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REVIEW

Resurrecting phenotypes from ancient DNA sequences: promises and perspectives[1]

K.L. Campbell and M. Hofreiter

Abstract: Anatomical changes in extinct mammalian lineages over evolutionary time, such as the loss of fingers and teeth and the rapid increase in body size that accompanied the late Miocene dispersal of the progenitors of Steller's sea cows (*Hydrodamalis gigas* (Zimmermann, 1780)) into North Pacific waters and the convergent development of a thick pelage and accompanying reductions in ear and tail surface area of woolly mammoths (*Mammuthus primigenius* (Blumenbach, 1799)) and woolly rhinoceros (*Coelodonta antiquitatis* (Blumenbach, 1799)), are prime examples of adaptive evolution underlying the exploitation of new habitats. It is likely, however, that biochemical specializations adopted during these evolutionary transitions were of similar or even greater biological importance. As these "living" processes do not fossilize, direct information regarding the physiological attributes of extinct species has largely remained beyond the range of scientific inquiry. However, the ability to retrieve genomic sequences from ancient DNA samples, combined with ectopic expression systems, now permit the evolutionary origins and structural and functional properties of authentic prehistoric proteins to be examined in great detail. Exponential technical advances in ancient DNA retrieval, enrichment, and sequencing will soon permit targeted generation of complete genomes from hundreds of extinct species across the last one million years that, in combination with emerging in vitro expression, genome engineering, and cell differentiation techniques, promises to herald an exciting new trajectory of evolutionary research at the interface of biochemistry, genomics, palaeontology, and cell biology.

Key words: paleophysiology, ancient DNA, extinct species, adaptation, protein structure.

Résumé : Les changements anatomiques chez des lignées de mammifères disparues au fil de l'évolution, comme la perte de doigts et de dents et l'augmentation rapide de la taille du corps qui ont accompagné la dispersion, au Miocène tardif, des ancêtres des rhytines de Steller (*Hydrodamalis gigas* (Zimmermann, 1780)) dans les eaux du Pacifique Nord et l'apparition convergente d'un pelage épais et les réductions associées de l'aire des oreilles et de la queue des mammouths de Sibérie (*Mammuthus primigenius* (Blumenbach, 1799)) et des rhinocéros laineux (*Coelodonta antiquitatis* (Blumenbach, 1799)), sont de parfaits exemples d'évolution adaptative sous-jacente à l'exploitation de nouveaux habitats. Il est toutefois probable que des spécialisations biochimiques adoptées durant ces transitions évolutives aient été tout aussi importantes, sinon plus, d'un point de vue biologique. Parce que ces processus « vivants » ne se fossilisent pas, l'acquisition d'information directe sur les attributs physiologiques d'espèces disparues demeure généralement hors de portée de l'étude scientifique. La capacité d'obtenir des séquences génomiques à partir d'échantillons d'ADN ancien, combinée à des systèmes d'expression ectopique, permet maintenant l'examen très détaillé des origines évolutives et des propriétés structurales et fonctionnelles de protéines préhistoriques authentiques. Des avancées techniques exponentielles en matière de récupération, d'enrichissement et de séquençage d'ADN ancien rendront bientôt possible la génération ciblée de génomes complets de centaines d'espèces disparues durant le dernier million d'années, ce qui, combinée à de nouvelles techniques d'expression in vitro, de génie génomique et de différenciation cellulaire, promettent une nouvelle trajectoire enlevante de recherche sur l'évolution à l'interface de la biochimie, de la génomique, de la paléontologie et de la biologie cellulaire. [Traduit par la Rédaction]

Mots-clés : paléophysiologie, ADN ancien, espèces disparues, adaptation, structure des protéines.

Our molecular past

As famously lamented by Charles Darwin (1859), the paleontological record is depressingly incomplete. This is, however, not unexpected as only a tiny fraction of carcasses ever become fossils and only a tiny fraction of these are discovered by humans. Moreover, as only the hard parts—in vertebrates mostly fragments of bones and teeth—tend to be preserved, much of what we know about the biology, behaviour, and evolution of most extinct species is inferred from partial remains. For a few species, like the woolly mammoth (*Mammuthus primigenius* (Blumenbach, 1799)) and the woolly rhinoceros (*Coelodonta antiquitatis* (Blumenbach, 1799)), much more detailed inferences are gleaned from occasional finds—albeit much less common than we are led to believe—of near complete mummified carcasses. Such discoveries have allowed stomach contents and internal organs of extinct organisms to be examined together with visual phenotypes such as the shape of ears or the length of tails and fur (e.g., Boeskorov et al. 2011; Fisher et al. 2012). While the latter anatomical changes are prime

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examples of adaptive evolution underlying the exploitation of Arctic habitats by these species, it is likely that physiological specializations may have been of similar or greater importance during their adaptation to the harsh environment of the Pleistocene Ice Ages. These dynamic processes are largely controlled by proteins that, for example, form cellular channels, bind and transport ligands, or drive chemical reactions; unfortunately, most are degraded quickly following death and become completely lost during fossilization, precluding their analysis in long-dead species.

