for instance landscapes, ecosystems, species, populations, individuals or genes. In this context, the relationships between biodiversity and the functionality of ecosystems seem to be very complex naturally, acting in spatial and temporal dimensions. To explore the functional aspects of biological diversity presupposes on a regular scale the restriction to one hierarchical level as well as to one or few functions, to be in a position to break down in this way the complexity of connections into components which facilitate the formulation of examinable hypotheses of cause-effect relationships (see e.g. RISSER 1995).

As above mentioned, genetic diversity reflects the biodiversity at the levels of populations and individuals. Owing to its genetic structure a population is more or less adequately adapted to a specific environmental situation. Often, a spatial or temporal alteration of the environment (including the effects of anthropogenic impacts) means that the extent of the adaptation to this new situation is changing. In this case, genetic adaptability is gaining importance.

Recent projects are focussing on the question, as to how genetic studies may be integrated into any future conservation measures of endangered species like Black grouse (*Tetrao tetrix*). Genetic structures thus may serve as an indicator for long-term adaptability of a population in question and thus they may help to evaluate its status of threat. Moreover, genetic differentiation of populations will provide us informations about isolating effects or certain environmental (and thus selective) conditions.

The first objective of such a project consists in developing and applying molecular genetic marker systems for the purpose of assessing and monitoring genetic variation and differentiation parameters in populations of Black grouse (*Tetrao tetrix*). These marker systems are to be developed as analysis and control tools with special respect to measures of species protection, as well as to be applied in the field. In the time to come they are to facilitate the assessment and supervision of genetic structures as a mirror image of long-term adaptability and thus survivability of endangered populations, thus enhancing the prospects for success of management measures.

However, the identification of appropriate marker systems requires some important preconditions : first, we need biochemical or molecular traits. It would be an advantage if these traits can be observed even in non-invasive ways such as, in the case of birds, e.g. from feathers. Moreover, a formal genetic analysis of complete families is an indispensable precondition to identify these traits as genetic markers. When the mode of inheritance has been made clear by genetic analysis, we should combine a set of markers beeing inherited biparenal as well as monoparental, allowing to study particular problems of species conservation. In addition, it would be helpful that several groups dealing with one and the same species should apply identical marker systems to make their results comparable.

Conservation management

The management of endangered wild species in close-to-nature and likewise anthropogenic ecosystems is by tradition a central task of nature conservation. In addition to economic motivations mentioned in various connections the latter is essentially an ethic commitment – not least in regard to future generations.

Over the past few decades the idea of species protection experienced a changing from a largely static mode of consideration towards more dynamic concepts which do not solely refer to the individual species, but to their incorporation in ecosystems and development over time. Local adaptations and peculiarities are eventually merely intermittent stages of an evolution, which virtually always happen at the present moment. If elucidating this aspect, one readily recognises, that finally adaptation to a present environmental situation (and the local peculiarity of organisms being nothing else but this) can virtually not be the long-term objective of a protection strategy, but always only its basis. The objective of a dynamic protection concept can exclusively relate to the future environmental situation, thus being currently unknown. This, in turn, means, that eventually only the maintenance of adaptability of one or several populations to future environmental situations can be the objective of species protection, the foundation of which, in turn, being genetic diversity.

Identification of genetic markers

To estimate genetic diversity by routine tests, mostly biochemical-genetic marker systems have been applied in wildlife until now. However, their applicability to highly endangered mammalian species is much restricted, because of the fact that a sufficient amount of investigation material (blood, tissues) on the living animals can often not or not at all be procured without detrimentally affecting the animals.

A possible solution to this problem is to apply molecular-genetic marker systems, i.e. those systems based on the investigation of DNA. As compared to the traditionally used biochemical-genetic markers these appear to have some drawbacks, but considerable advantages at the same time. The latter regard mainly the possibility of developing marker systems which either cover vast parts of the genome or being largely specific for individual gene loci. Moreover, certain molecular methods of analysis have the advantage particularly in connection with the investigation of endangered faunal species to cope with very few amounts of investigation material, so that the investigation does not necessarily mean to affect the health or even kill the animal to be examined.

The identification of genetic markers is often only facilitated in front of this background, for it necessarily presupposes to examine complete families, with the relationships of which being precisely known, possibly through several generations.

Since numerous threatened faunal species can often be found to be bred in captivity in connection with reintroduction programmes, it often occurs that such known families exist.

But until now it has not been possible due to too invasive methods of investigation or at least because of missing acceptance to obtain investigation material from these individuals. This problem can, however, be solved by using molecular marker systems.

Biparentally inherited marker systems such as microsatellites may serve for studies on variation within and differentiation between populations. Identification of certain nuclear genes, in addition, may help to study particular problems of selective forces concerning certain gene loci.

On the other hand, presumably maternally inherited marker systems on the basis of mitochondrial (mt)DNA will help us to get more knowledge about differentiation processes and also migration phenomena.

Outlook

If we agree that genetic diversity is representative of the biodiversity at population level and thus the evolutionarily most relevant part of biodiversity, and if we also agree that anthropogenic influences on the biocoenoses often result in uncontrolled changes of genetic diversity parameters, it is an essential task of genetics in view of management measures for species protection to minimise or to control these influences.

This requires genetic monitoring as an essential part of any conservation concept of an endangered species such as the Black grouse (*Tetrao tetrix*). Such a genetic monitoring program is recommended to be an essential part of a quality management system, beenig also necessary for any conservation programme. However, neither quality management nor genetic monitoring are well integrated into the existing conservation concepts.

