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Research proposal: HistoGenes [Part B2]

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Part B2: The scientific proposal (max. 15 pages, excluding the Resources section and References)

Section a. State-of-the-art and objectives

a1. The historical problem: State of the art and directions of research

HistoGenes addresses one of the formative periods in European history: between c. 400 and c. 900 CE, medieval Europe emerged after the dissolution of the Western Roman Empire, in a process that involved migrations and demographic change, the rise of post-Roman Christian kingdoms in the West and of non-Roman 'barbarian' societies in the East (Brown 2003; Smith 2005; Halsall 2007; Heather 2009; Wickham 2009). For centuries, the frontier of the Roman Empire, stretching along the Rhine and Danube rivers, had divided the continent into a Roman south and a 'barbarian' north. Now, a Latin and Christian West was separated from a largely 'pagan' east, which only gradually came to be christianised and integrated among the medieval societies that emerged in much of the continent. The area where these fault-lines crossed was perhaps most affected by these changes: the Carpathian Basin, the macro-region along the Middle Danube, roughly between Vienna and Belgrade. In the period, it was a node in the population history of Europe: new groups arrived from the North and East, and continued their migration or expansion towards the South and West (Bóna 1976; Pohl 2005; Wolfram 2018). It was situated between the core areas of the Roman world and the wide and thinly populated regions in which, in Roman perception, 'barbarians' lived. Many former provinces of the Roman Empire experienced fundamental political changes, but only a gradual social and cultural transformation. In the Carpathian Basin, the break with classical civilisation was almost complete, although it stayed in touch with areas of continuing Romanness to the South and West.

In the former province of Pannonia, the traces of the 'Roman' population gradually disappear during the 6th and 7th centuries, and archaeological and historical sources give only a blurred picture of what became of them (Bierbrauer 2004; Vida 2009). In the 5th and 6th centuries, the Carpathian Basin was successively (or simultaneously) dominated

by Huns, Goths, Gepids, Sarmatians, Eruli, Suebi and Longobards (Pohl 1980; Bemmman et al. 2008; Vida 2017). A dramatic shift occurred in 567/68: the Gepid kingdom in the east of the Carpathian Basin was destroyed, and the victorious Longobards and other groups moved from Pannonia to Italy. The Avars, whose core had recently arrived from central Asia, led by their khagan, conquered the entire area (Pohl 2018a). They raided the Balkan provinces of the Byzantine empire, and supported the expansion of the Slavs across almost the whole of eastern Europe. The Avar khaganate ruled over the Carpathian Basin until it was destroyed by Charlemagne's armies in c. 800 (Pohl 2018a). The c. 70,000 excavated graves from the Avar period, often with substantial grave goods, constitute one of the richest bodies of evidence from funerary archaeology from any historical realm in Europe (Bálint 1989; Daim 2003; Gavrituchin 2008; Tomka 2008; Bollók et al. 2016; Vida 2016). In spite of some minor remaining disagreements, the material is well-dated, mostly well-preserved and often well-published. It is classed in three periods, early, mid- and late-Avar. In the course of the ninth century, a mixed population led by Slavic groups and controlled by the Carolingian empire lived along the Middle Danube, before the Hungarians conquered it in c. 900 (Wolfram 1995).

Several very different social models coexisted or replaced each other in the area: the complex society of the Christian Roman Empire; the military elites of 'barbarians' more or less ready to be integrated in privileged positions in these late Roman societies; post-Roman rural populations under 'barbarian' rule; steppe warriors who built their often short-lived realms on tribute and plunder from Roman heartlands and their subsistence on local farmers; decentralized Slavic groups who had no need of Roman infrastructure, and only in the course of centuries began to build regional political units; and the Christian empire of the Franks. What is particular about the Carpathian Basin is that for much of the period, and unlike most neighbouring regions, steppe empires following a Central Eurasian model dominated it (Golden 2011; Bemmman et al. 2015; Kradin 2015; Schmauder 2015; Pohl 2015; Di Cosmo et al. 2018). Quite paradoxically, the rather ephemeral Hunnic Empire of Attila is well-known even among a general public and much-studied by scholars (Maenchen-Helfen 1973; Maas 2014; de la Vaissière 2014), whereas the Avar Empire, which existed for almost 250 years, has not received much scholarly and public attention in the West. The first ever monograph about them in English, written by the cPI of the present project, published in December 2018, can provide a basis for further interdisciplinary study (Pohl 2018a).

