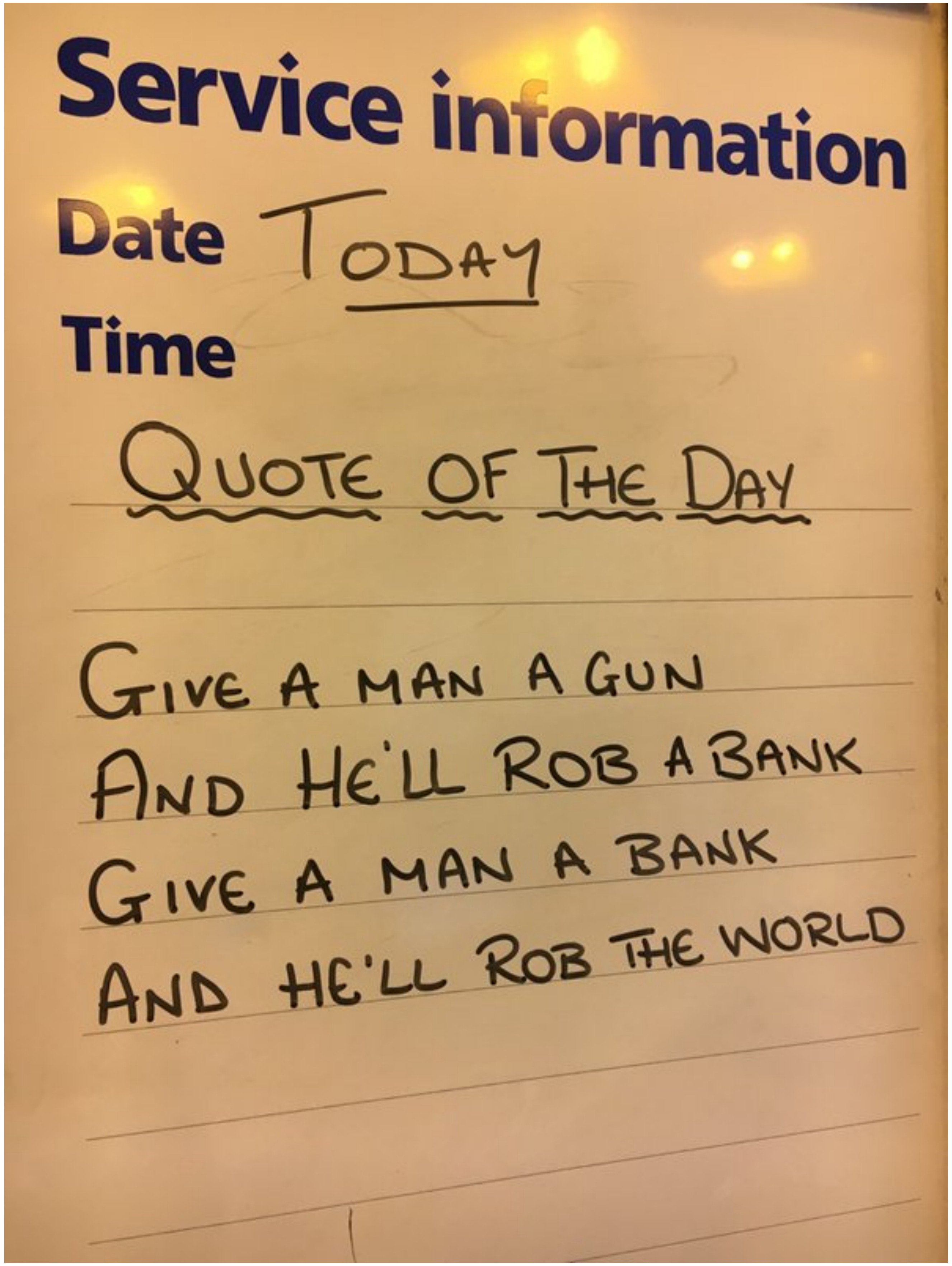

Service information

Date TODAY

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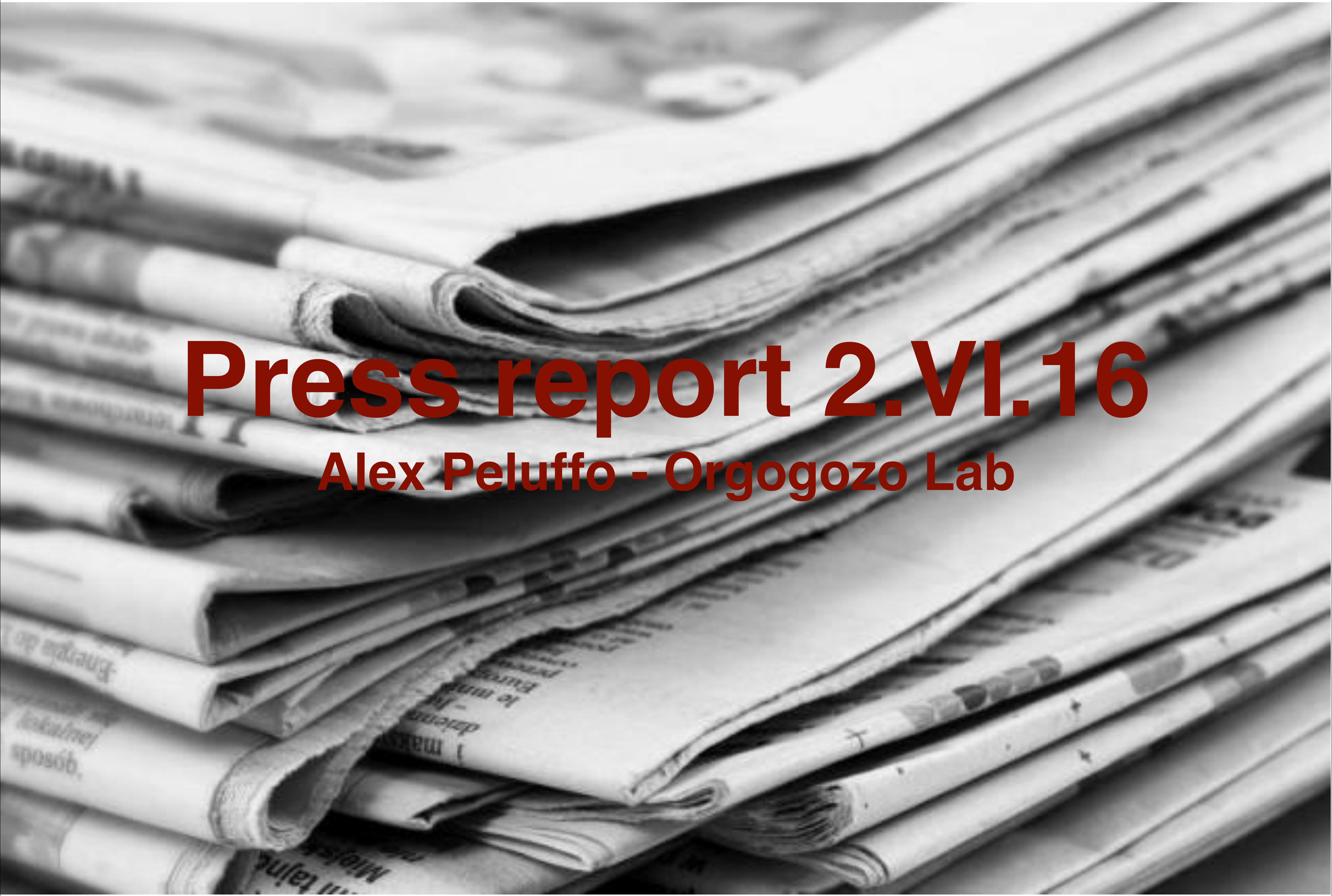
QUOTE OF THE DAY

GIVE A MAN A GUN
AND HE'LL ROB A BANK
GIVE A MAN A BANK
AND HE'LL ROB THE WORLD



Press report 2.VI.16

Alex Peluffo - Orgogozo Lab

Org Divers Evol
DOI 10.1007/s13127-016-0286-2

REVIEW

ORGANISMS
DIVERSITY &
EVOLUTION

Unresolved questions in genitalia coevolution: bridging taxonomy, speciation, and developmental genetics

Amir Yassin[1]

Received: 18 January 2016 / Accepted: 16 May 2016

Abstract Systematists and geneticists study biological diversity, but they use different approaches that rarely intersect. A very common pattern that is of interest for both researchers is the rapid evolution of genitalia, a trait of significant taxonomic utility in several sexually reproducing animal clades. The idea that both male and female genitalia are species-specific and play a role in reproductive isolation has long been controversial but has recently gained a renewed interest by speciation and developmental geneticists. Here, I highlight six unresolved questions in genitalia coevolution and I argue that systematists, with their well training in comparative morphology, usage of large and geographically diverse collections, and ability to apply molecular genetics techniques, can make important contributions. Such an extension of systematics into the speciation and developmental genetics realms is a promising opportunity to expand "integrative taxonomy" comparisons between DNA and morphology into more explanatory relationships between the two sources of taxonomic data.

LETTER

doi:10.1038/nature18005

How sexual selection can drive the evolution of costly sperm ornamentation