More than 50 years ago, however, Pauling and Zuckerkandl (1963) recognized that the proteins of all living species contain a record of their historical past and proposed that ancestral sequence reconstruction could be used to deduce the primary structures of polypeptides in the ancestors of contemporary species. Presciently, they moreover suggested that via molecular "restoration studies", these archaic proteins could one day be synthesized and used to "study the physico-chemical properties of these molecules and to make inferences about their functions…[such as]…the oxygen affinity and its dependence on pH of ancestral hemoglobins…as well as the affinity of ancestral enzymes for various substrates and the probable nature of these substrates in past evolutionary history" (Pauling and Zuckerkandl 1963). This ambition was realized when two independent research groups used site-directed mutagenesis and protein engineering techniques to "resurrect" and study the kinetic behaviour of a ribonuclease from a shared common ancestor of swamp buffalo, river buffalo, and ox that lived ~5 million years ago (Ma) (Stackhouse et al. 1990), and the activity, thermostability, and three-dimensional structure of lysozymes from a game bird progenitor in the order Galliformes (Malcolm et al. 1990). Similar phylogenetically informed biotechnological approaches have subsequently been used to pinpoint the timing and molecular underpinnings of key adaptive functional changes in ancient proteins, including pancreatic ribonucleases in leaf-eating monkeys (Zhang 2006), visual pigments (rhodopsins) from archosaurs and early vertebrates (Chang et al. 2002; Shi and Yokoyama 2003), a primordial hormone receptor from a Proterozoic protostome–deuterostome common ancestor (Thornton et al. 2003), and even an elongation factor protein from 0.5 to 3.5 billion year old forbearers of modern bacteria (Gaucher et al. 2008).

Although a strength of this methodology is that it allows for the testing of hypotheses regarding molecular adaptations in deep evolutionary time (e.g., Jermann et al. 1995; Thornton 2004), it is unable to examine lineages with no living descendants, such as the many recently extinct Ice Age species that presumably evolved under strong selective pressures (Campbell et al. 2010). Notably, these species represent a substantial fraction of recent mammalian diversity, as large-scale mass extinction events over the past 40 000 years annihilated ~80% of large-bodied (>100 kg) North American and ~35% of northern Eurasian mammalian species (Stuart 1991). Herein, we review how combining technical advances in ectopic expression systems with methodologies that permit the retrieval of nuclear gene and protein sequences from ancient biological remains has not only opened an exciting new chapter in palaeobiological research, but promises to add a new dimension to the study of natural selection of both extinct and extant species.

Extinct species as exemplars of the August Krogh Principle

Given their small ears, short tail, stocky legs, thick woolly undercoat, and intimate association with frigid northern environments, it is a surprise for many to learn that the ancestors of woolly mammoths not only originated in subtropical Africa some 6.7 Ma, but that they are more closely related to Asian elephants (*Elephas maximus* L., 1758) than either species are to the African bush elephant (*Loxodonta africana* (Blumenbach, 1797)) and the African forest elephant (*Loxodonta cyclotis* (Matschie, 1900)) (Rohland et al. 2007, 2010). Moreover, it is clear from the fossil record that the first ancestral mammoths only entered northern Siberia ≤2 Ma (Lister et al. 2005), at the dawn of one of the most profound global cooling events in the Earth's history, the Pleistocene Ice Ages. Hence, in contrast to their almost certainly sparsely haired tropical ancestors (and their extant Asian and African relatives), the above-noted morphological specializations indicate that a strong selection pressure faced by early Siberian mammoths regarded the conservation of metabolic heat. It thus stands to reason that woolly mammoths, together with other recently extinct species that independently evolved to exploit cold Arctic and sub-Arctic environments, such as woolly rhinoceros and Steller's sea cows (*Hydrodamalis gigas* (Zimmermann, 1780)), provide particularly attractive model systems to study physiological adaptations to cold climates. Indeed, each lineage exhibits a relatively low rate of molecular evolution (Meredith et al. 2011) that, together with relatively recent divergence dates from their closest living ancestors (e.g., 17.5–22.8 Ma for the woolly rhinoceros–Sumatran rhinoceros (*Dicerorhinus sumatrensis* (G. Fischer [von Waldheim], 1814)) split; Willerslev et al. 2009), should facilitate the identification of key amino acid replacements underlying functional adaptation since the accumulation of additional random changes are expected to be minimal. Finally, each group is of an easily manageable size for comparative phylogenetic analyses (i.e., simple three-species comparisons; Garland and Adolph 1994) and for tests of convergent evolution. Taken together, these features align nicely with the August Krogh Principle, which states "for such a large number of problems there will be some animal of choice or a few such animals on which it can be most conveniently studied" (Krogh 1929). Extant high-Arctic mammals (e.g., muskox (*Ovibos moschatus* (Zimmermann, 1780)), reindeer (*Rangifer tarandus* (L., 1758)), and polar bears (*Ursus maritimus* Phipps, 1774)), by comparison, do not have a clear evolutionary history of recent movement from tropical to Arctic environments, nor do they have nontemperate sister taxa for phylogenetically informative three-species comparisons. However, despite the advent of a bacterial expression system for the ectopic synthesis of proteins in the late 1970s (Itakura et al. 1977), functional studies on woolly rhinoceros, mammoths, and Steller's sea cows (together with a host of other recently extinct "August Krogh Principle" exemplar species for addressing separate biological questions; Table 1) were previously hindered by an inability to obtain nucleotide-sequence data from these species.

