

Early Description of the Black Vulture on the American Continent

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The biology of the Black Vulture (*Coragyps atratus*) has been well documented (e.g. Stewart 1974, McHargue 1981, Rabenold 1986), although recent authors have not reported early records of this bird on the American continent. An interesting account of the Black Vulture was written by Gonzalo Fernández de Oviedo y Valdés (a notorious official chronologist of the Spanish conquest of America) in "Summary of the Natural History of the Indies" (1526, Volume I, Chapter XXXIX, Toledo, Spain). A complete revision of this work was published by Avalle-Arce (1963), which enabled us to document what appears to be the first published mention of the Black Vulture from the New World. The textual translation of the chapter on the Black Vulture, which is entitled "Fragrant Chickens" is as follows: "There are many Spanish chickens here and they increase in number because they do not allow their eggs to be removed from under their wings; these have originated from chickens brought to the Americas [from Spain]. Other than these, there are some fierce chickens, big as turkeys, black in the head and part of the neck with some dark gray, although not as dark as the rest of them, and the less dark areas are not the plumage, but the hide. Their meat is bad and tastes awful, and [they] are very voracious and eat much filth, dead Indians, and animals. But they smell like almizcle [an animal

secretion used in certain cosmetics and perfumes] and very well, while they are alive. After they are killed, they lose their odor and are good for nothing, except the feathers are used for darts and arrows. They can withstand a great blow, and a crossbow must be powerful to kill one if it is not hit in the head or one of its wings broken. They are very inopportune and like to be in or near town to eat filth."

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Can Passerines Synthesize Vitamin C?

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L-gulonolactone oxidase (GLO) is an enzyme essential for the synthesis of vitamin C (ascorbic acid) that has been lost in several mammalian and avian lineages. Among mammals, the enzyme is present in

all major lineages except bats (Chatterjee 1973; Birney et al. 1976, 1980; Jenness et al. 1980), anthropoid primates (Pollock and Mullin 1987), and guinea pigs (Chatterjee 1973). In mammals, the presence of GLO seems to be a phylogenetically conservative trait that is lost rarely and is unlikely to be recovered once lost

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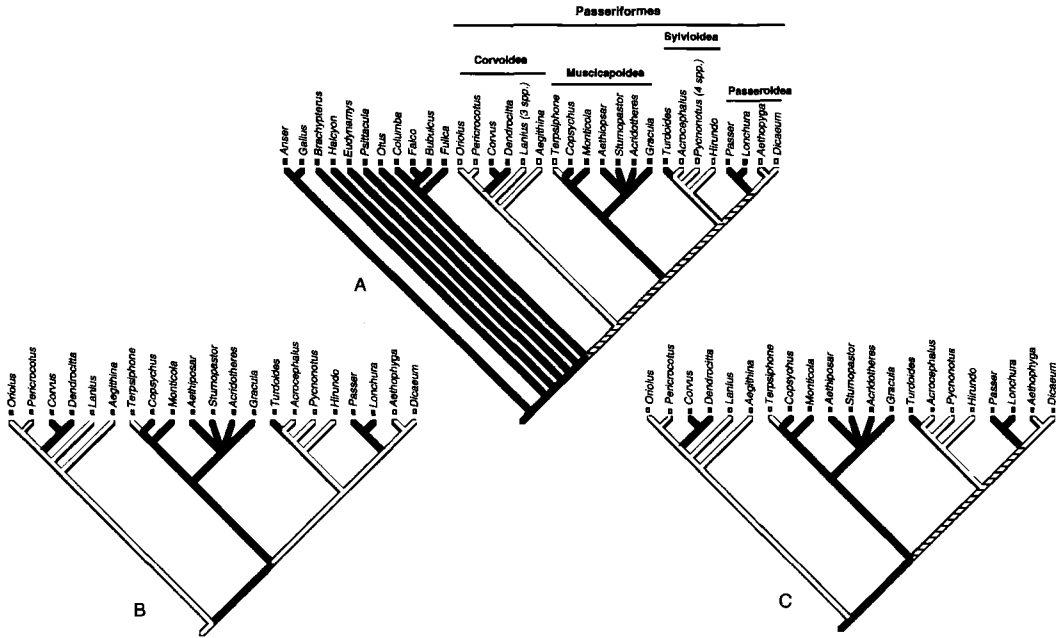