Stefan Lüpold[1,2]*, Mollie K. Manier[1,3], Nalini Puniamoorthy[1,4], Christopher Schoff[1], William T. Starmer[1], Shannon H. Buckley Luepold[1], John M. Belote[1] & Scott Pitnick[1]*

Post-copulatory sexual selection (PSS), fuelled by female promiscuity, is credited with the rapid evolution of sperm quality traits across diverse taxa[1]. Yet, our understanding of the adaptive significance of sperm ornaments and the cryptic female preferences driving their evolution is extremely limited[1,2]. Here we review the evolutionary allometry of exaggerated sexual traits (for example, antlers, horns, tail feathers, mandibles and dewlaps), show that the giant sperm of some *Drosophila* species are possibly the most extreme ornaments[3,4] in all of nature and demonstrate how their existence challenges theories explaining the intensity of sexual selection, mating-system evolution and the fundamental nature of sex differences[5–9]. We also combine quantitative genetic analyses of interacting sex-specific traits in *D. melanogaster* with comparative analyses of the condition dependence of male and female reproductive potential across species with varying ornament size to reveal complex dynamics that may underlie sperm-length evolution. Our results suggest that producing few gigantic sperm evolved by (1) Fisherian runaway selection mediated by genetic correlations between sperm length, the female preference for long sperm and female mating frequency, and (2) longer sperm increasing the indirect benefits to females. Our results also suggest that the developmental integration of sperm quality and quantity renders post-copulatory sexual selection on ejaculates unlikely to treat male–male competition and female choice as discrete processes.