Ancient DNA

The sole purpose of numerous processes in the bodies of all living organisms is to constantly repair the organic molecules (e.g., DNA, proteins, carbohydrates, and lipids) from which they are made. However, immediately following death, endogenous nucleases together with an army of invading organisms (predominantly bacteria and fungi) begin the inexorable degeneration of organic molecules within the body, leading to the near-complete abolishment of organic matter within a few decades (Hofreiter et al. 2001). However, upon desiccation or following freezing (i.e., in permafrost), the rate of degradation may be dramatically slowed, pushing the envelope back many thousands of years. Regardless, even under the best circumstances, DNA extractions from ancient specimens tend to be heavily contaminated with foreign DNA from invading microorganisms and contain only relatively small amounts of endogenous DNA. Hydrolytic damage moreover degrades these remaining molecules into short fragments—often 100 base pairs (bp) or less (Poinar et al. 2006; Green et al. 2010; Dabney et al. 2013)—that are fraught with chemical modifications arising from radiation, oxidation, and deamination (Lindahl 1993; Hofreiter et al. 2001).

Table 1. Extinct species as exemplars of the August Krogh Principle.

Ideally suited to test	Species
Cold tolerance	Woolly mammoth (*Mammuthus primigenius*), woolly rhinoceros (*Coelodonta antiquitatis*), Steller's sea cow (*Hydrodamalis gigas*)
Rapid dietary change	Mediterranean pygmy elephants (e.g., Cretan dwarf mammoth, *Mammuthus creticus* Bate, 1907; pygmy elephant, *Palaeoloxodon falconeri* Busk, 1867)
Fully aquatic adaptation	Great Auk (*Pinguinus impennis*)
Gigantism	Haast's Eagle (*Harpagornis moorei* Haast, 1872), Steller's sea cow, giant ground sloth
Wing reduction	Moas, elephant bird
Changes in hair and tail lengths	Woolly mammoth, woolly rhinoceros
Loss of fingers and teeth	Steller's sea cow

It is thus impressive that the field of ancient DNA was already established 30 years ago (prior to the advent of the polymerase chain reaction (PCR)) via the successful extraction, cloning, and sequencing of two small fragments (totaling 229 bp) of endogenous DNA from 140 year old dried muscle samples from an extinct subspecies of zebra (quagga, *Equus quagga quagga* Boddaert, 1785) (Higuchi et al. 1984). However, this study and the many that followed over the next 15 years concentrated on the small circular mitochondrial DNA molecules that are generally present in hundreds to thousands of copies per cell, but accounts for only a minute fraction (~16 500 bp or <0.00005%) of all genetic material in mammals. It also encodes only a handful of mitochondrial proteins, precluding its applicability for functional studies. It was not until 1999 that the use of dedicated ancient DNA facilities and strict adherence to procedures that minimize extraneous DNA contamination from modern sources demonstrated that small fragments (43–58 bp) of Pleistocene nuclear DNA—present in only two copies per cell—can survive in amounts sufficient for PCR amplification in at least some permafrost remains (Greenwood et al. 1999). Although these nuclear gene sequences provided little to no information about the structure and function of the ancient proteins they encoded, this work represented an important early advance in the development of the field.

Linking genotype with phenotype

With rare exceptions, such as those involving pseudogenization of tooth-specific (e.g., enamelin; Meredith et al. 2009; Springer et al. 2015) or eye-specific genes (e.g., retinal opsins; Meredith et al. 2013), our ability to ascribe a genotype to a specific phenotypic variant in extinct organisms is virtually nonexistent (Shapiro and Hofreiter 2014). However, the ability to obtain ancient nuclear DNA sequences, together with the ability to create and ectopically express recombinant proteins, in theory opened the door to the genetic reconstruction of extinct phenotypes from subfossil material. It nonetheless remained largely impractical to sequence the hundreds to thousands of nucleotides—often spanning multiple coding exons—that comprise most genes until the development of two-step multiplex approach that allowed for the simultaneous amplification of the first complete Ice Age mitochondrial genome (not surprisingly, a woolly mammoth) in two reactions (Krause et al. 2006). This advance quickly lead to the retrieval of the first complete nuclear encoded gene, the melanocortin 1 receptor (*MC1R*; 1236 bp), from an extinct species: again, from the woolly mammoth (Römpler et al. 2006). This gene is one of a large number of genes known to be involved in colour determination of both birds and mammals (Rees 2003), and was examined to test whether differences in hair coloration—from blond to red to almost black—of permafrost-preserved mammoths could be explained by variations in gene function as opposed to chemical factors in the sediments to which the hairs had been exposed for tens of thousands of years (see e.g., Tridico et al. 2014). A follow-up study focused on a short (128 bp) fragment of this locus from two Neanderthal specimens (Lalueza-Fox et al. 2007). Notably, both studies revealed heterozygous alleles with one copy exhibiting unique amino acid exchanges not found in living elephants or humans, respectively. In vitro functional analyses of proteins harbouring these amino exchanges expressed in an immortalized line of monkey kidney cells further demonstrated sharp reductions in both basal activity and responses to two agonists, aMSH and NDP-aMSH, in the derived mammoth and Neanderthal alleles suggesting the presence of blond and fair-skinned – red-head phenotypes, respectively (Römpler et al. 2006; Lalueza-Fox et al. 2007). However, for mammoths at least, single nucleotide polymorphism typing of *MC1R* fragments from 47 additional mammoths revealed the presence of only a single heterozygous individual carrying the derived allele, indicating that light-coloured mammoths, if present in the population, were extremely rare (Workman et al. 2011). Nonetheless, these pioneering studies demonstrated that the genetic reconstruction of phenotypes from extinct species had become a practical reality.

