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АЗИЯДАГЫ ЖЫРТКЫЧ КУШТАРДЫН ГЕНЕТИКАЛЫК ЖАНА ГЕНОМИКАЛЫК ИЗИЛДӨӨЛӨРҮНҮН АЗЫРКЫ АБАЛЫ

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СОВРЕМЕННАЯ СИТУАЦИЯ С ГЕНЕТИЧЕСКИМИ И ГЕНОМНЫМИ ИССЛЕДОВАНИЯМИ ХИЩНЫХ ПТИЦ В АЗИИ

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CURRENT SITUATION OF GENETIC AND GENOMIC RESEARCH OF BIRDS OF PREY IN ASIA

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Abstract: Among avian species, birds of prey are often studied because of their ecological significance. There has been an increase in genetic and genomic studies of wildlife to better understand their evolution, taxonomy, and to inform conservation strategies, especially for endangered species. Here, a comprehensive review of published studies on such genetic and genomic research of birds of prey was conducted, with a focus on Asian populations/species. Investigation of temporal trends and methods employed revealed an increase in the number of studies and advances in sequencing technology applied. However, there were considerably fewer studies using nuclear DNA and whole genomes in Asia. Implications for future developments in academic research and conservation are also summarized, based on these results.

Keywords: birds of prey, genetics, genomics, Asia, literature review.

Ключевые слова: хищные птицы, генетика, геномика, Азия, обзор литературы.

Негизги сөздөр: жырткыч канаттуулар, генетика, геномика, Азия, адабияттарды кароо.

Research in the field of genetics and genomics has revealed the importance of assessing genetic diversity and differentiation for evaluating population viability, defining units of conservation, identifying signals of hybridization, and to plan appropriate conservation management strategies [4]. This is especially the case for endangered populations, which are more likely to experience to inbreeding and genetic drift, which have significant consequences on fitness and adaptive potential [3].

Birds of prey, or raptors, are a group of birds including eagles, hawks, kites, ospreys, buzzards, harriers, vultures, falcons, caracaras, secretarybirds and owls. Many birds of prey serve ecologically important roles as predators and indicator species of terrestrial (and some aquatic) ecosystems [2]. Yet, a large proportion of them are also classified as endangered, indicating the necessity of conservation genetic/genomic studies [5]. However, a recent review found that population genetic studies have only been conducted in about one fourth of species under the threat of extinction [5]. The same study also showed a lack of studies in the Southern hemisphere.

Here, we conducted a comprehensive review of raptor studies in the fields of conservation-, ecological-, evolutionary-, and forensic genetics, in addition to population genetics. Temporal trends in the number of published studies, along with the types of methodologies employed were evaluated, especially in Asia, to investigate whether the lack of studies is limited to countries in the southern hemisphere. Lastly, we discuss possible directions and developments in this field.

MATERIAL AND METHODOLOGY

The literature survey was conducted through the Web of Science Zoological Record database, using keywords to specify the types of research and taxa studied. Specific keywords used in the query are shown in Figure 1. To restrict the taxa, names of 111 extant genera listed in the orders Accipitriformes (71 genera), Catharthiformes (5 genera), Falconiformes (10 genera), and Strigiformes (25 genera) were used. The nomenclature followed The Clements Checklist of Birds of the World [1]. The results from this search were then filtered manually, by removing unrelated studies, such as studies on non-raptor species, avian pathogens, quantitative genetic studies focusing on phenotypes, and studies mentioning but not employing genetics/genomics. The same procedure was repeated for Asian studies, by including the names of 57 countries/territories, and abstract regional terms: Asia, Far East, South Asia, Southeast Asia, Central Asia, Caucasus, and Middle East. The filtered studies from across the world and Asia were then categorized by the types of genes studied: nuclear markers (short sequences such as microsatellites, allozymes, etc.), mitochondrial DNA (mtDNA), combination of nuclear markers and mtDNA, functional genes, combination of non-functional and functional genes, sex identification markers, whole genomes, chromosome data. The year published was also noted. In addition, types of analyses (phylogenetics/taxonomy, genetic diversity, genetic structure, functional genetics, population monitoring, species/sex identification, marker development/mtDNA sequence generation, demographic history) and sampling regions were identified for studies from Asia.