a2. Challenges: Big issues and small communities

These transformations raise a number of fundamental historical questions, many of which are controversially debated. First, the dissolution of the Roman system has been one of the big issues in the historical disciplines since the controversy between Abbé Dubos und Boulainvilliers, and Edward Gibbon's massive work 'The Decline and Fall of the Roman Empire' in the 18th century (Wood 2013). Recent debates have circled around 'fall or transformation of Rome' (Pohl 2005; Heather 2005; Ward-Perkins 2005;

Halsall 2007; Pohl 2016). Evidence was mostly taken from Britain (fall), Gaul (continuity) or Italy (contentious). Eastern Central Europe has rarely featured in these debates, even Chris Wickham's ground-breaking comparative study 'Framing the Early Middle Ages' has left out the Middle and Lower Danube regions (Wickham 2005). There are, of course, a number of regional studies (Várady 1969; Bóna 1976; Curta 2005; Curta 2006; Poulter 2008; Curta 2015), but much can still be gained from looking at East Central Europe within the broader perspective. What became of the 'Roman' provincials and their Christian culture (Pohl et al. 2018c)?

This leads to the second issue, the Roman-barbarian dichotomy: Binary models (Romans-barbarians, Christians-pagans, sedentary-nomadic etc.) still shape the way people think about Late Antiquity; but they are often unhelpful or misleading (Geary 2007; Pohl 2007). How different were the emerging post-Roman structures on the ground between this area of apparent de-Romanisation and neighbouring regions with more gradual transformation? What, for instance, were the differences between the ways of life under Longobard rule in Pannonia before 568, and in Italy and Pannonia after 568 (Barbiera 2005)? There is a variety of aspects that merit attention: kinship structures, status differences, agricultural labour, modes of production, the distribution of wealth, diet, diseases etc. In spite of the excellent archaeological evidence, there are hardly any comprehensive studies making use of it. Biomolecular archaeology can contribute additional evidence, and further personalise our evidence.

A third issue, the role of ethnicity, follows from these considerations. From early medieval chronicles to modern scholarly narratives, the history of the period has always been told in terms of collectives whose cohesion was taken for granted: 'the' Romans, 'the' Longobards, 'the' Avars, 'the' Slavs. That represents a cognitive scheme in the written sources, by which collective agency and political distinctions were understood in ethnic terms. That was not inadequate, and more often than not, roughly corresponded to self-identifications. Current attempts to minimize the role of ethnicity are unhelpful, because it is a key feature in the sources. Yet we cannot take these ethnic classifications for granted as modern scholarly categories.

Decades of research on early medieval ethnicity and identity have shown that ethnic affiliations do not necessarily match areas of shared cultural features or common biological origin (Wolfram 2018; Geary 1999; Geary 2002; Pohl 1998; Pohl 2013). There were many ways to be an Avar or to live under the rule of the Avar khagans, and exploring their variety and their changes over time is more promising than to simply label them as Avars (or as something else) (Daim 1998; Pohl 2018a; Pohl 2018b). This raises serious issues about the classification of the material culture. For a long time, the archaeological evidence has unproblematically been ascribed to ethnic units, down to single objects, such as 'Longobard' fibulae or 'Avar' belt-sets. Only recently has this methodology of ethnic interpretation of archaeological evidence been questioned (Halsall 1995; Daim 1998; Brather 2004; Rummel 2007; Curta 2007; Halsall 2010; Curta 2011). This debate has somehow disjointed the older ties between history and archaeology. As long as we attribute all distinctive features in the archaeological record to particular

