letters to nature

genotypic exclusion, meaning that a male could be assigned paternity only if he met the strict 95% assignment level and was the only perfect genotypic match among sampled males. Details of the CERVUS analysis are given in Supplementary Table 3.

This set of conservative criteria lead to the assignment of 75 of 325 offspring to a known, sampled male. Although many of the unassigned offspring were probably fathered by unsampled males, others were fathered by known males but could not be assigned to them. CERVUS generates a test statistic (Δ) based on the difference in LOD scores (cumulative log-likelihood ratio of parentage compared with non-parentage) between the two most likely sampled males. The program then compares this value with a user-defined

critical value based on the percentage of simulations (here, 95%) that correctly assigned an offspring to the actual parent. The more genotypically similar that two candidate parents are, the more likely they are to have similar LOD scores and therefore to generate a smaller Δ score. Given the wild turkey's unique kin structure, coalition males were handicapped by necessarily having close relatives among the set of candidate males.

Received 20 November; accepted 30 December 2004; doi:10.1038/nature03325.

- McDonald, D. B. & Potts, W. K. Cooperative display and relatedness among males in a lek-mating bird. *Science* 266, 1030–1032 (1994).
- 2. Watts, C. R. & Stokes, A. W. The social order of turkeys. Sci. Am. 224, 112–118 (1971).
- Hamilton, W. D. The genetical theory of social behavior. I and II. J. Theor. Biol. 7, 1–52 (1964).
 Lucas, J. R., Creel, S. R. & Waser, P. M. How to measure inclusive fitness, revisited. Anim. Behav. 51, 225–228 (1996).
- Balph, D. F., Innes, G. S. & Balph, M. H. Kin selection in turkeys: a critical assessment. Auk 97, 854–860 (1980).
- Höglund, J., Alatalo, R. V., Lundberg, A., Rintamaki, P. K. & Lindell, J. Microsatellite markers reveal the potential for kin selection on black grouse leks. *Proc. R. Soc. Lond. B* 266, 813–816 (1999).
- Petrie, M., Krupa, A. & Burke, T. Peacocks lek with relatives even in the absence of social and environmental cues. *Nature* 401, 155–157 (1999).
- Shorey, L., Piertney, S., Stone, J. & Höglund, J. Fine-scale genetic structure on Manacus manacus leks. Nature 408, 352–353 (2000).
- 9. Brown, J. L. Helping and Communal Breeding in Birds (Princeton Univ. Press, Princeton, 1987).
- Emlen, S. T. Benefits, constraints and the evolution of the family. *Trends Ecol. Evol.* 9, 282–285 (1994).
- Clutton-Brock, T. H. Breeding together—kin selection and mutualism in cooperative vertebrates. Science 296, 69–72 (2002).
- Griffin, A. S. & West, S. A. Kin descrimination and the benefit of helping in cooperatively breeding vertebrates. *Science* 302, 634–636 (2003).
- Kokko, H. & Linström, J. Kin selection and the evolution of leks: whose success do young males maximize? Proc. R. Soc. Lond. B 263, 919–923 (1996).
- Höglund, J. Lek-kin in birds—provoking theory and surprising new results. Ann. Zool. Fenn. 40, 249–253 (2003).
- 15. Wilson, E. O. Sociobiology: the New Synthesis (Harvard Univ. Press, Boston, Massachusetts, 1975).
- Goodenough, J., McGuire, B. & Wallace, R. A. Perspectives on Animal Behavior 2nd edn (Wiley, New York, 2001).
- Blouin, M. S. DNA-based methods for pedigree reconstruction and kinship analysis in natural populations. *Trends Ecol. Evol.* 18, 503–511 (2003).
- Buchholz, R. Female choice, parasite load, and male ornamentation in wild turkeys. Anim. Behav. 50, 929–943 (1995).
- Buchholz, R. Male dominance and variation in fleshy head ornamention in wild turkeys. J. Avian Biol. 28, 223–230 (1997).
- 20. Lank, D. B. et al. High frequency of polyandry in a lek mating system. Behav. Ecol. 13, 209–215 (2002).
- Healy, W. M. The Wild Turkey: Biology and Management (ed. Dickson, J. D.) 46–65 (Stackpole, Mechanicsburg, Pennsylvania, 1992).
- Donoghue, A. M., Sonstegard, T. S., King, L. M., Smith, E. J. & Burt, D. W. Turkey sperm mobility influences paternity in the context of competitive fertilization. *Biol. Reprod.* 61, 422–427 (1999).
- Reed, K. M., Roberts, M. C., Murtaugh, J., Beattie, C. W. & Alexander, L. J. Eight new dinucleotide microsatellite loci in turkey (*Meleagris gallopavo*). Anim. Genet. 31, 140 (2000).
- Mock, K. E., Theimer, T. C., Rhodes, O. E., Greenberg, D. L. & Keim, P. Genetic variation across the historical range of the wild turkey (*Meleagris gallopavo*). *Mol. Ecol.* 11, 643–657 (2002).
- Raymond, M. & Rousset, F. GENEPOP (version 3.1b). An updated version of GENEPOP version 1.2: population genetics software for exact tests and ecumenicism. J. Hered. 86, 248–249 (1997).
- Queller, D. C. & Goodnight, K. F. Estimating relatedness using genetic markers. *Evolution* 43, 258–275 (1989).
- Marshall, T. C., Slate, J., Kruuk, L. E. B. & Pemberton, J. M. Statistical confidence for likelihood-based paternity inference in natural populations. *Mol. Ecol.* 7, 639–655 (1998).