Another highly conspicuous externally visible characteristic of woolly mammoths is their extremely thick overcoat that carried hairs up to a metre long. As similar (though less dramatic) long-hair phenotypes in mice, dogs, and cats are associated with non-functionalization of the fibroblast growth factor 5 (*FGF5*) gene, this locus together with four keratin genes were investigated (Roca et al. 2009). However, only synonymous (silent) mutations were identified on the mammoth *FGF5* locus, while the mammoth keratin genes did not possess any unique substitutions, indicating that other loci must underlie the thick woolly phenotype of mammoths (Roca et al. 2009). In this regard, 38 candidate genes that may underlie both coat colour and hair morphology in this lineage were identified in a recent study that sequenced the genomes of two woolly mammoths to ~20-fold coverage (Lynch et al. 2015). These authors also revealed mammoth-specific residue exchanges in four transient receptor potential (TRP) channels—TRPA1, TRPM4, TRPV3, and TRPV4—implicated in temperature discrimination in mammals (Lynch et al. 2015). Computer modelling of these exchanges onto cryo-electron microscopic structures moreover pinpointed residues on the TRPA1 and TRPV4 proteins that are predicted to alter their gating properties (i.e., maximal activity and range of temperatures over which they are activated). Intriguingly, a woolly mammoth mutation (N647D) located in a loop region of TRPV3 that forms an ion pore for Ca^{2+} was predicted to have similar effects and has been shown to abolish heat sensitivity in the orthologous mouse protein (Grandl et al. 2008). Briefly, this heat-activated cation channel is expressed in skin, sensory neurons, and epidermal keratinocytes and is stimulated at temperatures >33 °C in mice (Moqrich et al. 2005). Intriguingly, this channel also co-localizes with hair follicles, where it further operates as a regulator of hair morphogenesis (Cheng et al. 2010). Functional expression of the mammoth and inferred ancestral Asian elephant – mammoth TRPV3 channels in HEK293 cells revealed that while the activation temperatures (~29 °C) of both proteins were similar, the maximal activity of mammoth TRPV3 was reduced by ~20% relative to that of the ancestral elephantid Ca^{2+} channel (Lynch et al. 2015). As TRPV3 activation inhibits hair-shaft elongation and hair-follicle regression in mice, the authors accordingly suggest the N647D substitution may in part underlie the evolution of a woolly phenotype in mammoths. Phenotypic

characterization of genes relating to hair cover and (or) thermal sensation in other cold-adapted species (e.g., woolly rhinoceros, Steller's sea cow) have yet to be examined and offer a fertile avenue for research.

As noted earlier, morphological adaptations often play key roles in a species' adaptation to new environments. However, in certain instances these modifications require the presence of specific biological or physiological traits prior to, or concurrent, with their evolution. One example is the countercurrent heat exchangers of regionally heterothermic vertebrates, which allow for large temperature gradients between the core and the extremities. For cold-adapted mammals, this vascular arrangement reduces heat loss to the environment, thereby lowering daily energy requirements when thermal costs are at their highest and when forage quality and forage availability are often at their lowest (i.e., during winter). Unlike tropical species, such as humans, which possess blood with a high thermal sensitivity (whereby small increases in temperature cause relatively large increases in oxygen offloading), ostensibly to promote increased oxygen delivery to warm exercising muscles, temperate species appear to require blood that exhibits a relatively low thermal sensitivity to maintain appropriate oxygen delivery to cold tissues (Weber and Campbell 2011). This altered blood phenotype arises from amino acid substitutions in the hemoglobin molecules that inherently lower the energetic transition of the protein from the tense (T) deoxygenated state to the relaxed (R) oxygenated state (Weber et al. 2014), and (or) via the binding of other molecules inside the red blood cells (primarily protons, chloride ions, and organic phosphates such as 2,3-diphosphoglycerate) to hemoglobin which release heat, which can be used to help break the heme–oxygen bond (Weber and Campbell 2011). In the latter case, it should be noted that hemoglobins of noncold-adapted species may also bind these same effector molecules; "cold-adapted" hemoglobins are simply able to bind more effector molecules and thus their oxygen affinity is less sensitive to changes in temperature.

Given the Arctic habitat of woolly mammoths, it was hypothesized that they evolved substitutions in their hemoglobin that may, at least in part, underlie their physiological adaptation to the cold (Campbell et al. 2010). DNA sequencing revealed that the mammoth β-type (β/δ) globin chain only differed from Asian elephants at 3 of 146 amino acid positions, while the α-type chain had not acquired any substitutions following the split of these two lineages. As predicted from computer modelling, the oxygenation properties of the recombinant mammoth protein measured in the presence and absence of red blood cell effector molecules and at various physiologically relevant temperatures revealed radically different functional attributes relative to those of Asian elephants (Campbell et al. 2010; Yuan et al. 2011). The most striking change was a strong increase in the inherent oxygen affinity of the molecule likely caused by a charge-changing residue exchange (β/δ101Glu→Gln) within the sliding interface of the protein. Remarkably, however, this same amino acid substitution also appeared to establish additional effector binding sites for chloride and protons that not only negated this deleterious effect, but also significantly lowered the proteins' sensitivity to temperature (Campbell et al. 2010; Yuan et al. 2011). From an evolutionary standpoint, it bears mentioning that no other amino acid replacement at this residue position appears to be able to create this new binding site, indicating that mammoths evolved the only possible beneficial mutation at this position. These conclusions were corroborated by X-ray crystallography and solution nuclear magnetic resonance (NMR) studies (Yuan et al. 2011; Noguchi et al. 2012), coupled with site-directed mutagenic experiments whereby individual and paired mammoth changes were introduced into the Asian elephant background (Yuan et al. 2013), that permitted the structural and mechanistic dissection of this extinct physiological phenotype. Such investigations are required to elucidate the functional role of novel amino acid replacements not found in living species or for pinpointing the relative contributions of individual mutations and are likely to be employed more in future as more archaic proteins are resurrected.