ethnic groups, they can easily be integrated into an overall historical narrative. That may seem to provide plausible pictures of the past; but it may also be misleading. Most of all, it cannot adequately represent cultural change and hybridity. We know that Romanized Longobards did not cease to be Longobards, while Italian Romans could become Longobards. Do Longobards, Pannonians or Gepids who adopt late-Avar culture turn into Avars? This question needs to be re-opened on a paradigmatic and methodological level. We are still searching for new ways in which the written evidence and the archaeological record can be related. Now also genetic data need to be accounted for. HistoGenes will deal with this issue on a fundamental and theoretical level, using a particularly suited set of cases. It will not take any ethnic identities for granted, even though for the sake of brevity, conventional definitions of archaeological groupings ('late Avar' etc.) are sometimes used in this proposal.

A fourth issue is migration. The conventional image of 'the great migrations', as represented by coloured lines on a map, has been deconstructed in the last decades. Current discussion have dealt with the extent to which these 'migratory events' were in fact simplifying perceptions condensing long-term mobility into a single violent mass migration. Migration theory has shown that in human history, migration was the norm and not the exception (Hoerder 2002; Han 2006); theorists prefer to speak of transnationalism (understood as networks of mobility) rather than of migration (Glick Schiller et al. 1992; Bauböck 2017). For late/post- Roman Eastern Central Europe, this needs to be taken into account: the Roman Empire had always favoured, and often enforced mobility, and in the Central Eurasian steppe, mobility ('nomadism') was a way of life.

Still, large-scale military exploits, such as the Longobard conquest of parts of Italy and the Avar move to the Carpathian Basin in 567/68, could only be achieved by groups of at least 15-20.000 warriors, probably with families and following (Pohl 2005). This combination of long-term mobility, often along established 'transnational' routes, and one-off mass movements requires particular caution in interpreting archaeological and genomic evidence – they cannot prove 'migratory events', but give indications of substantial human movements. It is an old question in archaeology whether and when objects travelled with people who produced or used them (through migration or long-distance marriage), or without them (through trade or plunder). Therefore, object distribution cannot per se be taken as proof of migration. Genetics and isotope analysis can provide clues. In the careful and fine-tuned combination of absolute dates in written sources, (mostly) relative dates in the archaeological record, and the corresponding genetic data, we can reach robust hypotheses on migratory movements. Of course, we have to avoid 'mixed arguments', most of all, routinely dating archaeological evidence by dates given in the texts (for instance, pre- or post-568: Koncz 2015).

A fifth, and rather understudied issue are local communities, their social structure and cohesion, and the role of kinship and of status. Written evidence is patchy, and indeed rare for early medieval Eastern Central Europe. Substantial early medieval evidence from written sources has been collected by an international working group on 'Local

identities' (Patzold et al. 2016; Davis et al. 2019) in the context of the ERC AdG SCIRE (Walter Pohl). Relatively little has been done so far to integrate the historical information that we have with the extensive archaeological record. This is a promising perspective for HistoGenes, and also regards the relationship of local communities with wider, if looser affiliations, cultural affinities and identities. A challenge will be to relate the micro-studies of small communities and their cemeteries, as accessible through the methods of archaeology, genetics and other scientific methods, to the more general narrative perspectives offered by historical accounts.