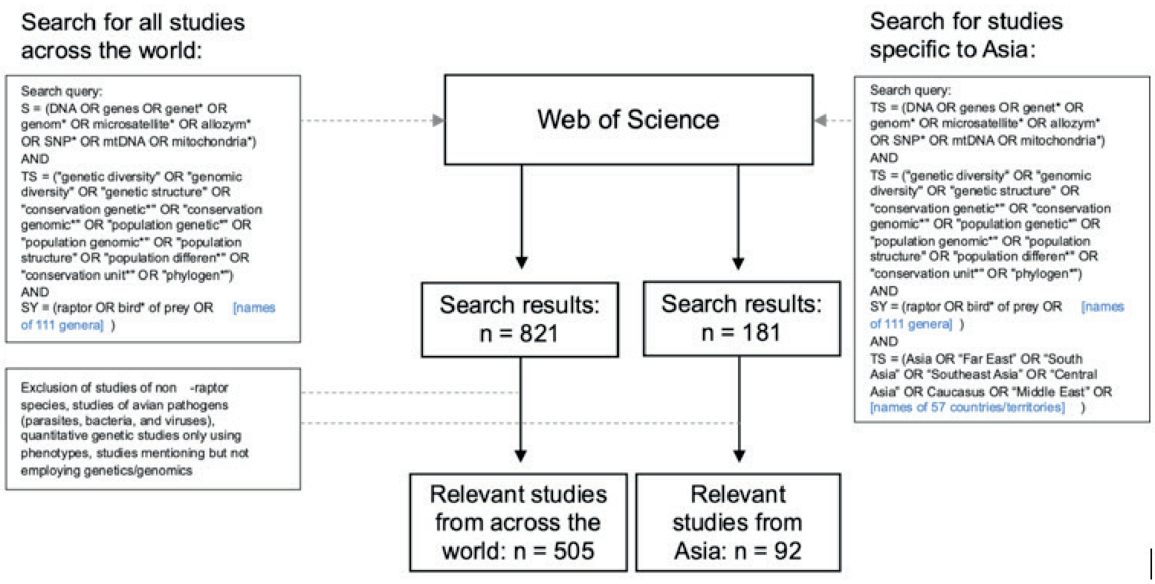

Figure 1. Flow of literature search and screening process to find relevant studies about raptor genetics/ genomics from the world and in Asia.

RESULTS

Globally, the number of genetic/genomic studies of raptor species increased over the past 35 years. Studies using mtDNA and short nuclear sequences especially increased until the 2010s, after which functional genetic studies also began to increase. In the most recent 6 years, short nuclear sequence analyses decreased, while whole genome analyses increased. In Asia, the number of genetic/genomic studies also increased. However, the number of studies using nuclear DNA and whole genomes was significantly fewer compared to the global sum, despite of the large landmass and numbers of species inhabiting Asia. Functional genetic studies were also scant.

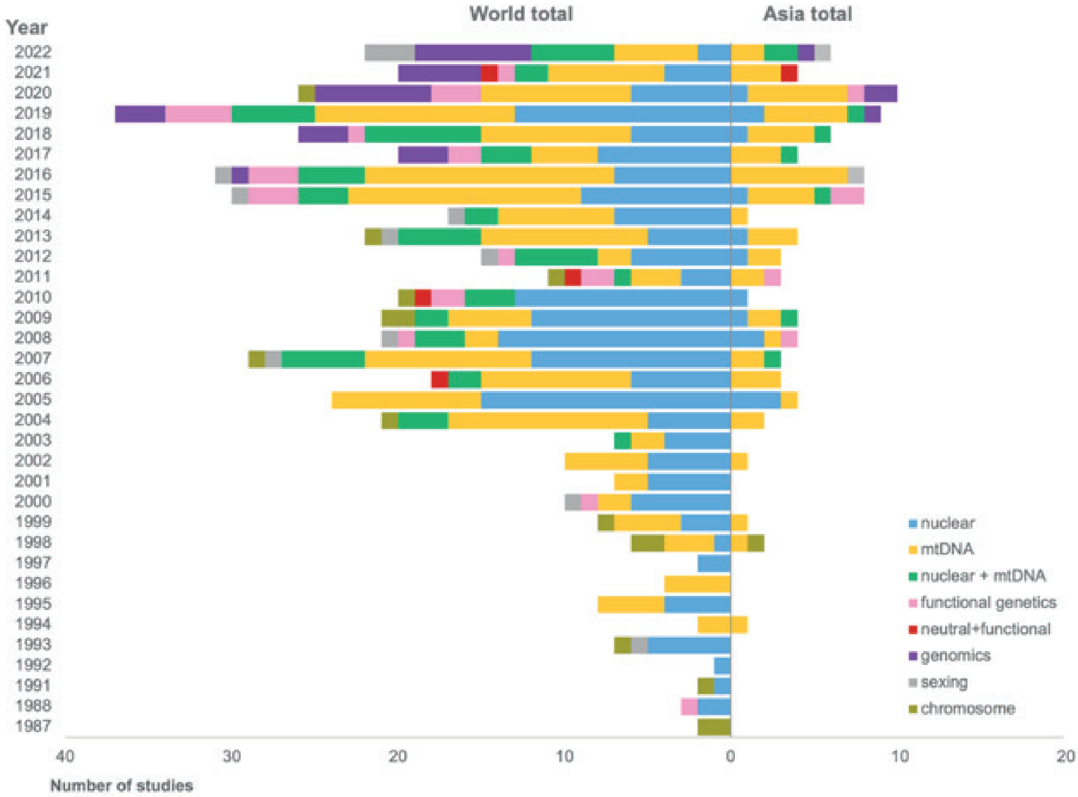

Figure 2. Number of genetic/genomic studies in raptors from across the world and Asia