In vivo expression

While amino acid polymorphisms and gene inactivation presumably drive many phenotypic differences observed in extinct species relative to their extant relatives, variations in noncoding *cis*-regulatory elements that govern the location, timing, or level of expression of functional loci may also underlie important phenotypic innovations (Wray 2007). Unfortunately, relatively few of these regions have been identified and characterized in model taxa, let alone extinct species. Early progress in this latter area was achieved by generating an expression construct containing the transcriptional enhancer element of the Tasmanian tiger (*Thylacinus cynocephalus* (Harris, 1808)) proα1(II) collagen (*Col2a1*) gene with the human β-globin basal promoter flanked by a *lacZ* (β-galactosidase) reporter gene. Histological staining 2 weeks after injection of this construct into mouse zygotes resulted in chondrocyte-specific expression in the developing fetuses. Although the nucleotide differences in the thylacine enhancer compared with the mouse version did not alter the function of this element (Pask et al. 2008), this work was the first to illustrate the future promise of elucidating variations in the function of regulatory sequences from extinct species in an in vivo model system.

More recently, an in vivo system was also used to investigate the functionality of the *tbx5* gene in extinct, New Zealand endemic moas. The transcription factor encoded by this locus is known to play a critical role in forelimb development in all vertebrates (Ng et al. 2002; Agarwal et al. 2003). Moas show the most extreme reduction of the forelimb skeleton among ratites, a (paraphyletic) group of flightless birds from the southern hemisphere, though, phylogenetically, they form the sister group to the fully flighted South American tinamous (Phillips et al. 2010). Briefly, Huynen et al. (2014) investigated the moa *tbx5* sequence structure and transcription activity in both cell culture and chicken embryo assays. Surprisingly, and despite wingless moa likely having lost their entire forelimb girdles >20 Ma (save for a small residual shoulder bone, the scapulocoracoid), their *tbx5* gene not only showed transcription activation similar to that of the chicken homolog in cell culture assays, but it also triggered the development of forelimb features when injected into the hind limb of chicken embryos (Huynen et al. 2014). These results demonstrate that while the moa *tbx5* gene presumably maintains a role in initiating development of the forelimb and pectoral girdle (scapulocoricoid), it is not sufficient for continued forelimb growth (Huynen et al. 2014).

Another example explored the effects of two amino acid changes in a gene (*FOXP2*) critical for the development of speech and language in humans using a mouse model system. Earlier studies identified two residue replacements in the human protein that arose following the split of humans from chimpanzees (*Pan troglodytes* (Blumenbach, 1775)) (5–10 Ma), but prior to the divergence of humans from other archaic (i.e., Neanderthal and Denisovan) human lineages (Enard et al. 2002, Krause et al. 2007). Introduction of these "humanized" changes into mice altered neuronal properties of basal ganglia that affect ultrasonic vocalizations, suggesting an important role in the evolution of human vocal communication (Enard et al. 2009). More recently, a nucleotide substitution in a highly conserved region of intron 8 of *FOXP2* conserved in most (98%) modern humans, but not found in other anthropoid primates including Neanderthals and Densiovans, was revealed to affect a binding site for another transcription factor (*POU3F2*) exclusively expressed in the central nervous system (Maricic et al. 2013). Intriguingly, in vitro functional assays further revealed that the ancestral (premodern human) version

was more efficient in activating transcription from a reporter construct, suggesting a prominent role for this mutation in a recent selective sweep of this locus in modern humans (Maricic et al. 2013). However, studies employing transgenic mice that carried each of the *POU3F2* variants fused to a *lacZ* reporter failed to detect enhancer activity, suggesting that the archaic and modern 1.8 kb long human sequences do not work in the mouse genetic background (Maricic et al. 2013). Despite this setback, similar in vivo approaches are likely to be central to deciphering the roles of derived mutations in regulatory elements or complex biochemical pathways of extinct species in the future.

Finally, novel insights into the physiological attributes of extinct species have also been achieved via inclusion of specific gene products into ancestral sequence reconstruction data sets of proteins known to strongly influence phenotypic traits. The oxygen-storing muscle pigment myoglobin, for example, plays a key role in the ability of air-breathing birds and mammals to hold their breath and actively forage under water. Using myoglobin sequence data from 128 extant and two extinct species (woolly mammoth and Steller's sea cow), Mirceta et al. (2013) revealed a molecular signature of increased surface protein charge in all lineages of diving mammals with an extended aquatic history—from 15 g American water shrews (*Sorex palustris* Richardson, 1828) to 80 000 kg whales—that underlies this phenotype via its mechanistic linkage with muscle myoglobin content and hence maximal dive time. Apart from providing insights into the tempo and multiple convergent routes of dive-capacity evolution across the mammalian phylogeny, the ancestral sequence reconstruction approach employed by these authors allowed for a comprehensive modelling of the muscle oxygen storage capacity and maximal submergence times—figuratively putting "flesh onto the bones"—of successive transitional forms of whales, sea cows, and seals over more than 50 million years of evolution. Importantly, inclusion of woolly mammoths and Steller's sea cow into this data set substantially increased the sample size and hence reliability of ancestral sequence reconstruction for the afrotherian clade that provided unique evidence for a shared early Palaeocene amphibious ancestor of sea cows, elephants, and hyraxes (Mirceta et al. 2013). The ability to trace protein evolution over geological time scales further permitted these authors to deduce that the longer maximal submergence time observed for Steller's sea cows (~300 s) by Georg Wilhelm Steller (Steller 1751) relative to extant sirenians primarily arose from massive increases in body size (up to 11 000 kg) in the former lineage as opposed to physiological specializations. As sequence data from Holocene and Pleistocene organisms becomes more readily available, we anticipate that similar approaches will allow the evolution and characterization of other phenotypic traits to be reconstructed for extinct species in unprecedented detail.