FIG. 1. (A) Presence (solid branches) and absence (open branches) of L-gulonolactone oxidase in bird lineages. Stippling labels branches for which there is more than one equally parsimonious character evolution reconstruction. The algorithm used to trace GLO's evolution in birds assumes that characters are unordered (i.e. a change from presence to absence of GLO and vice versa are counted as one step) and is based on Fitch (1971) as modified by Maddison and Maddison (1992). For consistency with Chaudhuri and Chatterjee (1969), I retained the name *Sturnopastor* in the phylogeny. The current nomenclature for this genus is *Sturnus* (Sibley and Monroe 1990). Note that the ancestral condition for passerines is uncertain and that the reconstruction suggests at least one loss and two reacquisitions of GLO in passerines. Panel (B) assumes that the absence of GLO is ancestral in passerines, whereas (C) assumes that the presence of GLO is ancestral.

(Pollock and Mullin 1987). Because GLO is present in all nonpasserine birds examined, but is absent in several passerines, an early analysis suggested that GLO was lost during a single phylogenetic event in "the most highly evolved" passerines (Chaudhuri and Chatterjee 1969). Here, I present a phylogenetic reanalysis of Chaudhuri and Chatterjee's (1969) hypothesis. This reassessment suggests two conclusions: (1) GLO has been repeatedly lost and regained in passerine birds; and (2) with the available data, its presence in passerines cannot be predicted from either phylogenetic affiliations or diet.

Phylogenetic analysis of GLO expression in birds.—I used Sibley and Ahlquist's (1990) tapestry as a hypothesis for avian phylogenetic relationships. To examine the evolution of GLO in birds, I used Chaudhuri and Chatterjee's (1969) data and Fitch's (1971) parsimony-tracing algorithm (Maddison and Maddison 1992). Because the presence or absence of GLO appears to be conserved within avian genera, I used genera rather than species in the analysis. The scanty data available do not allow one to identify whether the presence of GLO is ancestral or derived in pas-

serines, and hence whether the presence of GLO in the Passeroidea represents a gain or a loss (Fig. 1A).

At a minimum, GLO seems to have reappeared within passerines in two independent lineages (Corvoidea and Sylvioidea, sensu Sibley and Ahlquist 1990) and has been secondarily lost in one (Muscapoidea, Fig. 1A). If one assumes that the absence of GLO is ancestral in passerines, then parsimony tracing suggests that GLO expression has been reacquired four times and lost once (Fig. 1B). In contrast, if the presence of GLO expression is assumed to be ancestral in passerines, then the analysis suggest two independent reacquisitions and two losses (Fig. 1C). Because the data on GLO expression in birds are limited, the inferences of this analysis should be considered tentative. They allow two conclusions, however: (1) the notion that a single evolutionary event led to the loss of GLO in "most highly evolved" passerines is untenable (Chaudhuri and Chatterjee 1969: figure 1); and (2) there appears to be considerable evolutionarily lability in the expression of GLO in passerines. The pattern of occurrence of GLO expression in passerines is different than the one exhibited by

mammals in that the trait does not seem to be phylogenetically conservative.

Is the expression of GLO correlated with diet?—Diamond (1986) proposed two complementary answers to the question of why enzymes become genetically lost or repressed: (1) if a character becomes selectively neutral through disuse, then mutations will gradually remove the character even in the absence of positive selection to eliminate it; and (2) in addition, building and maintaining a character may impose biosynthetic and energetic costs. Disused characters may not be neutral, they may be selectively disadvantageous. These hypotheses predict that enzyme losses will be found in lineages where the metabolic pathways in which the enzymes participate are not used. Because GLO deficiency has been shown to account for scurvy in animals fed diets free of ascorbic acid (Chatterjee et al. 1975), and because foodstuffs vary dramatically in ascorbic-acid content (England and Seifter 1986), it is reasonable to hypothesize an association between dietary habits and the presence or absence of GLO. This association appears to be well established in the literature. Pauling (1970) suggested that "animals that have lost the ability to synthesize vitamin C evolved in environments with ample supplies of ascorbic acid in available foods," and Pianka (1994: 110) used vitamin C synthesis as a prime example of a trait molded by the action of natural selection.