LETTER

doi:10.1038/nature17961

The gene *cortex* controls mimicry and crypsis in butterflies and moths

Nicola J. Nadeau[1,2], Carolina Pardo-Diaz[3], Annabel Whibley[4,5], Megan A. Supple[2,6], Suzanne V. Saenko[4], Richard W. R. Wallbank[2,7], Grace C. Wu[8], Luana Maroja[9], Laura Ferguson[10], Joseph J. Hanly[2,7], Heather Hines[11], Camilo Salazar[3], Richard M. Merrill[2,7], Andrea J. Dowling[12], Richard H. ffrench-Constant[12], Violaine Llaurens[4], Mathieu Joron[4,13], W. Owen McMillan[2] & Chris D. Jiggins[2,7]

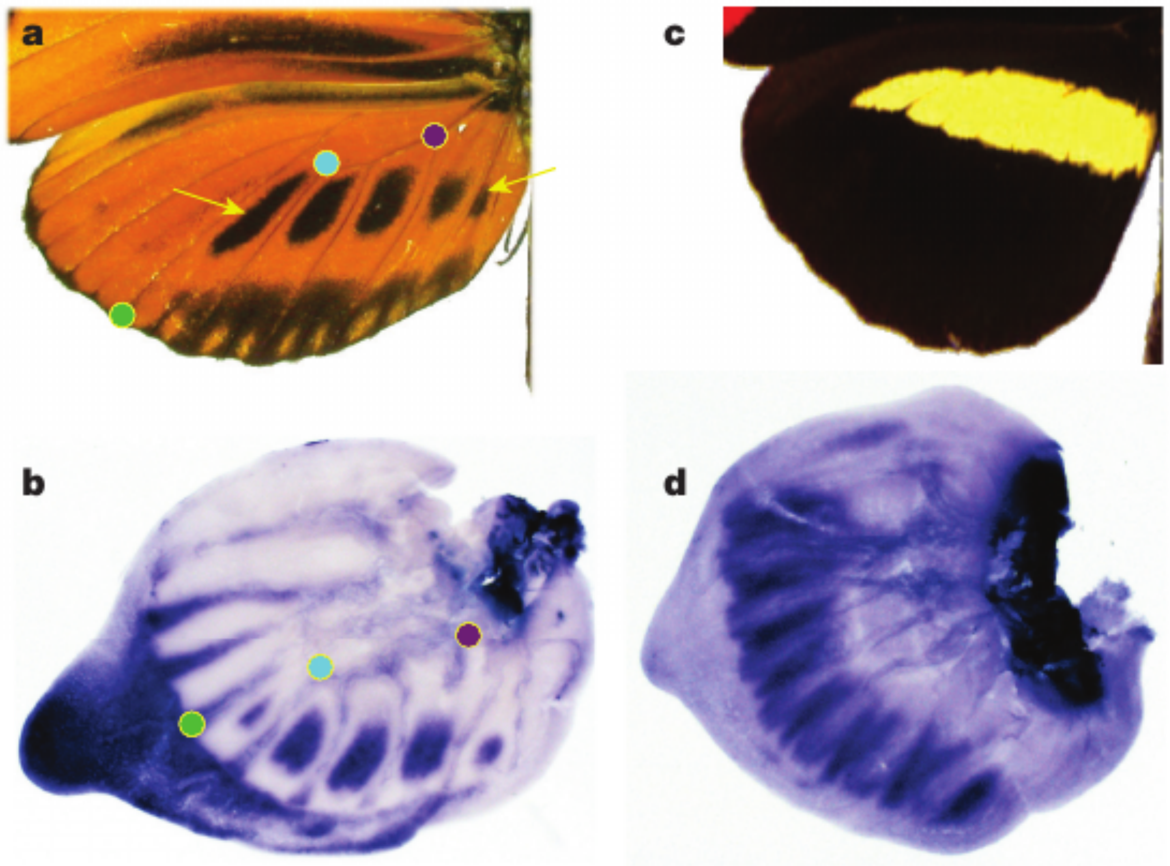


Figure 4 | *In situ* hybridizations of *cortex* in hindwings of final instar larvae. a, b, *H. numata tarapotensis* (replicated three times in the lab). Adult wing shown in **a**; coloured points indicate landmarks, yellow arrows highlight adult pattern elements corresponding to *cortex* staining. **c, d,** *H. melpomene rosina* (replicated twice in the lab). Adult wing shown in **c**; staining patterns in other *H. melpomene* races (*meriana*, $n = 11$, and *aglaope*, $n = 6$) appeared similar. The probe used was complementary to the *cortex* isoform with the longest open reading frame (also the most common; see Extended Data Fig. 5).