a3. Integrating population genetic analysis and the historical disciplines

Early attempts to find genetic traces of early medieval population movements relied on modern DNA, on the analysis of mtDNA and Y-chromosomes, and on the comparison of haplogroups. Results, for instance about the arrival of the Angles and Saxons on the British Isles (Weale et al. 2002; Capelli et al. 2003; Thomas et al. 2006; Schiffels et al. 2016) or on Viking migrations (McEvoy et al. 2006), remained controversial (for a critique, Jobling et al. 2016; Geary and Veeramah 2016). Haplogroups could easily be misunderstood as providing evidence of an 'Anglosaxon' or 'Viking gene'. Limited cooperation with archaeologists and hardly any involvement of historians made the historical interpretation of results precarious (but see Bowden et al. 2008), and misleading simplifications were often trumpeted by the media. At present, many of the scientific obstacles hampering paleogenetic research 20 years ago have been overcome. Contamination of ancient DNA samples by modern DNA can now be controlled (Key et al. 2017), sampling from the petrous bone has yielded better coverage (Pinhasi et al. 2015), whole genome sequencing and SNP capture have improved genetic data collection (Amorim et al. 2018), and advanced computer modelling and principal component analysis provide sophisticated tools for data analysis (see methodology section). So far, the spectacular progress of genetic methods to analyse aDNA has mainly had an impact on the history of human evolution and on prehistoric archaeology (e.g. Lazaridis et al. 2014, Haak et al. 2015, Allentoft et al. 2015). There is as yet a lack of accessible comparative data for the Early Middle Ages, but that will soon change, as several research groups are prepared to engage in this field. Now is the moment at which these methods begin to be applied on a greater scale to research on historical periods. On the other hand, many archaeologists and historians remain unconvinced by what could be called the 'bio-archaeological turn', and fear that it might come at the expense of the traditional strengths of the discipline; a recent themed issue of *Medieval Worlds*, 4/2016, edited by the cPI, has discussed these preoccupations (Brather 2016; Samida and Feuchter 2016).

Methodological debate how to integrate genomic data and archaeological cultures has begun (Geary and Veeramah 2016; Feuchter 2017; Eisenmann et al. 2018; Forum: Genetic History 2018). At this critical moment, it is crucial to establish a best practice

model in the field to avoid unsatisfactory use of data, methodological short-cuts and insufficient archaeological and historical interpretation.

To this end, HistoGenes proposes the following methodological principles:

First, an obstacle to genetic research at large is sample and data hoarding, be it in a competition between big academic players or, worse, channeled to commercial uses. Sample collection should be geared towards comprehensive scientific projects, data procession should be transparent, and the data be made accessible for control and comparison. The ERC, which imposes an open-access strategy, has an important contribution to make to reach this goal, and HistoGenes is fully committed to it.

Second, shortcuts in the interpretation of the data should be avoided. Research on the first millennium CE has to confront the problem that at that time, genetic differences in most of Europe were already much smaller than in prehistoric times, which requires a very fine-tuned workflow, a combination of analytical methods, and sophisticated data analysis and interpretation (see methodology section). The goal of HistoGenes is not simply a random mapping of the genetic landscape of early medieval Europe, but the project is driven by a number of historical questions calibrated to the potential of interdisciplinary collaboration.

Third, especially in some eastern European countries, genetic history is increasingly being directed towards 19th-century-style national histories to support identity politics with visions of a shared past. These new and revived national myths require the attention of historians, and establishing a best practice in the use of aDNA data that provides a convincing alternative to their use for partisan politics. This also requires a keen awareness of the history of modern historiography in the field, and of the risks of biological determinism linked to ideas of national or racial superiority.

Fourth, the evidence accessible in the field of late antique/early medieval archaeology largely consists of cemeteries counting a few dozen to a few hundred burials, in rare cases, also a few thousand. It is not sufficient to use a few samples from each cemetery to arrive at robust conclusions. As a pilot study to the present project (Amorim et al. 2018) has shown, 6th-/7th-century cemeteries may be composed of two or three distinctive genetic clusters; to grasp the population history of the period, it is therefore advisable to sample entire cemeteries or distinct parts of them. This is one of the innovative features of HistoGenes.