Supplementary Information accompanies the paper on www.nature.com/nature.

Acknowledgements I thank E. DuVal, E. Lacey and especially W. Koenig and M. Hauber for comments on the manuscript; J. Dickinson, S. Beissinger, B. Jones, B. Slikas and N. Johnson for training and discussion; B. Davis, A. Hsieh, F. Aguillar, C. Miller, J. Leyhe, R. Orben, L. Robinson, M. Nguyen, B. Loui, M. Nasiri and C. Chu and others for field and laboratory assistance; and P. Kephart for research access to Rana Creek Ranch. My research was funded by an NSF graduate fellowship and dissertation improvement grant, as well as the Animal Behavior Society, American Ornithologists' Union, Sigma Xi, and support from both Integrative Biology and the Museum of Vertebrate Zoology at the University of California, Berkeley.

Competing interests statement The author declares that he has no competing financial interests.

Correspondence and requests for materials should be addressed to the author (krakauer@berkeley.edu).

Disruptive coloration and background pattern matching

Innes C. Cuthill¹, Martin Stevens¹, Jenna Sheppard¹, Tracey Maddocks¹, C. Alejandro Párraga² & Tom S. Troscianko²

¹School of Biological Sciences, University of Bristol, Woodland Road, Bristol BS8 1UG, UK

²Department of Experimental Psychology, University of Bristol, Woodland Road, Bristol BS8 1TN, UK

Effective camouflage renders a target indistinguishable from irrelevant background objects. Two interrelated but logically distinct mechanisms for this are background pattern matching (crypsis^{1,2}) and disruptive coloration: in the former, the animal's colours are a random sample of the background^{1,2}; in the latter, bold contrasting colours on the animal's periphery break up its outline. The latter has long been proposed as an explanation for some apparently conspicuous coloration in animals^{3,4}, and is standard textbook material. Surprisingly, only one quantitative test⁵ of the theory exists, and one experimental test of its effectiveness against non-human predators⁶. Here we test two key predictions: that patterns on the body's outline should be particularly effective in promoting concealment and that highly contrasting colours should enhance this disruptive effect. Artificial moth-like targets were exposed to bird predation in the field, with the experimental colour patterns on the 'wings' and a dead mealworm as the edible 'body'. Survival analysis supported the predictions, indicating that disruptive coloration is an effective means of camouflage, above and beyond background pattern matching.