The association between environmental factors and the ability to synthesize vitamin C, however, is a lot more tenuous than suggested in the secondary literature. In mammals, no association between the ability to synthesize vitamin C and diet is found. Instead, a strong phylogenetic component of the loss is evidenced by the absence of the protein in whole lineages, such as all bats and all anthropoid primates (Elliot et al. 1966), irrespective of dietary habits and hence presumably of ascorbic acid intake. In passerines, the pattern of GLO gains and losses also is not obviously associated with dietary shifts. Among the Corvoidea, the enzyme is absent in carnivorous/insectivorous shrikes (*Lanius* spp.; Ali and Ripley 1972a), insectivorous Common Ioras (*Aegithina tiphia*) and Scarlet Minivets (*Pericocotus flammeus*; Ali and Ripley 1972b), and frugivorous Black-hooded Orioles (*Oriolus xanthornus*; Ali and Ripley 1972a). GLO is present, however, in the notoriously omnivorous House Crows (*Corvus splendens*) and Rufous Treepies (*Dendrocitta vagabunda*; Ali and Ripley 1972a). The gain of GLO in the Muscivapoidea (e.g. *Terpsiphone paradisi*) and its loss in the Sylvioidea (e.g. *Turdoides somervillei*), respectively, also are difficult to explain because both species are strict insectivores (Ali and Ripley 1972a, b).

Two factors may contribute to obscure the association of the presence of GLO with dietary habits in birds and mammals. Vitamin C has very diverse physiological functions and its presence in food is

quite heterogeneous. Vitamin C is involved in collagen formation, carnitine biosynthesis, iron absorption, synthesis of neurotransmitters, antioxidant defense, and immunocompetence (Jacob 1994). Vitamin C content can vary by two orders of magnitude among cultivated fruit species (Davies et al. 1991) and among the tissues within an animal (Hornig 1975). With very few exceptions (e.g. Hanssen et al. 1979), the factors that determine vitamin C intake and the vitamin requirements of wild birds are unknown. Without a better understanding of these factors, the phylogenetic patterns described above will remain enigmatic.

Because knowledge on presence of GLO in birds is based on a small and phylogenetically biased sample of passerines, it appears risky to attempt predicting GLO expression, and thus reliance on dietary intake of vitamin C, from either dietary habits or phylogenetic affiliations. Thus, the assertion made by Robbins (1993) that "approximately one-half of the Passeriformes are unable to synthesize vitamin C" seems premature. At this point, the occurrence of the ability to synthesize the vitamin in passerines appears to be unpredictable. The applied consequence of this uncertainty is that the levels of dietary vitamin C required for normal growth and adequate health and reproduction in captive passerine birds must be determined on a species-by-species basis.

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Sex Identification of South American Parrots (Psittacidae, Aves) Using the Human Minisatellite Probe 33.15

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Many species of South American parrots are endangered, and captive breeding has become a standard procedure for species conservation. Because most South American parrots are not sexually dimorphic, an efficient means of determining the sex of individuals is an important tool in establishing and maintaining a viable breeding population in captivity.

DNA fingerprinting (Jeffreys et al. 1985) has been

applied in a variety of wild species, including birds (Burke and Bruford 1987, Wetton et al. 1987). It was used to monitor genetic variability in captive Puerto Rican Parrots (*Amazona vittata*; Brock and White 1992) and to establish paternity in endangered species (Mathé et al. 1993). Recently, we used DNA fingerprinting to identify the sex of Peach-fronted (*Aratinga aurea*) and Golden (*Guaruba [Aratinga] guarouba*) parakeets (Miyaki et al. 1992) and suggested that fingerprinting also could be used to determine sex in other psittacines (Miyaki et al. 1993, 1995). Here, we present results on sex determination using the human minisatellite probe 33.15 (Jeffreys et al.

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