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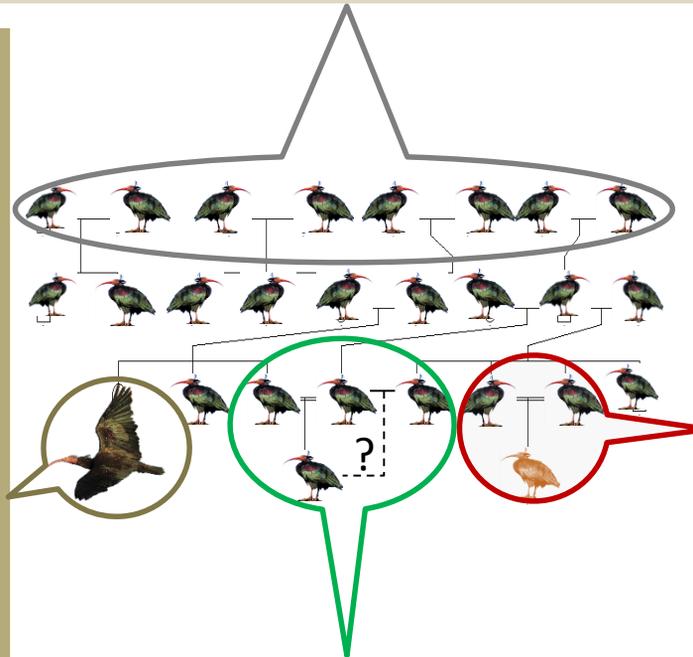
In captive breeding, pedigrees are typically used to manage **Genetic Diversity**, one of the key elements that guarantees long-term healthy populations. However, **pedigrees** are often incomplete and assumptions have to be made on pairwise relatedness or individuals might even need to be excluded from breeding. In recent years we have seen an increased use of genetic analysis to fill **pedigree "gaps"**, resulting in less assumptions and more individuals to breed with. Alongside, genetics is used to estimate the relative amount of genetic diversity captured within breeding programs when compared to wild populations, or even to study the role of specific genes in observed health issues, behaviours and morphologies. As such, one might question whether **DNA is coming to the rescue?**

Founders

As **high quality resources** are often needed to reach certain standards, the quality of **founders** is a key to success in conservation breeding. But what makes a good founder? Taxonomist would argue all founders should belong to the same **species**, which for some species is hard to evaluate outside their natural range. Comparing the genetic signature of founders vs. their wild counterparts, solves such problematic identifications. Furthermore, the quality of a founder depends on its **relatedness** to all other founders. It is assumed that all founders are unrelated, but defining the genetic relatedness between them might proof differently, which affects breeding recommendations.

Reintroductions

have become part of several EEPs. It remains challenging to monitor the success of such initiatives. While individuals might lose their tags, they never lose their unique genetic signature. They even pass it on to the next generation. As such, genetic screenings provide insights in e.g. which **released** individuals contribute most. Furthermore, genetics can be used to select the most appropriate candidates for reintroduction, those that **restore** or **complement** the wild population without disturbing the EEPs potential **back-up role**.



Parentage

In multi-male groups, **paternity** of new-borns is often unknown. A small set of highly variable DNA markers can be used to resolve those paternities.

Health & Genetics

Small populations are prone to suffer from **inbreeding**, which typically affects **fertility**. Also, random processes reshape small populations more severely, which might result in atypical phenotypes or increased prevalence of **diseases**. Patterns are species specific but, in the end, all affect the **long-term viability** of the populations under our (intensive) care. Genetic screenings can pinpoint genetic regions affecting **health** (eg. inheritable diseases).

Genetic analysis can improve ex-situ species management and as such conservation. If your interested in what might be in it for the program you manage, please contact us or our colleague geneticists e.g. via mail, at the **Molecular Genetics Q&A sessions** (Thursday morning or Friday evening) or during the breaks.

The first step to efficiently incorporate genetic analysis in your pedigree and population management, is to collect and store biological samples (blood, serum, tissue...). The **EAZA biobank** aims to facilitate sample storage for all EEPs. For more information please attend the plenary talk or read the article in ZooQuaria (Autumn 2016).