

IMPLICATIONS OF BROAD HOST SPECIFICITY OF AVIAN *ISOSPORA* SPP. FOR CONSERVATION BREEDING PROGRAMS

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Avian coccidia are differentiated mainly on the basis of oocyst morphology, developmental cycle, host occurrence and pathogenicity. Over 200 *Eimeria* spp. have been described; most from individual bird species. In comparison, only 60 *Isoospora* spp. have been described, most from multiple host species, especially passerines. Their broad host range and distribution confounds differential diagnosis and epidemiological investigations. Over the last two years, veterinary surveillance of two endangered bird species, black-eared miners (*Manorina melanotis*) in Victoria and regent honeyeaters (*Xanthomyza phrygia*) in New South Wales, detected high numbers of *Isoospora* oocysts in captive breeding colonies, occasionally in association with clinical disease in juveniles. Similar oocysts were detected in wild birds of both species from their native habitats which are geographically separate and remote. Morphometric characterization of all isolates revealed the presence of only one parasite species. The oocysts were colourless, subspherical (20-24 x 18-22 μ m), contained 1-3 polar granules but lacked a collar, micropyle, polar cap and oocyst residuum. Sporulated oocysts contained two ellipsoidal sporocysts (12-15 x 6-10 μ m) with a prominent macropylia-type Steida body and a granular sporocyst residuum. Their morphological characteristics were consistent with those of *I. chloridis* found in local sparrow populations (*Passer domesticus*) and previously reported in greenfinches (*Carduelis chloris*), chaffinches (*Fringilla coelebs*) and sparrows overseas. These findings suggest *I. chloridis* may be a cosmopolitan species infective to a range of passerine birds which has implications for the management of breeding colonies. Given the logistic problems and undesirability of conducting extensive cross-transmission studies (particularly involving endangered species), gene sequencing techniques have been initiated to characterize parasite species and indicate their host range and specificity.