Fifth, the new scientific methods still lack an established methodology through which the results of scientific analysis can be translated into valid historical conclusions. Genetic data should not simply be invoked as a kind of epistemic 'deus ex machina' to decide issues unresolved in previous research. They should be interpreted in a consequent collaboration between the disciplines involved. Recent approaches in research on early medieval identities should be taken into account (Geary 2002; Pohl 2013). Genetic clusters should not a priori be identified with ethnic groups, speakers of a particular language known from written sources, or archaeological 'cultures' as conceptualized by archaeologists. Such overlaps or even identifications may emerge as results in some

cases. In the period under study, linguistic models, often used in reconstructions of prehistoric migrations, will be of little use because of repeated changes of language in the same population, for instance the Romanisation of the western Franks and Longobards, or the Slavicisation of Eastern Europe (Pohl and Zeller 2012).

These methodological principles have been developed and tested in several smaller pilot projects in which the HistoGenes research group was involved. A pilot project headed by PI Patrick Geary in which all PIs and many team members were involved was funded by the Humboldt Foundation (Anneliese Meier grant), by the Swedish Bicentenary Funds, by the US National Science Foundation etc. It addressed the Longobard migration to Italy, and so far has compared two cemeteries in Pannonia (Hungary) and Piedmont (Italy), and discussed interpretation and methodology in a series of workshops. Analysis of the two sites yielded good evidence for migration between the two regions, and for the organization of the cemeteries in families and distinct cultural groups largely coinciding with genetic clusters (Amorim et al. 2018). First results were published in 'Nature Communications' in September 2018 and quickly found reassuring resonance; more data from Northern Italy will emerge in 2019. A further project conducted by PIs Tivadar Vida and Johannes Krause tested some of the richest seventh-century graves from the Avar empire, and established connections to Central Asian populations (Csáky et al. 2018). Extensive isotope analyses were carried out in the project "Mobility and Population Transformation in the Carpathian Basin from the 5th to the 7th Century AD: Changing Societies and Identities" (NKFIH/OTKA-DFG, 2014-2019) led by PI Tivadar Vida and Corina Knipper. The pilot studies have demonstrated the feasibility of the present project, have established a basic workflow in the group, and strengthen the source base for HistoGenes.

HistoGenes will collect c. 6,000 human samples of the fifth to ninth centuries, about half of which from the core area of the Avar Empire (mostly present Hungary), and half from selected sites in neighbouring macro- regions, including Southern and Eastern Germany, Austria, Moravia, Slovakia, Northern Italy, Slovenia, Serbia and Romania. The cemeteries in the Carpathian Basin will as far as possible receive a full analysis, sampling all graves for whole genome sequencing (WGS) or SNP capture, providing at least basic anthropological analysis for all skeletons, and including Sr-, C- and N-isotope analysis and ¹⁴C dating wherever this seems promising. In the neighbouring areas, a representative selection will usually suffice; in some of them, existing data can be used. HistoGenes will not only provide an unprecedented quantity of data, which will constitute a point of reference for all future studies. The scientific workflow will also be embedded in close multi-disciplinary cooperation to discuss research strategies and the selection of samples, and interpretation of the data. HistoGenes will not only unite four of the foremost researchers in their respective fields as PIs. Each of the PIs will assemble a complementary research team from several of the fields involved, and collaborate with senior researchers from other disciplines.

The region and the period under scrutiny – the Early Middle Ages – are exceptional for the combination of quite differentiated written evidence (not a 'dark age' at all, in spite of

some lacunes in the sources), an unusual wealth of archaeological finds, and, as has already been established, fair conditions for genetic surveys and the application of further scientific methods. If we could make these different angles of looking at the period match, that would help us to pose new questions, see old problems differently, and explore new research routines. The evidence produced by the three disciplines – history, archaeology and genetics/biomolecular archaeology – is in many ways complementary, but it needs a strong input from all three sides to validate it, and translate the different scholarly languages used into consensual results.

a4. Research aims and questions

The big issues in the focus of HistoGenes translate into a number of precise research questions, each of which will be addressed through a close study of several cemeteries in the core areas of the Carpathian Basin as compared with neighbouring regions. Below, only some of these sites are indicated; for a fuller list of sites to be targeted, see the map on p. 10 and the list of sites in the annex. Additionally, these case studies will be grouped into long-term studies of micro-regions where population change can be observed continuously from the 4th/5th to the 8th/9th century in well-documented and available sites – for instance, around Győr/Arrabona, around Keszthely on Lake Balaton, and in Srem (Sirmium and Singidunum). On the basis of these particular studies, the general questions sketched in sections a1-a2 can then be addressed by the team.