Thus, the development of genetic indicator and monitoring systems as predictors of a long-term survivability and the ability to evolutionary progress seems to be an indispensable prerequesite of any future conservation efforts. These are to function as analytical and controlling tools in the scope of management measures for species protection. They are to facilitate the survey and supervision of genetic structures as a mirror image of long-term adaptability and thus survivability of endangered populations, hence enhancing the prospects for success of various management measures.

REFERENCES

LOESCHKE, V.; TOMIUK, J.; JAIN, S.K. 1994. Introductory remarks : Genetics and conservation biology. In : LOESCHKE, V.; TOMIUK, J.; JAIN, S.K. (editors). Conservation Genetics, Birkhäuser verlag, Basel, Boston, Berlin, 3-8.

RISSER, P.G. 1995. Biodiversity and Ecosystem Function. *Conservation Biology* **9**, 742-746.

ZIEHE, M.; GREGORIUS, H.-R.; GLOCK, H.; HATTEMER, H.H.; HERZOG, S. 1989. Gene resources and gene conservation in forest trees : General concepts. In : Scholz, F.; Gregorius, H.-R.; Rudin, D. (editors). Genetic Effects of Air Pollutants in Forest Tree Populations. Springer-Verlag : Berlin, Heidelberg, New York, 173-185.

ZUSAMMENFASSUNG : Sinn und Unsinn genetischer Untersuchungen gefährdeter Arten

Genetische Diversität repräsentiert die Biodiversität auf der Ebene der Population und bildet damit die Grundlage der Stabilität und Anpassungsfähigkeit von Populationen. Im Hinblick auf gefährdete Arten hat diese Tatsache naturgemäss eine besondere Bedeutung.

Anthropogene Einflüsse auf Biozönosen bewirken oftmals unkontrollierte Veränderungen genetischer Strukturen. Es ist eine wichtige Aufgabe von Managementmassnahmen im Rahmen des Artenschutzes, diese Veränderungen zu minimieren bzw. zumindest kontrolliert zu gestalten.

Die Entwicklung von genetischen Inikator- und Monitoringsystemen zur Einschätzung der Fähigkeit zur Anpassung und damit zu evolotiver Fortentwicklung ist somit eine unerlässliche Voraussetzung aller künftiger Schutzmassnahmen.

Derartigen Systemen wird in Zukunft eine grosse Bedeutung als Analyse- und Kontrollelemente im Artenschutz zukommen. Ihre wesentliche Aufgabe wird darin bestehen, genetische Strukturen als Spiegelbild langfristiger Anpassungsfähigkeit und damit Überlebensfähigkeit gefährdeter Populationen zu erforschen und zu überwachen und auf diese Weise eine Möglichkeit zur pro- und retrospektiven Erfolgsbeurteilung von Artenschutzmassnahmen zu schaffen.

Die Identifikation geeigneter Markersysteme hat verschiedene Voraussetzungen : zunächst bedarf es biochemischer oder molekularer Merkmale. Es ist von Vorteil, wenn diese Merkmale mit nicht-invasiven Methoden beobachtbar sind, also etwa durch Verwendung von Haaren oder Federn. Darüberhinaus ist eine formale genetische Analyse vollständiger Familien eine unabdingabre Voraussetzung, um solche Merkmale als genetische marker zu identifizieren. Wenn der Vererbungsmodus durch genetische Analyse geklärt ist, sollten Marker so kombiniert werden, dass mittels bi- oder monoparental vererbter Marker auch spezifische Fragestellungen unstersucht werden können. Schliesslich ist es von grossem Vorteil, wenn verscheidene Arbeitsgruppen, welche an ein und derselben Art arbeiten, auch auf ein identisches Set genetischer Marker zurückgreifen, um ihre Ergebnisse vergleichbar zu halten.

Schlüsselwörter: Gefährdete Arten, Genetik, molekulare Marker, Biodiversität, Schutzmanagement

RESUME : Sens et non sens des études génétiques sur les espèces menacées.

La diversité génétique détermine la diversité biologique au niveau populationnel et est dès lors le fondement de la stabilité et de l'adaptabilité des populations. S'agissant des espèces menacées, ce facteur est évidemment de première importance.

Les influences anthropiques sur les biocénoses conduisent souvent à des changements dramatiques des structures génétiques. Etudier ces influences incontrôlées et les minimiser est une tâche essentielle des généticiens dans la perspective d'une gestion des efforts de conservation des espèces.

La mise au point de systèmes d'indicateurs et de surveillance génétiques en tant qu'outils d'évaluation des aptitudes adaptatives et donc, des processus évolutionnaires en cours, s'impose comme un pré requis de tout effort futur en matière de conservation. Ces systèmes pourront faciliter l'analyse en routine et le contrôle des structures génétiques — véritables images en miroir de l'adaptabilité des populations — et permettront de mieux cibler les mesures de gestion les plus appropriées.

Identifier des systèmes appropriés de marqueurs suppose deux conditions. En premier lieu, on a besoin de traits biochimiques ou moléculaires. Il serait intéressant que ces traits puissent être observés et identifiés de manière non invasive, par exemple à partir de cheveux, poils, ou plumes. Ensuite, il est indispensable de réaliser des études génétiques formelles de familles complètes, si on désire être à même d'identifier ces traits comme marqueurs génétiques. Lorsque le processus de transmission de ces traits aura été éclairci par une telle analyse génétique, il conviendra d'utiliser un jeu de marqueurs hérités tant par voie biparentale que par voie uniparentale, permettant ainsi d'étudier des problèmes particuliers de conservation des espèces. De plus, il conviendrait que les équipes travaillant sur une seule et même espèce utilisent les mêmes jeux de marqueurs, de façon que leurs résultats soient comparables.

Mots-clés : Espèces menacées, génétique, marqueurs moléculaires, biodiversité, gestion de la conservation.

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