Future perspectives

To date, functional ancient DNA studies have focused on one or only a couple of loci, yet many morphological and physiological phenotypes are determined by a complex interaction of genes. Unfortunately, even the most efficient multiplex PCR techniques are quite laborious and thus PCR is not really an option to study the myriad of genes potentially involved in, for example, the long-hair phenotype of woolly mammoths and woolly rhinoceros. However, the development of specifically tailored ancient DNA extraction methodologies that optimize recovery of the miniscule amounts of DNA within prehistoric samples (Dabney et al. 2013), together with parallel technical advances in DNA enrichment (e.g., hybridization capture) and high-throughput next-generation sequencing (NGS) techniques, now allow ancient nuclear genomes to be sequenced to high coverage and accuracy (e.g., Rasmussen et al. 2010; Meyer et al. 2012; Prüfer et al. 2014). Indeed, the field of ancient DNA was rapidly transformed by the application of NGS technologies (Margulies et al. 2005) to ancient DNA (Poinar et al. 2006). Since then, partial or complete nuclear genomes of 4 000 to 60 000 year old woolly mammoths (Miller et al. 2008; Lynch et al. 2015; Palkopoulou et al. 2015), three 75 000 to 130 000 year old extinct camelids (Heintzman et al. 2015), three 16 000 to ~700 000 year old horses (Orlando et al. 2013; Schubert et al. 2014), a 4 500 year old Saqqaq paleoeskimo (Rasmussen et al. 2010), several Neanderthals (Green et al. 2010; Prüfer et al. 2014), a previously unknown human lineage (Denisovans) from Siberia (Reich et al. 2010; Meyer et al. 2012), and numerous anatomically modern humans from the Late Pleistocene (e.g., Fu et al. 2014; Rasmussen et al. 2014) have been published. Unfortunately, this tour de force technique has so far been of very limited use to study the physiological peculiarities of extinct species because, due to the random nature by which these data are obtained, some sections of the genome are sequenced several times, while others are missed altogether. For instance, about 50% of all DNA sequences—2.1 billion base pairs—in the original 0.8× coverage mammoth genome were not sequenced at all (Miller et al. 2008). Moreover, low-coverage genomes contain too many errors due to postmortem damage of the ancient DNA templates and errors introduced during the sequencing process to be able to offer insights into the physiology of the individual studied. The only way to trust ancient gene sequences obtained with the shotgun approach is to sequence so heavily that most regions are covered many times over, as was done for the two recent mammoth studies (Lynch et al. 2015; Palkopoulou et al. 2015). Given the high levels of postmortem, exogenous DNA in most ancient specimens (>50% to >95%; e.g., Poinar et al. 2006; Green et al. 2010), this approach quickly becomes cost prohibitive, especially when one considers that studies should target multiple individuals of a species, because intraspecific variation often exists in such traits.

Fortunately, a recently developed approach called hybridization capture enables the targeting and enrichment of millions of base pairs within the genome (Hodges et al. 2007), even from degraded DNA with heavy exogenous contamination (Burbano et al. 2010; Skoglund et al. 2014), something that could never be achieved using PCR. Remarkably, this approach has also allowed for the retrieval of complete mitochondrial genomes from >300 000 year old nonpermafrost-preserved human and cave bear (*Ursus spelaeus* (Rosenmüller and Heinroth, 1794)) samples (Dabney et al. 2013; Meyer et al. 2014). The lower stringency of this approach moreover permits capture of gene coding sequences from lineages that diverged hundreds of millions of years ago (Li et al. 2013), with the caveat that capture efficiency is inversely proportional to genetic distance. Nonetheless, in combination with NGS platforms, this approach has recently demonstrated the simultaneous, high-coverage retrieval (~99%) of dozens of nuclear genes from five ~1000 year old Steller's sea cow samples using bait designed from dugong (*Dugong dugon* (Müller, 1776)), manatee (genus *Trichecus* L, 1758), and even elephant and hyrax sequences (Mirceta et al. 2013; Springer et al. 2015), the latter two of which diverged from sirenians in the Paleocene (~60 Ma; Meredith et al. 2011; Springer et al. 2015). The validation of cross-ordinal capture from ancient genomes opens the door to studying hundreds of vertebrate (largely avian and mammal) taxa with Pleistocene and Holocene extinction histories (e.g., glyptodonts, giant ground sloth, thylacine, Great Auk (*Pinguinus impennis* (L., 1758)), elephant bird, among many others), thus providing unparalleled insights into the phylogenetic affinities and divergence times of these species (see Fig. 1). This approach will also permit comprehensive studies on phenotypic evolution that focus, for example, on gene networks underlying the loss of teeth and fingers in Steller's sea cows and the long-hair – short-tail phenotypes of woolly mammoths and woolly rhinoceros. Given the large number of loci involved in these traits, such studies will benefit from positive selection analyses that help identify genes potentially underlying adaptive changes, as has been conducted for archaic humans (Meyer