The pioneers of modern military camouflage were both artists and keen observers of nature⁷. For example, the work of Thayer, who proposed the theory of countershading⁸ and developed Bates's ideas on disruptive coloration in animals³, was influential in persuading





the US government to form a special camouflage unit during the First World War (ref. 7). Thayer's theory of 'ruptive' coloration, that contrasting colours on an object help to break up its outline, is such a central feature of military camouflage-and similar patterns in the animal kingdom seem so obviously designed to fulfil the same role⁴—that it is easy to assume that what deceives humans deceives other animals. Yet it is unwise to extrapolate from human perception to that of other animals9-11, and there are many other explanations for colour patterns presumed by Thayer and successors to be camouflage^{3,4,12,13}. Before accepting that disruptive coloration has a role in anti-predator defence, two conditions must hold: that the distribution of colour patterns matches that predicted by the theory, and that these distributions reduce the detectability of prey to predators. There has only been one test of each condition. In one⁵, the spots on a marine isopod were shown to touch the body outline more often than predicted by background matching, which is consistent with the theory of disruptive coloration. In the other⁶, there was no effect on survival of experimentally removing the wing-stripes of a nymphalid butterfly that is highly palatable to birds, a finding inconsistent with the theory, although the methods might have unintentionally made the butterflies more similar to a co-occurring unpalatable species¹⁴ or altered their palatability directly. Clearly there is a pressing need for further empirical research before we can accept what has been described⁴ as "certainly the most important set of principles relating to concealment".

We tested two predictions⁵ arising from previous work^{3,4}: first, that patterns on the body's edge should be more effective than equivalent patterns placed randomly; second, that highly contrasting colours should be more disruptive than those of low contrast. In each case, provided that the colours and patterns on the prey were equally common in the background, the theory of background pattern matching^{1,2,15} would predict no difference in the effective-



Figure 2 High-contrast disruptive patterns enhance survival. **a**, Examples of 'moth' targets in experiment 2; **b**, survival curves. The differences between treatments were significant (Wald = 62.26, d.f. = 5, P < 0.001) in the order Edge–high-contrast (EH) > Edge–low-contrast (EL; Wald = 15.31, d.f. = 1, P < 0.001) > Inside–high-contrast (IH) (Wald = 5.20, d.f. = 1, P = 0.023) = Inside–low-contrast (IL) (Wald = 0.00, d.f. = 1, P = 0.952) = Average–low-contrast (AL) (Wald = 1.68, d.f. = 1, P < 0.195) = Average–high-contrast (AH) (Wald = 0.00, d.f. = 1, P = 0.951).

ness of the camouflage. Our artificial targets (see Methods), with their coloured 'wings' and edible 'bodies', were not designed to mimic any real lepidopteran, and the oak tree trunks on which they were pinned were merely a convenient complexly patterned substrate against which birds might detect prey. Thus, our experiments are best thought of as 'field psychophysics' rather than a study of moth predation risk.

In experiment 1, targets were dark brown with black markings designed, with regard to bird vision, to match the real patterns of dark and light on heavily ridged, mature, oak bark. There were five treatments (Fig. 1): markings overlapping the edges of the 'wings' ('Edge'), the exact same markings displaced inwards so that no edges were overlapped ('Inside 1'), other randomly selected markings placed so as not to overlap edges ('Inside 2'), monochrome brown, and monochrome black. The three bicoloured treatments all possessed life-sized pattern elements randomly sampled from the background, and so should have been equally cryptic in terms of background pattern matching (and better camouflaged than monochrome brown or black). Similarly, no difference would be predicted if bicoloured targets gained a crypsis advantage because, when viewed from a distance, predators would not be able to discriminate between the two colours and so would see a spatially averaged dark brown. Only the theory of disruptive coloration predicted that treatment Edge should survive better than the other bicoloured treatments. This prediction was fulfilled (Fig. 1). Treatment Inside 2 was included because of the possibility that moving the pattern elements present in treatment Edge from the periphery of the 'wings', to form treatment Inside 1, created pattern elements with straight lines that themselves could have enhanced conspicuousness. This indeed seemed to be so, because treatment Inside 2 survived better than Inside 1, which lacked these straight edges to the pattern elements (Fig. 1). The inwards displacement of pattern elements in Inside 1 also tended to enhance the outline of these targets, thus having the opposite effect to disruptive coloration. Nevertheless, all bicoloured treatments survived better than monochrome black or brown, indicating that background pattern matching was, as expected, itself effective as camouflage (Fig. 1).