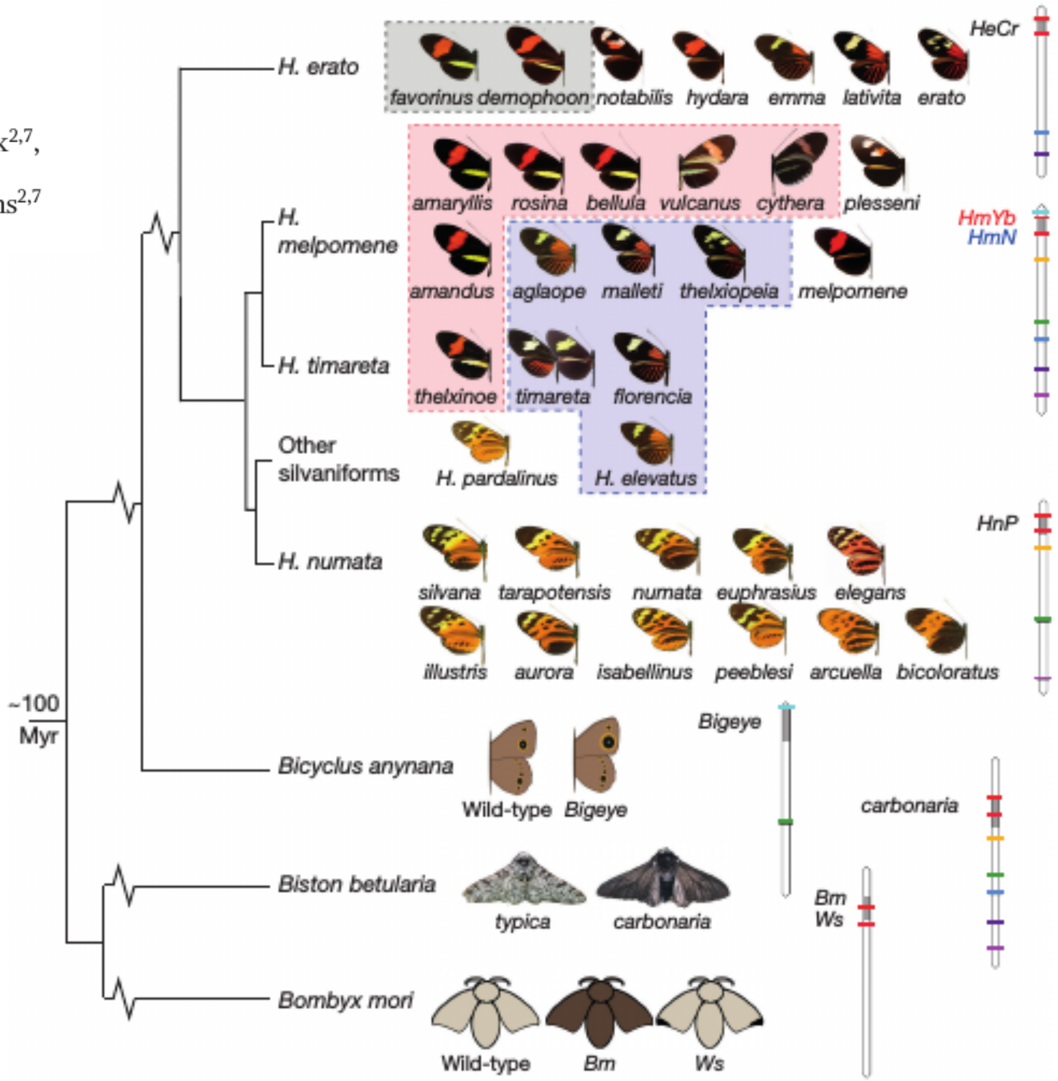


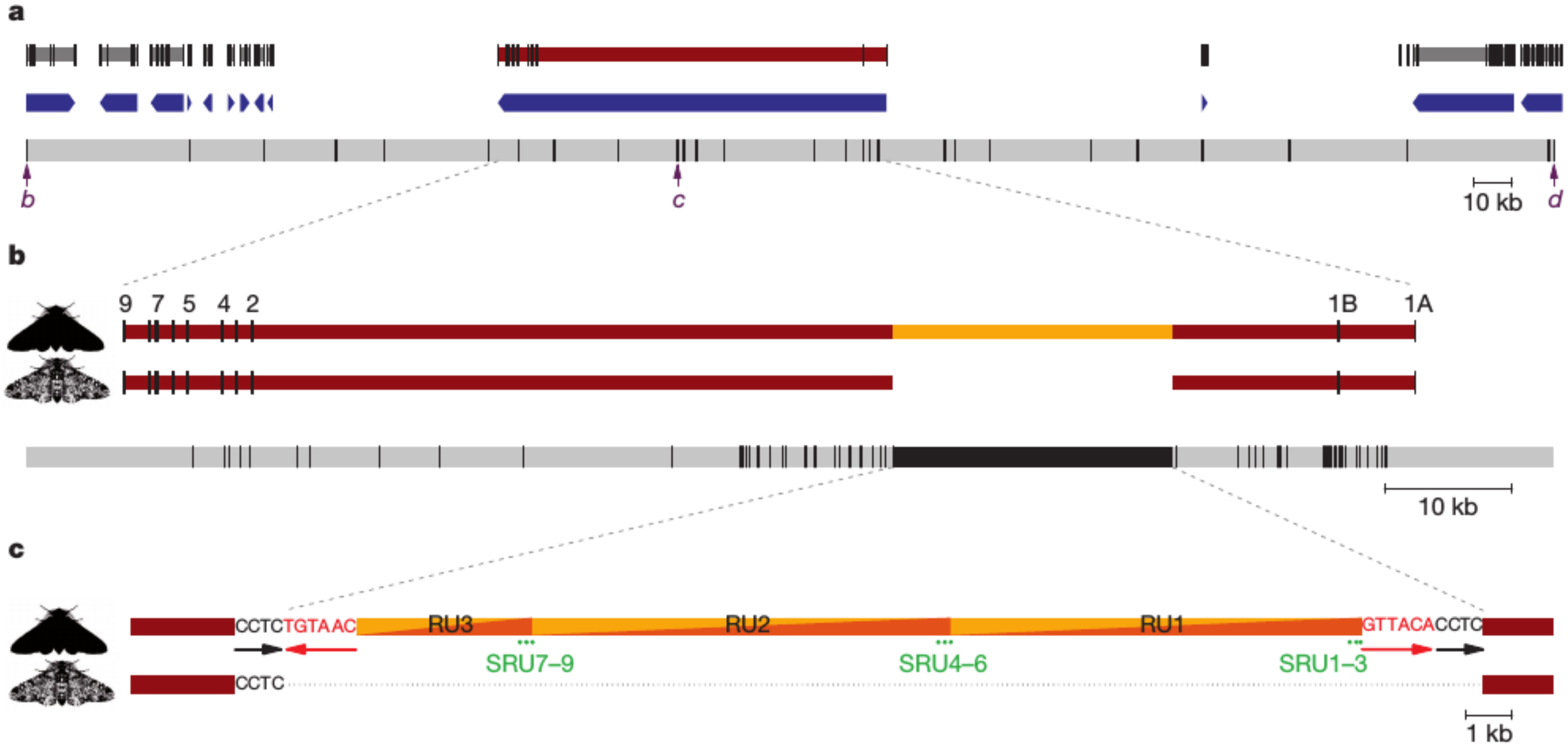
Figure 1 | A homologous genomic region controls a diversity of phenotypes across the Lepidoptera. Left, phylogenetic relationships[29]. Right, chromosome maps with colour pattern intervals in grey; coloured bars represent markers used to assign homology[5,8–10] and the first and last genes from Fig. 2 are shown in red. In *H. erato* the *HeCr* locus controls the yellow hindwing bar phenotype (grey boxed races). In *H. melpomene* it controls both the yellow hindwing bar (*HmYb*, pink box) and the yellow forewing band (*HmN*, blue box). In *H. numata* it modulates black, yellow and orange elements on both wings (*HnP*), producing phenotypes that mimic butterflies in the genus *Melinaea*. Morphs/races of *Heliconius* species included in this study are shown with names. All images are by the authors or are in the public domain.

LETTER

doi:10.1038/nature17951

The industrial melanism mutation in British peppered moths is a transposable element

Arjen E. van't Hof[1]*, Pascal Campagne[1]*, Daniel J. Rigden[1], Carl J. Yung[1], Jessica Lingley[1], Michael A. Quail[2], Neil Hall[1], Alistair C. Darby[1] & Ilik J. Saccheri[1]