Fig. 1. Schematic diagram outlining the steps from subfossil material to paleophysiology. Briefly, ancient DNA extracts from bone (or other material) are purified and ligated to adaptor strands housing a specimen-specific identifying index sequence. This step allows multiple samples to be pooled for subsequent hybridization capture and (or) sequencing (see below); these barcoded libraries moreover can be safely used in any standard DNA laboratory—and re-amplified if stocks become depleted—as any introduced contamination (i.e., DNA strands lacking an index sequence) is automatically removed from analyses following sequencing. Targeted regions of the genome are enriched via DNA hybridization with biotinylated oligos (typically 60–120 bp in length) carrying complementary sequence, captured with magnetic beads, and eluted for subsequent next-generation sequencing; nontarget DNA is discarded. Retrieved sequences are then assembled or mapped to reference sequences from closely related species. Depending on the specific question, obtained gene or promotor or enhancer sequences can be ectopically expressed for ensuing functional, structural, or developmental analyses.

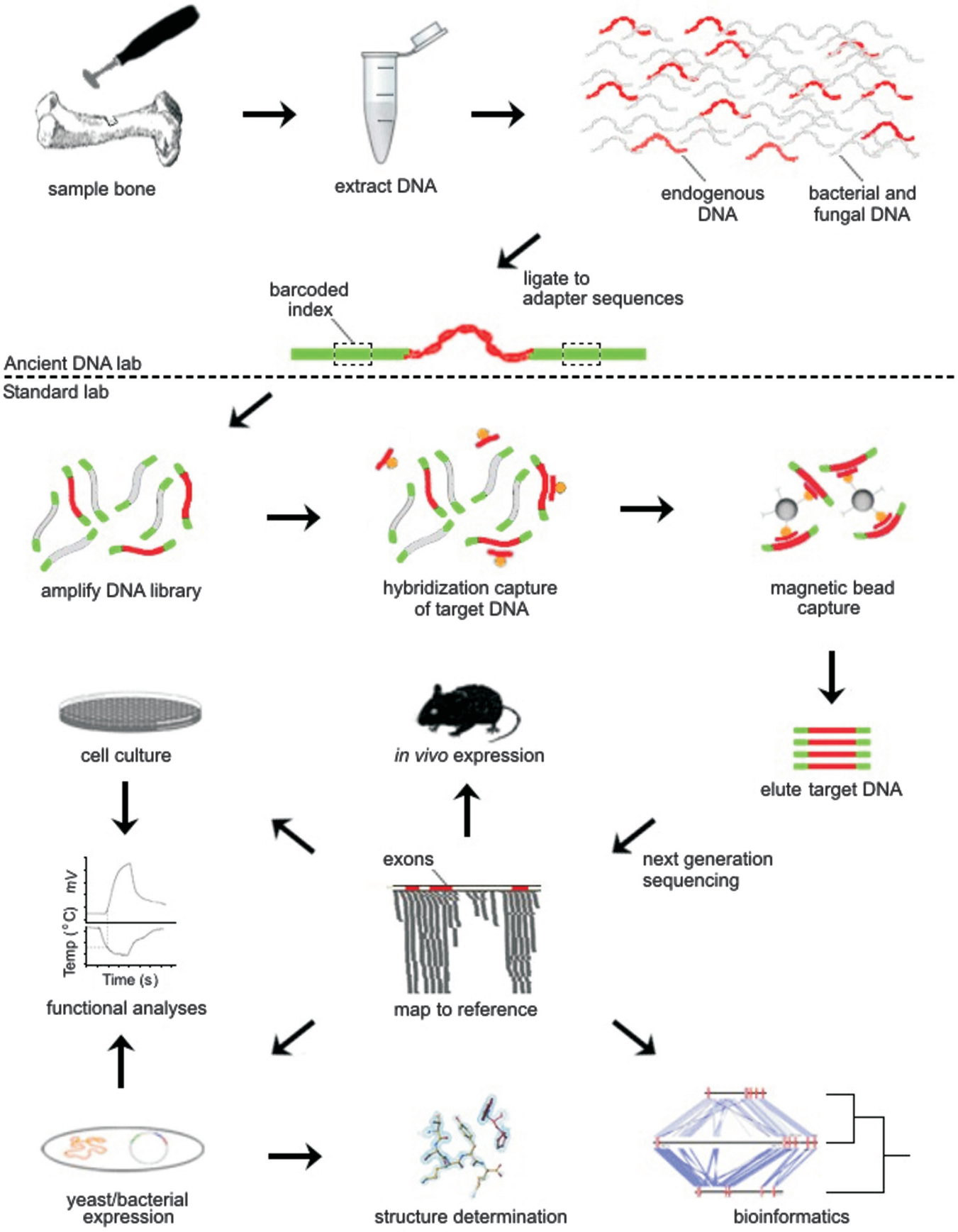
et al. 2012; Prüfer et al. 2014), mammoths (Lynch et al. 2015), and horses (Orlando et al. 2013; Schubert et al. 2014). As shown above, however, the gold standard will remain functional verification.

The development of improved sequencing platforms able to sequence billions of DNA fragments in combination with whole genome enrichment and capture—whereby genomes of extant species are fragmented, biotinylated, and used to capture corresponding sequences from closely related extinct taxa (Enk et al. 2014)—will further increase the efficiency of ancient DNA retrieval. This relatively low cost, massively parallel targeted sequencing approach also holds the potential for large-scale population-level studies, whereby, for example, the complete genomes of Siberian mammoths from relatively warm interglacial periods can be genetically compared and contrasted with individuals living during glacial maxima; direct geographical comparisons among Siberian, Spanish, and North American populations may also be possible.