Experiment 2 had six treatments: the 2×2 combination of bicoloured patterns with high or low contrast, placed as in experiment 1's treatment Edge or Inside 2, plus two monochrome treatments that were the average colour of either the high-contrast or the low-contrast colour pairs. As uniquely predicted by the theory of disruptive coloration, the high-contrast-edge treatment survived best (Fig. 2), with high contrast providing minimal benefit in non-disruptive 'Inside' treatments. The results apply to the conditions pertaining in our study (for example winter, and a given habitat type); the extent to which disruptive patterns provide a general advantage over simple crypsis, with different background types (for example varying spatial and/or chromatic complexity) or different light environments (for example direct or diffuse lighting) therefore awaits further experimentation. Nevertheless, our results provide the strongest support so far for the effectiveness of disruptive patterns against birds, the most commonly invoked visual predators shaping the evolution of protective coloration in insects. \square

Methods

'Prey' were dead (frozen overnight at -80 °C, then thawed) mealworms (*Tenebrio molitor* larvae) pinned onto coloured paper triangles 50 mm wide by 25 mm high. These were pinned onto oak trees in the mixed deciduous Leigh Woods National Nature Reserve, North Somerset, UK (2° 38.6' W, 51° 27.8' N) and their 'survival' was checked at about 2, 4, 6 and 24 h. Birds took all or most of the mealworm, spiders sucked fluids out, leaving a hollow exoskeleton, and slugs left slime trails; predation in the latter two categories, complete disappearance of a target, or survival to 24 h, were treated as 'censored' values in survival analysis. Both experiments had randomized block designs with ten replicate blocks, run in different areas of the wood on different dates between October 2003 and March 2004. Each block had 75 (experiment 1; 15 per treatment) or 84 (experiment 2; 14 per treatment) targets in a nonlinear transect). Treatments were randomly allocated to trees,

letters to nature

subject to the constraints that no lichen covered the trunk and no young trees with a trunk circumference less than 0.9 m were used. Colour matches of treatments to natural bark were verified by spectrophotometry of stimuli and bark, followed by modelling of predicted photon catches¹⁶ of a typical passerine bird, the blue tit's (*Parus caeruleus*) single cone photoreceptors¹⁷, with irradiance spectra from overcast skies in the study site. Our acceptance criterion was simply that cone captures for the experimental stimuli fell within the measured range of those for oak bark.

Experiment 1 used black patterns printed onto dark brown card. Patterns were samples of digital photos of the oak trees at 1:1 reproduction, converted using Image¹¹⁸ to greyscale and thresholded at 50% to binary (black/white) images to provide, when printed onto brown card, bark-like brown/black spatial variation (Fig. 1). Different samples, from different trees, were used for each replicate target.

Experiment 2 used bicoloured targets printed onto waterproof paper (Hewlett Packard Laserjet Tough Paper) with a Hewlett Packard Colour Laserjet 2500 (600 dots per inch) printer, with colour pairs chosen to have either high or low contrast. Colours were chosen from frequency distributions of the eight-bit RGB (red, green, blue) values from digital photographs of the oak trees in the study site, reduced to 16 bins in each colour channel. Photos (about 267 mm \times 200 mm; 2,560 pixels \times 1,920 pixels) were taken with a Nikon Coolpix 5700 camera, calibrated¹⁹ to linearize the relationship between radiance and the greyscale in each colour channel, and saved as uncompressed TIFF files. Digital photographs lack ultraviolet information that birds can see²⁰, but lichen-free oak bark reflects negligible ultraviolet²¹. Even a properly calibrated RGB image does not precisely simulate the avian-perceived colour of many natural objects, owing to differences in the spectral sensitivity of bird long-wave, medium-wave and short-wave cones compared with human cones²². However, because our treatments varied only in relative colour contrast, any error associated with this method was considered minor, an assumption verified retrospectively by spectrophotometry and colour-space modelling. We chose colour pairs from the eight most frequent RGB triplets in the bark photos as follows: a 'background' colour, then a triplet that was similar to the background (low contrast), and one that differed markedly (high contrast). The major difference between colours was in overall brightness not hue, but we could not systematically vary only one colour dimension within the available common bark colours. Sample numbers of background and contrasting colours were balanced for which was darker/lighter, and so there were no significant differences between bicoloured treatments in the brightest or darkest colour or average colour (analyses of variance on RGB sums and all possible ratios; P > 0.9). Monochrome treatments were also created as the means of the respective R, G and B values of the two colours in bicoloured high-contrast and low-contrast treatments. Different colour pairs and patterns, from different trees, were used for each replicate target.

