**Table S1**. Number of times toxic substances (grouped in seven classes) were tested for their occurrence in 48 Griffon vultures affected by poisoning from 2000 to 2020 in the central Apennines. The percentage of vultures tested for each class of substance is also given.

|  |  |  |
| --- | --- | --- |
| **Active substance** | **Times tested** | **% Birds tested** |
| Aldicarb | 40 | 83 |
| Carbaryl | 43 | 90 |
| Carbofuran | 42 | 88 |
| Methiocarb | 41 | 85 |
| Methomyl | 8 | 17 |
| **Carbamates** | **174** | **92** |
| Arsenic | 1 | 2 |
| Zinc phosphide | 11 | 23 |
| **Inorganic compounds** | **12** | **23** |
| Metaldehyde | 1 | 2 |
| **Molluscicides** | **1** |  **2** |
| Aldrin | 14 | 29 |
| Dieldrin | 13 | 27 |
| Endosulfan (alpha) | 25 | 52 |
| Endosulfan (alpha +beta) | 12 | 25 |
| Endosulfan (beta) | 21 | 44 |
| Hexachlorobenzene | 14 | 29 |
| HCH (alpha) | 14 | 29 |
| HCH (beta) | 14 | 29 |
| Heptachlor | 14 | 29 |
| Heptachlor Epoxide | 24 | 50 |
| Lindane | 14 | 29 |
| Methoxychlor | 24 | 50 |
| Mirex | 24 | 50 |
| O,P-DDD | 24 | 50 |
| O,P-DDE | 14 | 29 |
| O,P-DDT | 24 | 50 |
| P,P-DDD | 24 | 50 |
| P,P-DDE | 19 | 40 |
| P,P-DDT | 24 | 50 |
| **Organochlorines** | **356** | **54** |
| Azinphos ethyl | 24 | 50 |
| Azinphos methyl | 24 | 50 |
| Chlorpyriphos ethyl | 6 | 13 |
| Chlorpyriphos methyl | 6 | 13 |
| Diazinon | 25 | 52 |
| Dimethoate | 14 | 29 |
| Fenthion | 24 | 50 |
| Malathion | 16 | 33 |
| Mevinphos (Phosdrin) | 24 | 50 |
| Parathion ethyl | 25 | 52 |
| Parathion methyl | 25 | 52 |
| Phorate | 25 | 52 |
| Ronnel | 13 | 27 |
| **Organophosphates** | **251** | **52** |
| Coumarin | 3 | 6 |
| Strychnine | 20 | 42 |
| **Plant Toxins** | **23** | **44** |
| Crimidine | 1 | 2 |
| Brodifacoum | 3 | 6 |
| Bromadiolone | 3 | 6 |
| Coumachlor | 3 | 6 |
| Coumatetralyl | 3 | 6 |
| Difenacoum | 3 | 6 |
| Warfarin | 3 | 6 |
| **Rodenticides (anticoagulants or not)** | **19** | **8** |

**Supporting information 2.** Description of the model used to estimate the annual variation in mortality according to population size.

Annual mortality is the ratio of individuals found dead over the number of individuals in the population, but the actual population size was unknown to us. We therefore assumed that population size in year *t* (*Nt*) was proportional to the number of breeding pairs in the same year (*Bt*):

*Nt = kBt*.

We then modelled the temporal variation in mortality of the population with a negative binomial regression model with a log link function:

ln(E(*Dt*/ *kBt*)) = b0 + b1 × year

where *Dt* denotes the number of individuals found dead in each year, E is the expected value, and b0 and b1 are the intercept and the slope of the negative binomial regression.

This model can be re-written as:

ln(E(*Dt*)) = b0 + b1 × year + ln(*k*) + ln(*Bt*)

and posing d0 = b0 + ln(*k*), we have

ln(E(*Dt*)) = d0 + b1 × year + ln(*Bt*)

This latter equation shows that a negative binomial regression model where the log-number of breeding pairs is entered as an offset is able to model annual variation in mortality.

**Supporting information 3.** Mathematical description of the model used to estimate within-year variation in mortality and the related R code.

Harmonic analysis was used to test for within-year variation in mortality. To do so, we first converted months into angles (March = 90°, June =180°, September = 270°, December = 360°) and then built a GLMM model whereby the number of individuals found dead in each month is the response variable, while the sines and cosines of the angles corresponding to the months, and their interaction are the predictors. The GLMM model assumed a negative binomial distribution of the data and included the year as a random grouping factor. Preliminary analyses also showed that the optimal random structure for this model included sine as a random slope within year. This procedure can be mathematically described as follows:

 *= i-th month of each year*

 *= number of death vultures in the i-th month of the j-th year*

 *and*

The R code used for the GLMM analysis was:

Model1 <- glmmTMB (y ~ sin\*cos + (1+sin|year), data=data, family="nbinom2")