1. Tracing the population history of the Carpathian Basin in the fifth and sixth centuries

1.1 'Pannonians' – the degree of continuity of the late Roman population: We tend to class the heirs of the provincial population of the Roman Empire after the end of Roman rule as 'Romans', but that was an increasingly ambiguous and elusive status all over the former Western Empire; often, former provincial identities came to the fore, as the work package 'Being Roman after Rome' in the ERC AdG 'SCIRE' demonstrated (Pohl et al. 2018c). Continuity of settlement after the end of provincial administration in Pannonia is a much-debated issue (Bierbrauer 2004; Vida 2009). 'Pannonii' are mentioned in the Longobard army that marched into Italy in 568. To what extent were they descended from the provincial population of the fifth century? Is there evidence for continuous settlement in genetic and isotope data?

1.2 'Barbarians' – ethnic distinctions, mobility and admixture in the 5th/6th century: The Carpathian Basin was a node in the migratory movements of the 5th and 6th centuries; many smaller and larger groups passed through here, some of them stayed for longer or shorter periods. Numerous, mostly short-lived kingdoms formed here: Huns, Gepids, Goths, Sarmatians, Suebi, Eruli, Sciri, and Longobards (Bóna 1976; Pohl 1980; Steinacher 2017). Does the variety of ethnonyms attested in the written sources correspond to a similarly varied genetic profile? Or were most of these ruling groups too hybrid or closely related for any clear distinctions? To what extent did the movements recorded in the texts have an impact on the composition of the population of the region?

The development of post-Roman Pannonia will also be compared to the eastern half of the Carpathian Basin, which had never been part of the Empire, and where the Gepid kingdom ruled from 454 to 567.

1.3 Pannonia under Longobard rule: In the first two thirds of the 6th century, the Longobard kingdom expanded from southern Moravia and eastern Austria into Pannonia. In the early Empire, Longobards had been attested along the Elbe, but then there is a gap of more than 300 years (Pohl 1997). The pilot project identified a genetic structure involving at least two groups with different ancestry that were very distinct in their funerary customs at Szólád (Amorim et al. 2018); does that correspond to other cemeteries from the Longobard kingdom between Pannonia and Moravia? Is it closely related to cemeteries in Thuringia that we can build a plausible hypothesis on Longobard origins, and sufficiently distinct from other barbarian groups? Furthermore, the material culture of the Longobards is so directly connected to the Merovingian world within the so-called 'Reihengräberkreis' that the chronology of the Longobard period in Pannonia depends on Merovingian archaeology; was this cultural continuum also based on human mobility?

2. Reconstructing the populations of the Avar Empire and the neighbouring regions, 568-c. 800

2.1 Population continuity between the Longobard/Gepid and Avar period: The written sources record that a substantial and mixed group left Pannonia in 568. What became of the pre-568 population? Some cemeteries seem to have continued in use even after 568, particularly around Lake Balaton. Can the post-provincial population that has left its genetic footprint in a part of the mid-6th-century Szólád cemetery still be detected in early Avar contexts (Amorim et al. 2018)? This is closely linked to question 2.2, and will require looking at the same cemeteries. East of the Danube, Gepids are still mentioned under (and after) Avar rule (Pohl 2018a). Archaeological continuity is still hard to prove here, although it seems that Gepid-period cemeteries continued in use.