Of the studies focusing on Asian species/populations of raptors, most studies focused on phylogenetics (e.g. [6]) and taxonomy (e.g. [8]) and genetic diversity (e.g. [9]). Genetic structure analyses also accounted for a large proportion of studies, followed by method papers (e.g. microsatellite marker development [7], mtDNA sequence generation [13]) and studies on demographic history (e.g. [11]). Few studies focused on species/sex identification (e.g. [15]), functional genetics (e.g. [12]), and population monitoring (e.g. [10]).

The majority of studies using Asian samples were used in a global context (26%). The rest of the studies were primarily from Japan (17%) and China (13%), followed by Russia (8%), India (6%), Kazakhstan (5%), South Korea (4%), the Philippines (4%), and Mongolia (3%). The rest of the countries, mostly in Southeast and Western Asia had relatively fewer number of studies (1~2%).

An example of a Japanese study conducted by the authors highlights the potential of genetic studies in the context of conservation of raptors threatened by extinction [9]. Figure 3, adapted from this study, shows the genetic diversity and population structure of wild and captive populations of the endangered Japanese golden eagle (Aquila chrysaetos japonica) using microsatellite markers. The lack of differences in genetic diversity indices and small genetic distances imply that captive individuals retain the diversity of the wild population, and belong to the same gene pool. Thus, it is suggested that there are likely no genetic risks, such as inbreeding, outbreeding, and genetic disturbance, associated with releasing captive individuals to reinforce wild populations.

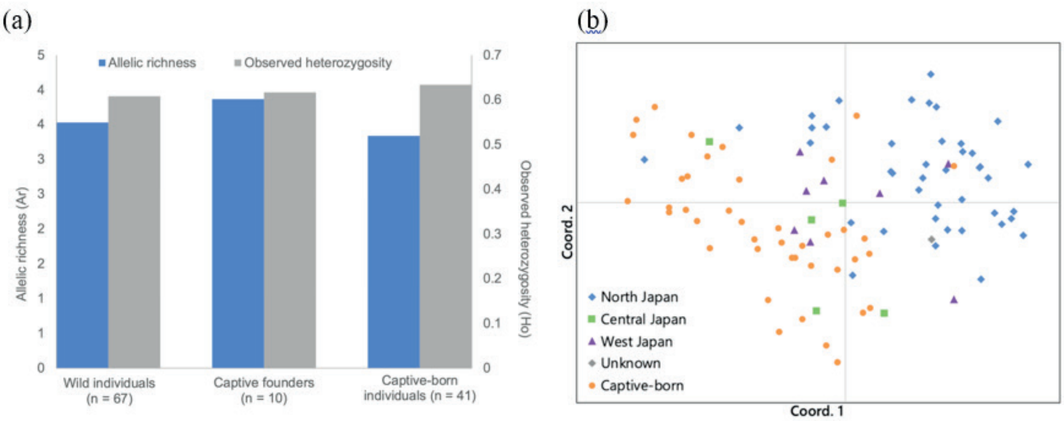

Figure 3. (a) Comparison of genetic diversity between wild and captive Japanese golden eagles, as shown by microsatellite allelic richness and observed heterozygosity. (b) Principal coordinate analysis plot based on genetic distances calculated using microsatellite genotypes of wild and captive Japanese golden eagles. (Figures adapted from [9]).

CONCLUSIONS

Our review of literature highlights an increase of the number of genetic and genomic studies in birds of prey across the world and in Asia. However, while the global trend is shifting toward whole genome studies, many studies from Asia still relied primarily on mtDNA. Although these techniques are useful in population and conservation genetics, advanced genomic analyses are allowing for estimation of high-resolution demographic histories and extinction risks, which are extremely beneficial for deepening our understanding of the evolution of populations, as well as improving conservation management strategies [14]. Given that Asia is a large continent with high diversity of bird species, it is likely that the genetics/genomics of many endangered species are yet to be studied. From these results, we suggest increased efforts be made in the field of genomics in Asian birds of prey, especially for endangered species.

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РАДИОЭКОЛОГИЧЕСКАЯ ОЦЕНКА КАДЖИ-САЙСКОЙ УРАНОВОЙ ПРИРОДНО-ТЕХНОГЕННОЙ ПРОВИНЦИИ

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