Survival analysis was by Cox regression^{23,24} with the factors treatment and block. Cox regression assumes that all survival functions have the same shape; this proportional hazards assumption was checked by plotting partial residuals against ranked survival times²⁴. There were significant block effects in both experiments (in experiment 1, Wald = 121.78, d.f. = 9, P < 0.001; in experiment 2, Wald = 271.50, d.f. = 9, P < 0.001), reflecting differences in average predation rates in different parts of the woods on different dates, but this was not relevant to our hypotheses.

Received 23 September; accepted 30 December 2004; doi:10.1038/nature03312.

- Endler, J. A. Progressive background in moths, and a quantitative measure of crypsis. *Biol. J. Linn. Soc.* 22, 187–231 (1984).
- Endler, J. A. An overview of the relationships between mimicry and crypsis. *Biol. J. Linn. Soc.* 16, 25–31 (1981).
- Thayer, G. H. Concealing Coloration in the Animal Kingdom; An Exposition of the Laws of Disguise through Color and Pattern; Being a Summary of Abbott H. Thayer's Discoveries (Macmillan, New York, 1909).
- 4. Cott, H. B. Adaptive Coloration in Animals (Methuen, London, 1940).
- Merilaita, S. Crypsis through disruptive coloration in an isopod. Proc. R. Soc. Lond. B 265, 1059–1064 (1998).
- Silberglied, R. E., Aiello, A. & Windsor, D. M. Disruptive coloration in butterflies lack of support in Anartia fatima. Science 209, 617–619 (1980).
- 7. Behrens, R. R. False Colors: Art, Design and Modern Camouflage (Bobolink, Dysart, Iowa, 2002).
- 8. Thayer, A. H. The law which underlies protective coloration. Auk 13, 124-129 (1896).
- Endler, J. A. On the measurement and classification of colour in studies of animal colour patterns. Biol. J. Linn. Soc. 41, 315–352 (1990).
- 10. Endler, J. A. A predator's view of animal color patterns. Evol. Biol. 11, 319-364 (1978).
- Bennett, A. T. D., Cuthill, I. C. & Norris, K. J. Sexual selection and the mismeasure of color. Am. Nat. 144, 848–860 (1994).
- Kiltie, R. A. Countershading: universally deceptive or deceptively universal? *Trends Ecol. Evol.* 3, 21–23 (1988).
- Ruxton, G. D., Speed, M. P. & Kelly, D. J. What, if anything, is the adaptive function of countershading? Anim. Behav. 68, 445–451 (2004).
- Waldbauer, G. P. & Sternburg, J. G. A pitfall in using painted insects in studies of protective coloration. Evolution 37, 1085–1086 (1983).
- Merilaita, S., Tuomi, J. & Jormalainen, V. Optimization of cryptic coloration in heterogeneous habitats. *Biol. J. Linn. Soc.* 67, 151–161 (1999).
- Maddocks, S. A., Church, S. C. & Cuthill, I. C. The effects of the light environment on prey choice by zebra finches. J. Exp. Biol. 204, 2509–2515 (2001).
- Hart, N. S., Partridge, J. C., Cuthill, I. C. & Bennett, A. T. D. Visual pigments, oil droplets, ocular media and cone photoreceptor distribution in two species of passerine: the blue tit (*Parus caeruleus* L.) and the blackbird (*Turdus merula* L.). J. Comp. Physiol. [A] 186, 375–387 (2000).
- Rasband, W. ImageJ v. 1.30 (http://rsb.info.nih.gov/ij/docs/, National Institutes of Health, USA, 2003).
- Parraga, C. A., Troscianko, T. & Tolhurst, D. J. Spatiochromatic properties of natural images and human vision. *Curr. Biol.* 12, 483–487 (2002).
- 20. Cuthill, I. C. et al. Ultraviolet vision in birds. Adv. Stud. Behav. 29, 159-214 (2000).