2.2 Who lived in Pannonia under the early Avar khaganate? One of the most puzzling features of the late 6th/early 7th century in Pannonia is the flourishing of a population with objects and cultural traits that resemble that of the Western and Southwestern neighbours in Italy and the Frankish kingdoms (Vida 2008; Vida 2016). Were they locals who had become rich and started to use fancy apparel in their funerary rites? Freed captives from Byzantine provinces? Were they contingents from the Avar army that had adapted quickly to the new cultural environment? Or was there immigration from the west and south, unattested in the written sources? Was this a recently-amalgamated hotchpotch population, or a rather homogeneous group that indulged in displays of cultural hybridity? This is an issue relevant beyond this particular context, because it is a test case for the relationship between a cultural and a biological definition of the group (while any written identification with an ethnonym is lacking in this case).

2.3 Avar origins and the genetic composition of the Avar elite: The preliminary analysis of some of the richest Avar graves (7th century) showed a substantial degree of (East) Central Asian genetics with little or no Western Eurasian ancestry (Csáky et al. 2018).

This is very relevant for an old historical debate: Were the European Avars essentially survivors from the Rouran khaganate in Mongolia that had been destroyed by the Turks, or a mix of other groups fleeing from the Turks, or did most of them rather come from the Western Eurasian steppes? Who migrated – a military elite, their families, or can we speak about a larger-scale migration (Pohl 2018a)? Early ‘Avar’ cultural habitus was not homogeneous. For instance, in the region east of the Tisza river burial customs differ from those observed between Danube and Tisza or in Pannonia. It also seems that a group with an Eastern European profile settled in the area between the Tisza, Körös and Aranka rivers and assimilated the local population. HistoGenes cannot engage in systematic comparison with finds all over Central Asia, material that is also targeted in other projects, but it can plot the principal component analysis on existing genetic data. Most of all, it can test genetic similarity or difference between top level graves, wealthy warriors and poorer graves displaying Avar-type cultural habitus in the early Avar period, to explore the relative genomic unity or hybridity of the ruling population of the khaganate.

2.4 Eastern influx and migrations into the Avar khaganate: On the basis of changes in archaeological culture, scholars have variously assumed an impact of a new wave of immigration in the 7th century (Szőke 2008).

Was there indeed a significant population growth at the beginning of the Middle Avar period, which would make immigration likely, or did this period begin earlier and take longer (Bálint 2008; Gavrituchin 2008; Pohl 2018a)? We can surely assume recurrent migration to the Carpathian Basin, but its origin and impact is so far hard to assess.

2.5 Cultural homogenization and admixture in the Avar Empire: In the course of the 7th century, the material culture in the Avar settlement area became more and more homogeneous, and the Western influences faded out in Pannonia. In the eighth century, shared cultural features span the entire area of Avar dominion; this is also a time when a large percentage of the burials display, if generally poorer, grave goods. Was this a cultural unification of a population that continued to be genetically rather heterogeneous, or did it correspond to a process of admixture and homogenization? This also regards the relationship between Avars and Slavs within the khaganate (see also 3.2). The written sources indicate that under Avar rule, other ethnic groups, mainly Slavs and Bulgars, formed along clear lines of economic and social differentiation. Do social distinctions in burials correspond to genetic differences? So far, we have few clues to Slavic presence in the archaeological record from the Avar core area, although Slavs are already attested there in texts in the late sixth century. It is not unlikely that some people buried in Avar fashion in the eighth-century Carpathian Basin were directly related to those regarded and buried as Slavs in the ninth. Genetic data cannot track Slavic or Avar self-identification, but show whether social and cultural divides corresponded to genetic differences, or whether close interaction along the Middle Danube had redrawn the boundaries.