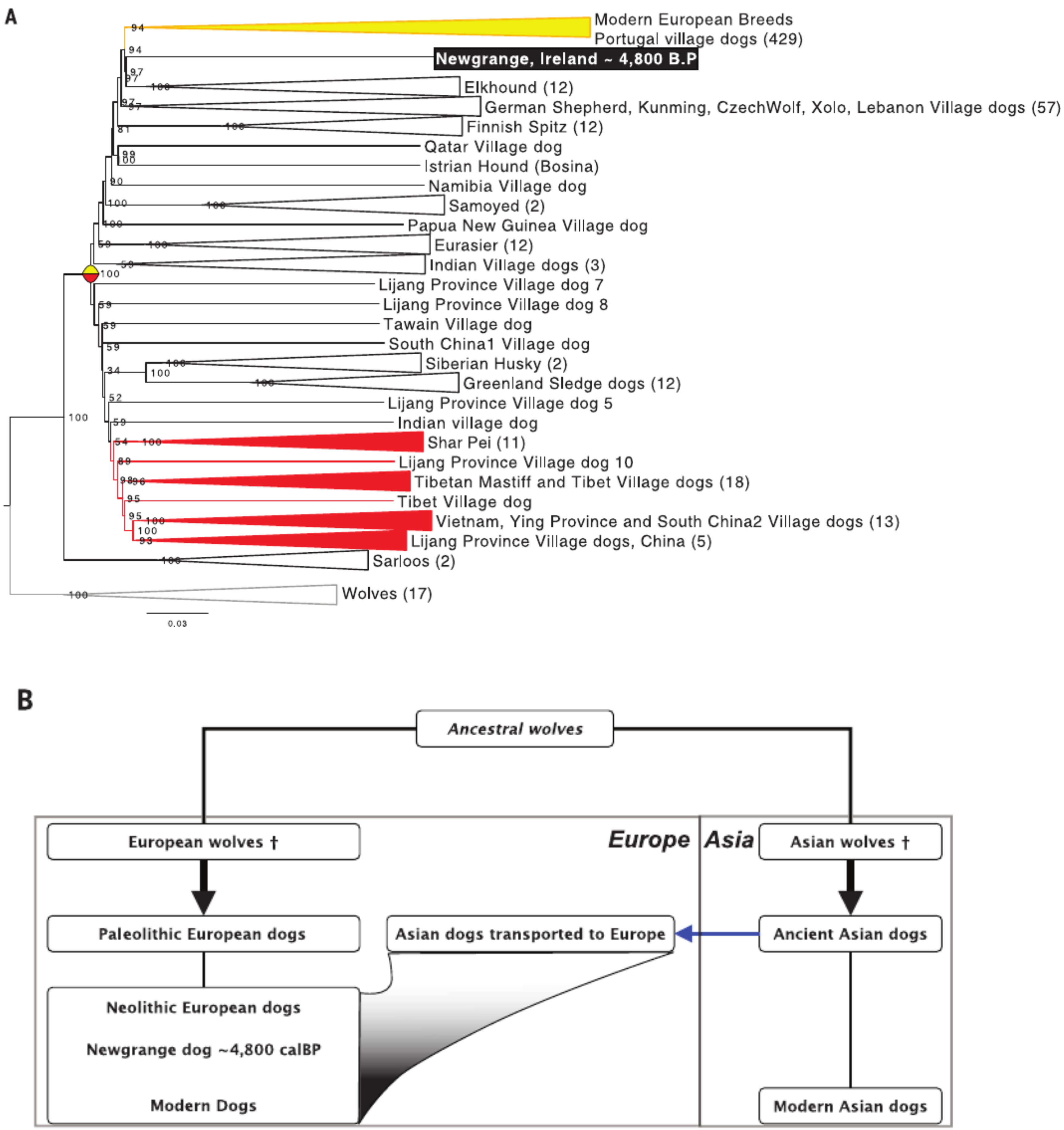


NONHUMAN GENETICS

Genomic and archaeological evidence suggests a dual origin of domestic dogs

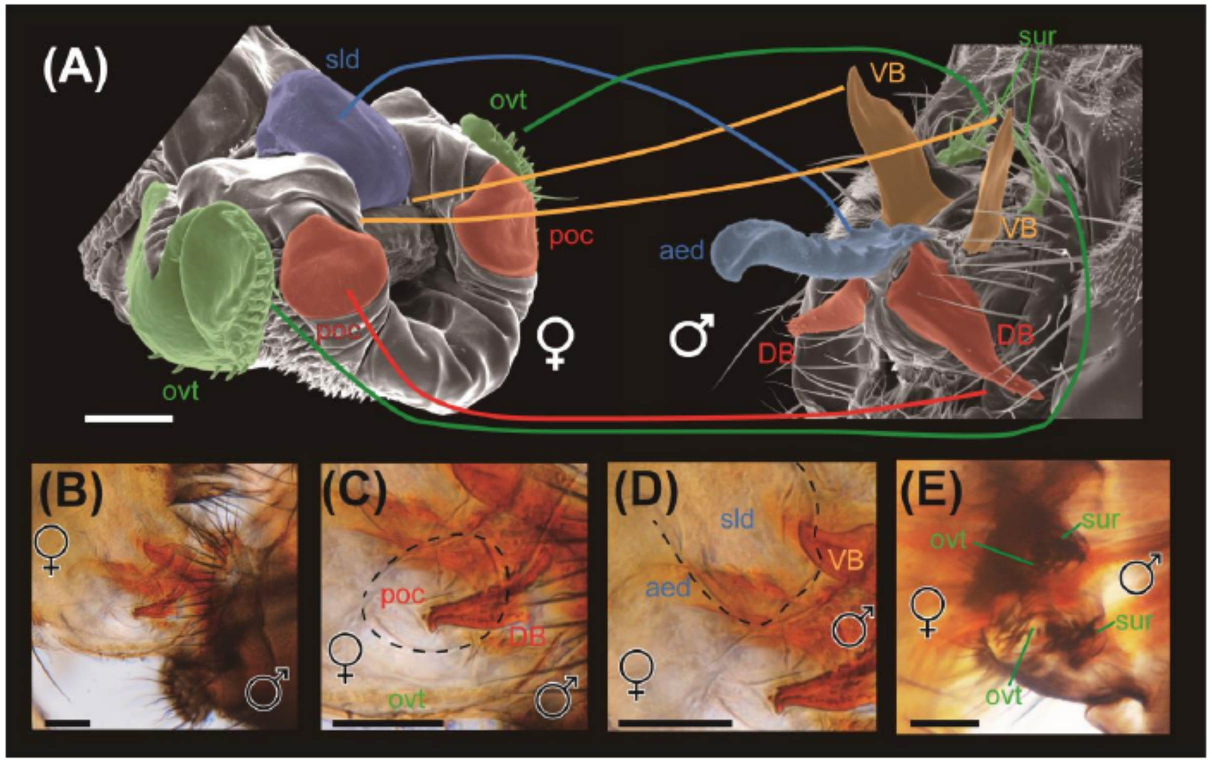
Laurent A. F. Frantz,[1*†] Victoria E. Mullin,[2†] Maud Pionnier-Capitan,[3,4] Ophélie Lebrasseur,[1] Morgane Ollivier,[3] Angela Perri,[5] Anna Linderholm,[1,6] Valeria Mattiangeli,[2] Matthew D. Teasdale,[2] Evangelos A. Dimopoulos,[1,7] Anne Tresset,[4] Marilyne Duffraisse,[3] Finbar McCormick,[8] László Bartosiewicz,[9] Erika Gál,[10] Éva A. Nyerges,[10] Mikhail V. Sablin,[11] Stéphanie Bréhard,[4] Marjan Mashkour,[4] Adrian Bălăşescu,[12] Benjamin Gillet,[3] Sandrine Hughes,[3] Olivier Chassaing,[3] Christophe Hitte,[13] Jean-Denis Vigne,[4] Keith Dobney,[14,15] Catherine Hänni,[3] Daniel G. Bradley,[2*] Greger Larson[1*]

