News & views

Figure 1 | A yellow-breasted bunting (*Emberiza aureola*). This species is highly threatened with extinction, mainly owing to illegal hunting.

Conservation

Convictions show scale of wildlife hunting in China

David P. Edwards

An analysis of convictions reveals that around one-fifth of China's terrestrial vertebrate species were illegally hunted over a six-year period. Improved efforts to reduce such crimes are needed to control this threat to biodiversity. **See p.100**

The illegal harvest and trade in wildlife is a problem on a global scale that is driving many species towards extinction[1,2]. Detailed records of legal international trade of wildlife to supply pets and products, such as those under the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES), point towards a high number of species traded, often between major exporter and importer nations[3]. What is lacking is a coordinated, spatially explicit assessment of the diversity of species in illegal trade in individual nations. On page 100, Liang *et al.*[4] present a landmark study quantifying the severity of illegal wildlife hunting in China. The country is a centre of high biodiversity (seventh globally for vertebrates[5]), has strong domestic demand for wildlife products and had a fast-growing economy during the time frame studied.

Many individual studies have been carried out in local markets of wild-animal meat (bushmeat), particularly in Africa, or key bird markets, especially in Indonesia, to identify species in legal and illegal national trade. The information generated has been collated in International Union for Conservation of Nature (IUCN) Red List assessments to determine species' extinction risk, and in turn, used to generate an understanding of the global hotspots of diversity in trade[6–8]. It has been much harder to quantify the extent of illegal trade at scales within national boundaries and to discern the geographical patterns and socio-economic drivers of illegal hunting.

Liang and colleagues benefited from the publication in OpenLaw (a nationwide record of criminal trials in China) of around 9,200 wildlife-related court convictions, relating to more than 3 million animals hunted between January 2014 and March 2020. The authors' analysis makes for uncomfortable and worrying reading from a conservation perspective, given that it unearths illegal domestic hunting in China on a vast scale. The authors' headline finding is that 673 species — equating to 21% of all Chinese terrestrial amphibians, birds, mammals and reptiles — were illegally hunted, mostly for commercial use (73% of convictions) and these incidents were concentrated in the eastern and central prefectures. Convictions included those for

hunting of birds such as the yellow-breasted bunting (*Emberiza aureola*; Fig. 1), which is a heavily targeted species.

The illegally hunted species included 25% of the 363 species of terrestrial vertebrates in China that are threatened with extinction (as assessed by the IUCN Red List) and more than 20% of vertebrates in the IUCN's near-threatened category. For mammals and reptiles, the percentage of threatened and near-threatened species in trade was substantially higher than the percentage of traded species that are not of conservation concern (IUCN least concern category), underscoring the observation that illegal hunting can be a driver of extinction risk[1,2].

Although the number of species affected are important, so too is understanding how the evolutionary tree is affected by illegal hunting of wildlife. By constructing evolutionary trees for each taxon that included all Chinese species and then marking these phylogenies with the species lineages associated with at least one court verdict, the authors revealed two key points. First, trade in China is widely distributed across the tree of life, with 80% of the nation's 45 orders of taxa affected. Second, there was a strong phylogenetic signal of illegal hunting especially in mammals and reptiles, indicating that hunting was particularly focused on certain families.

It is widely acknowledged that not all illegal hunting activity will be detected and result in arrest and conviction, owing to the difficulty in detecting crimes and identifying the species involved. Indeed, the authors point to field evidence that detected crimes might represent less than 1% of all such incidents. To quantify the degree of error that undersampling of the true number of crimes generates in the estimated number of species and the identity of those species, the authors applied two approaches that are more commonly used in research that quantifies the effects of land-use change on biodiversity – a scenario in which undersampling is also probable because of the sheer spatial scale of deforestation and degradation.

First, Liang and colleagues used the method of sample-based extrapolation to project how the 'accumulation curve' of species that were illegally hunted, based on the number of court verdicts, would change if more court verdicts had been made. The expectation is that a rise in the number of verdicts (increased sampling efficiency) would increase the number of species detected. Assuming that 10% of incidents result in conviction, the authors estimate that at least 866 vertebrate species (28% of China's vertebrate species) were hunted illegally during the six-year study period, pointing to 193 overlooked species. These 866 species include 39% of China's birds, 22% of mammals and 19% of reptiles.

Second, given the strong phylogenetic signal in illegal hunting, Liang and colleagues

used the method of phylogenetic logistic regression to predict ecological traits that correlate with whether a species is hunted or not. Among other findings, they discovered that species with larger distributions and body mass tended to be more affected by illegal hunting, which is a conclusion supported by previous global-scale assessments[6,9]. The authors' approach of using a best-fitting model of key ecological traits and phylogenetic relatedness identified that 781 species were not mentioned in court verdicts but have a high likelihood of being hunted. These include 90 species classified by the IUCN as being globally threatened.

Taken together, this evidence indicates that it is highly probable that a substantial number of illegally hunted species are yet to come under the attention of law enforcement. Liang and colleagues' list of species with a high likelihood of being hunted is a crucial conservation resource because it can guide authorities towards monitoring these potentially overlooked species. So too is the fact that only 5% of convictions accounted for 90% of the individual animals taken – focused enforcement and strict penalties for the most egregious perpetrators could help to reduce the volume and diversity of illegally hunted species for commerce.

Moving forwards, I predict that the analysis of hunting-related convictions and the use of underpinning modelling approaches, as demonstrated by Liang and colleagues, will

provide the blueprint from which to quantify the severity of detected and overlooked hunting crimes in other hotspots of national-level trade. Thereafter, as the authors affirm, we must quantify the degree to which illegal hunting reduces vertebrate populations – of both imperilled species and those considered to be (formerly) common. Then we should examine how the consequences of this affects aspects of ecosystem function, such as crop pollination (especially by bats), pest predation and maintenance of forest carbon stocks through seed dispersal.

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Genetics

Master regulator of a mosquito X chromosome

Maggie P. Lauria Sneideman & Victoria H. Meller

In organisms with X and Y chromosomes, gene expression must be equalized between the sexes. A protein that causes upregulation of gene expression of the X chromosome in male mosquitoes has been discovered. **See p.175**

In organisms that have X and Y sex chromosomes, females have two X chromosomes but males have only one. The first and most essential aspect of sexual development in such organisms is the adjustment of X-chromosome gene expression – a process called dosage compensation – to ensure similar expression levels in both sexes. Dosage compensation is remarkable not only because it modulates hundreds of genes, of which the only common feature is residence on the X chromosome, but also because of the diversity of mechanisms used. On page 175, Kalita *et al.*[1] identify

a key regulator of dosage compensation in the malaria-carrying mosquito *Anopheles gambiae*.

Sex chromosomes evolve rapidly, and dosage compensation has arisen independently in each lineage of organisms[2]. Only a few examples of compensation are well understood[3]: mammalian females inactivate expression of one of their two X chromosomes; hermaphrodites of the roundworm *Caenorhabditis elegans* downregulate expression of both of their two X chromosomes; and males of the fruit fly *Drosophila melanogaster* double the amount of expression from their single X chromosome.