As proteins tend to be more resistant than nucleic acids to degradation, ancient proteomic methodologies promise to substantially extend both the age and the range of organisms beyond that currently available to DNA-based approaches, while offering additional benefits such as developmental stage and tissue-specific expression patterns (Cappellini et al. 2014). Specifically, liquid chromatography – tandem mass spectrometry (LC–MS/MS) techniques allow ancient peptides to be directly sequenced from subfossil material. To date, this approach has primarily been employed to obtain collagen sequences (which is highly abundant in bone) and elucidate the phylogenetic position of extinct species from temperate and tropical latitudes for which ancient DNA methodologies have failed, such as the endemic South American notoungulates (Welker et al. 2015; Buckley 2015) and the enigmatic "Malagasy aardvark" of Madagascar (Buckley 2013). However, the great potential of LC–MS/MS for paleophysiological characterizations of extinct species was perhaps best demonstrated by the partial retrieval of 126 mostly low-abundance bone matrix and blood plasma proteins (Cappellini et al. 2011) from the same 43 000 year old woolly mammoth femur sample used in the *MC1R* and hemoglobin studies described above. As generally comparable results have been obtained from archeological bovine samples dating back hundreds of thousands of years (Buckley and Wadsworth 2014; Wadsworth and Buckley 2014), with a partial MS-generated collagen sequence even reported from a 80 million year old hadrosaur (*Brachylophosaurus canadensis* Sternberg, 1953; Schweitzer et al. 2009), this approach currently offers the best hope of directly resurrecting pre-Pleistocene phenotypes.

Another recent development, which may have a major impact on the field lies in the ability to reveal epigenetic changes between the genomes of modern and ancient specimens. The first publication showing that it is in principle possible to study DNA methylation patterns from ancient DNA sequences was published in 2010 (Briggs et al. 2010). Briefly, ancient DNA extracts were first treated with uracil N-glycosylase (UNG), an enzyme that removes uracils, which are common in ancient DNA due to cytosine deamination (Pääbo 1989; Hofreiter et al. 2001); as DNA breaks at these abasic sites, DNA damage artifacts are effectively removed from the resulting sequences. In contrast, methylated cytosins—a hallmark of epigenetic modifications—are deaminated to thymins, which are not removed by UNG and thus appear as C→T changes in the sequences of UNG-treated ancient DNA. Alternatively, cytosine methylation can also be measured directly on individual genomic regions (Llamas et al. 2012) or inferred from NGS data if polymerases are used that cannot read over uracils during the initial library amplification (Pedersen et al. 2014). Despite the large potential of ancient epigenetics, there are so far only a handful of studies on this topic (Briggs et al. 2010; Llamas et al. 2012; Pedersen et al. 2014; Gokhman et al. 2014; Smith et al. 2014). While the first three were mostly proof-of-principle publications, Gokhman et al. (2014) found a number of regions that were differentially methylated between modern humans, Denisovans, and Neanderthals. Some of these are quite intriguing because they affect regions that seem to make morphological sense, such as a methylation difference in the HOXD cluster, which affects limb development (Gokhman et al. 2014). However, methylation of the HOXD complex is preserved across great apes, which raises questions about the reliability of the results (Schneider et al. 2014), although the authors of the original study took considerable effort to exclude any artefactual results. Even more surprising was the finding of hypermethylation of a nonprotein-coding RNA gene (H19) in Neanderthals (Gokhman et al. 2014), as methylation of this locus is conserved across 170 million years of evolution in placental and therian mammals (Schneider et al. 2014), arguing for at least some false positive results in this study. A possible cause may lie in the fact that DNA methylation patterns diminish over time in the fossil record (Smith et al. 2014), although the authors of the Neanderthal–Denisovan study tried to take this factor into account. Thus, while ancient epigenetics may have substantial promise, further studies are required to reveal both its potential and pitfalls (for a comprehensive review on this topic see Orlando et al. 2015).

Perhaps the most exciting future perspective for the field lies in available technologies that may soon allow ancient DNA adherents to overcome limitations inherent to single gene targeting and (or) the use of inappropriate in vivo and in vitro genetic background models (e.g., mouse, chicken). For instance, available genome-editing techniques that enable precisely targeted modifications (i.e., mutations, insertions, deletions) to be introduced into living cells (Gaj et al. 2013), in conjunction with recent developments in cell biology that allow differentiated adult cells to be reprogrammed into pluripotent stem cells (Takahashi and Yamanaka 2006), theoretically provides a means to simultaneously engineer numerous gene mutations from an extinct species into cells of a closely related taxon. Subsequent in vitro differentiation of these cells into isolated tissue cultures of interest (e.g., retinal cells, melanocytes) can then be used to faithfully reconstruct and study complex biological phenotypes of long-dead species. Several authors have speculated this approach could one day even allow for the "de-extinction" of iconic Ice Age (and more recently extinct) species (Zimmer 2013; Seddon et al. 2014), though considerable ethical and technological hurdles remain.


sample bone
extract DNA
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ligate to adapter sequences
barcoded index
Ancient DNA lab
Standard lab
amplify DNA library
hybridization capture of target DNA
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cell culture
in vivo expression
next generation sequencing
exons
mV
Temp (°C)
Time (s)
functional analyses
map to reference
yeast/bacterial expression
structure determination
bioinformatics

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