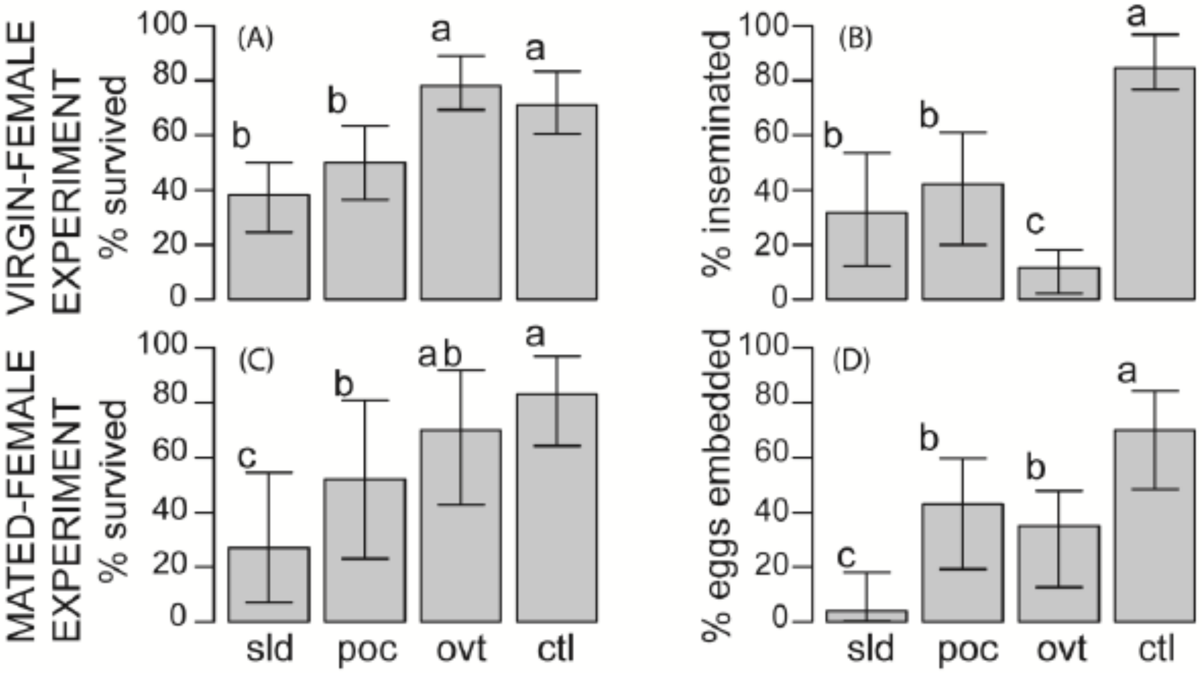
The geographic and temporal origins of dogs remain controversial. We generated genetic sequences from 59 ancient dogs and a complete (28x) genome of a late Neolithic dog (dated to ~4800 calendar years before the present) from Ireland. Our analyses revealed a deep split separating modern East Asian and Western Eurasian dogs. Surprisingly, the date of this divergence (~14,000 to 6400 years ago) occurs commensurate with, or several millennia after, the first appearance of dogs in Europe and East Asia. Additional analyses of ancient and modern mitochondrial DNA revealed a sharp discontinuity in haplotype frequencies in Europe. Combined, these results suggest that dogs may have been domesticated independently in Eastern and Western Eurasia from distinct wolf populations. East Eurasian dogs were then possibly transported to Europe with people, where they partially replaced European Paleolithic dogs.