- Majerus, M. E. N., Brunton, C. F. A. & Stalker, J. A bird's eye view of the peppered moth. J. Evol. Biol. 13, 155–159 (2000).
- Cuthill, I. C. et al. Avian colour vision and avian video playback experiments. Acta Ethol. 3, 29–37 (2000).
- 23. Cox, D. R. Regression models and life-tables. J. R. Stat. Soc. B 34, 187-220 (1972)
- 24. SPSS for Windows Release 9.0 (SPSS Inc., Chicago, 2003).

Acknowledgements We thank J. Endler for suggestions. The research was supported by a BBSRC grant to I.C.C., T.S.T. and J. C. Partridge.

Authors' contributions I.C.C. designed the experiments and stimuli; M.S., J.S., T.M. and I.C.C. performed the experiments; A.P. wrote the programs for colour analysis and camera calibration; T.S.T. advised on design and colour modelling.

Competing interests statement The authors declare that they have no competing financial interests.

Correspondence and requests for materials should be addressed to I.C. (i.cuthill@bristol.ac.uk).

An anaerobic mitochondrion that produces hydrogen

Brigitte Boxma¹*, Rob M. de Graaf¹*, Georg W. M. van der Staay¹*, Theo A. van Alen¹, Guenola Ricard², Toni Gabaldón², Angela H. A. M. van Hoek¹†, Seung Yeo Moon-van der Staay¹, Werner J. H. Koopman³, Jaap J. van Hellemond⁴, Aloysius G. M. Tielens⁴, Thorsten Friedrich⁵, Marten Veenhuis⁶, Martijn A. Huynen² & Johannes H. P. Hackstein¹

¹Department of Evolutionary Microbiology, Faculty of Science, Radboud University Nijmegen, Toernooiveld 1, NL-6525 ED Nijmegen, The Netherlands ²Centre for Molecular and Biomolecular Informatics,

³*Microscopical Imaging Centre and Department of Biochemistry, Nijmegen Centre of Molecular Life Sciences (NCMLS), Radboud University Nijmegen Medical Centre, NL-6500 HB Nijmegen, The Netherlands*

⁴Department of Biochemistry and Cell Biology, Faculty of Veterinary Medicine, Utrecht University, PO Box 80176, NL-3508 TD Utrecht, The Netherlands ⁵Albert-Ludwigs-Universität, Institut für Organische Chemie und Biochemie, Albertstrasse 21, D-79104 Freiburg i. Br., Germany ⁶Department of Eukaryotic Microbiology, Groningen University, PO Box 14,

"Department of Eukaryotic Microbiology, Groningen University, PO Box 14, NL-9750 AA Haren, The Netherlands

* These authors contributed equally to this work

† Present address: RIKILT, Institute of Food Safety, Bornsesteeg 45, NL-6708 PD Wageningen, The Netherlands

Hydrogenosomes are organelles that produce ATP and hydrogen¹, and are found in various unrelated eukaryotes, such as anaerobic flagellates, chytridiomycete fungi and ciliates². Although all of these organelles generate hydrogen, the hydrogenosomes from these organisms are structurally and metabolically quite different, just like mitochondria where large differences also exist³. These differences have led to a continuing debate about the evolutionary origin of hydrogenosomes^{4,5}. Here we show that the hydrogenosomes of the anaerobic ciliate Nyctotherus ovalis, which thrives in the hindgut of cockroaches, have retained a rudimentary genome encoding components of a mitochondrial electron transport chain. Phylogenetic analyses reveal that those proteins cluster with their homologues from aerobic ciliates. In addition, several nucleus-encoded components of the mitochondrial proteome, such as pyruvate dehydrogenase and complex II, were identified. The N. ovalis hydrogenosome is sensitive to inhibitors of mitochondrial complex I and produces succinate as a major metabolic end product—biochemical traits typical of anaerobic mitochondria³. The production of hydrogen, together with the presence of a genome encoding respiratory chain components, and biochemical