A
Modern European Breeds
Portugal village dogs (429)
Newgrange, Ireland ~ 4,800 B.P
Elkhound (12)
German Shepherd, Kunming, CzechWolf, Xolo, Lebanon Village dogs (57)
Finnish Spitz (12)
Qatar Village dog
Istrian Hound (Bosina)
Namibia Village dog
Samoyed (2)
Papua New Guinea Village dog
Eurasier (12)
Indian Village dogs (3)
Lijang Province Village dog 7
Lijang Province Village dog 8
Tawain Village dog
South China1 Village dog
Siberian Husky (2)
Greenland Sledge dogs (12)
Lijang Province Village dog 5
Indian village dog
Shar Pei (11)
Lijang Province Village dog 10
Tibetan Mastiff and Tibet Village dogs (18)
Tibet Village dog
Vietnam, Ying Province and South China2 Village dogs (13)
Lijang Province Village dogs, China (5)
Sarloos (2)
Wolves (17)
0.03
B
Ancestral wolves
Europe
Asia
European wolves †
Asian wolves †
Paleolithic European dogs
Asian dogs transported to Europe
Ancient Asian dogs
Neolithic European dogs
Newgrange dog ~4,800 calBP
Modern Dogs
Modern Asian dogs

Significance of constraints on genital coevolution: why do female *Drosophila* appear to cooperate with males by accepting harmful matings?

Running title: Constrained genital coevolution in *Drosophila*





Male density and rapid evolution of genital morphology in the seed beetle *Callosobruchus maculatus*

D.M. Soper[1,2*] and W. L. Macy[1]

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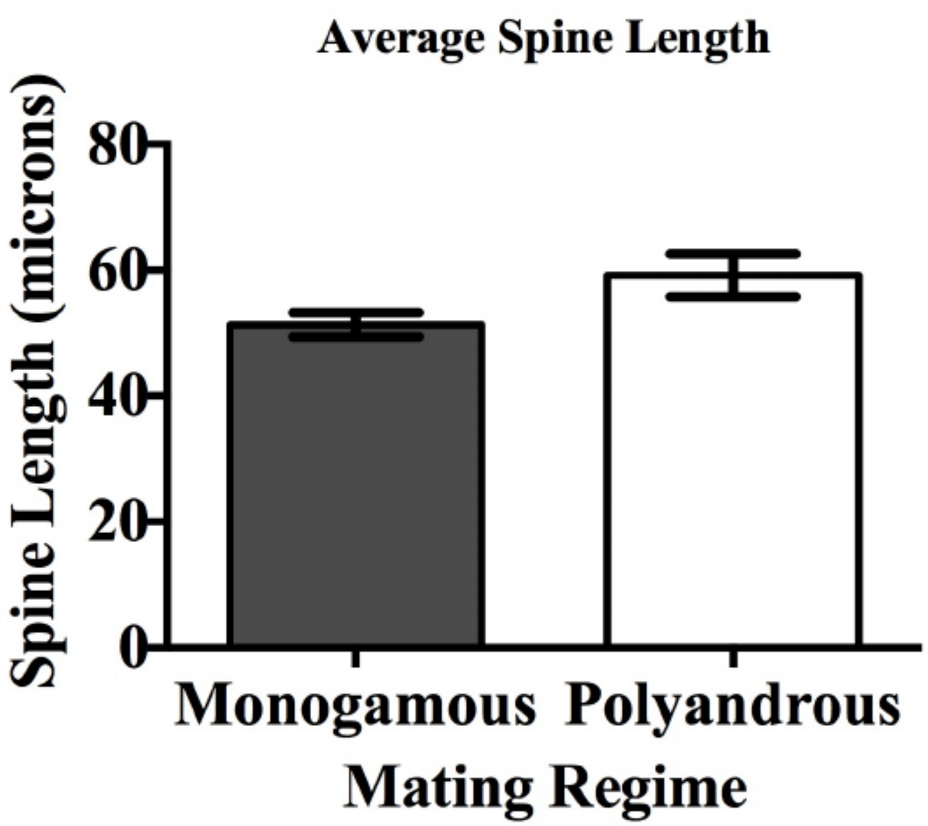

REVIEWS

EPIGENETICS

Genetic sources of population epigenomic variation

Aaron Taudt[1], Maria Colomé-Tatché[1,2] and Frank Johannes[3,4]

Abstract | The field of epigenomics has rapidly progressed from the study of individual reference epigenomes to surveying epigenomic variation in populations. Recent studies in a number of species, from yeast to humans, have begun to dissect the *cis*- and *trans*-regulatory genetic mechanisms that shape patterns of population epigenomic variation at the level of single epigenetic marks, as well as at the level of integrated chromatin state maps. We show that this information is paving the way towards a more complete understanding of the heritable basis underlying population epigenomic variation. We also highlight important conceptual challenges when interpreting results from these genetic studies, particularly in plants, in which epigenomic variation can be determined both by genetic and epigenetic inheritance.