2.6 Internal migration: Isotope analysis and perhaps genetic traces may shed light on internal migration – was there a high degree of mobility within the Avar realm, or did

regional populations rather remain where they were? For instance, in the Avar period cemetery of Leobersdorf in Lower Austria, excavated by a collaborator, significant cultural changes (although within the orbit of Late Avar culture) occur in the middle of the eighth century, which cannot be connected to any attested overall events (Daim 1988). Could that be a trace of short- or medium-range migration within the Avar Empire? Did only objects move or people as well? Particularly interesting are communities living at a (cultural) border. Do patterns of cultural exchange also point to intermarriage and admixture, for instance between Avar and Slavic communities in southern Lower Austria (see 3.2)?

3. Placing the Avar khaganate in relation to its neighbours and successors

3.1 The Avars and the West: Comparison and the study of connectivity of the Avar realm with the neighbouring Bavarian, Alemannic, Frankish and Longobard regions will be continued for the Avar period (until the grave good habit ends in the West in the 7th/8th centuries). Small-scale mobility across the border is attested, for instance, at Linz-Zizlau. One question will be whether cultural exchanges corresponded to human mobility, and whether their decrease also meant a decline in ‘transnational’ contacts. Another issue is the structural development in the Avar core areas where only residual Christianity is attested as compared to the increasingly Christianised western regions. Like the Huns before them, the Avars followed a pattern that was ostensibly different from their western neighbours: they remained outside the former Roman heartland and supported their rule by the transfer of riches from Byzantium through plunder, tribute and the sale of prisoners. They organized their realm largely following the model of the Central Asian steppe empires (Golden 2011; Pohl 2018a). The Longobards, on the other hand, transferred their kingdom to Italy, where the ancient infrastructure was to a considerable extent still in place. They inserted themselves into late Roman society as a military elite and as recipients of regular dues from estates, became Christians and ultimately adopted the Romance language of their subjects. We will look at the implications of these differences on grassroot level, in the mostly small rural settlements that we can grasp in the archaeological evidence, relying also on the evidence the pilot project (Amorim et al. 2018).

3.2 Avars and Slavs: One of the long-term outcomes of Avar domination over wide areas of Central/Eastern Europe was its impact on the Slavic expansion, which the khaganate favoured but sought to control. The earliest Slavs in the 6th and 7th century are clearly mentioned in the written sources, but in many regions have left little archaeological traces (Curta 2001; Dzino 2001). Early Slavs usually cremated their dead and in many regions are not directly accessible to aDNA testing. However, skeletal evidence in Slavic environments becomes more substantial from the 8th century in Austria, Slovakia, Eastern Germany, and from the ninth century also in Hungary. This allows assessing traces of Avar-Slav interaction, especially in border areas. A case study will look at the 8th-century ‘Avar’ cemetery at Frohsdorf and the ‘Slavic’ cemetery at Pitten, which are situated in vicinity – do their distinct cultural profiles with some exchanges correspond

with genetic differences, is there admixture, or was that a rather homogeneous local population with divergent cultural markers?

3.3 After the Avars – continuity and change after the fall of the Avar Khaganate: Within less than 30 years after the destruction of their empire in 795/96, the Avars completely disappear from the written sources (Pohl 2018a). Avar cemeteries become impoverished and fade out. ‘To disappear like the Avars’ even became proverbial in Byzantium. What happened to the population that had been buried in Avar style in the 8th century? Did they more or less disappear, or only change their cultural habitus? The question of Avar survivals, and of the further population groups in ninth-century Pannonia, will be studied in particular in the Carolingian centre of Mosapurc-Zalavár on Lake Balaton (Szőke 2010). Some 1200 Carolingian-period graves have been uncovered around the churches of St. Mary and St. Hadrian. The Slavic *dux* Priwina gathered a sizeable population of families from different regions, Slavs, Franks, Bulgars, apparently even people from the Baltic regions (Alsórajk). As yet, little is known about the make-up and the physical and biological condition of this population. The proportion of the local Avar-period population and of immigrants remains to be established. Is there any correlation between genetically related individuals and grave goods? What genetic variations can be identified and how do these reflect internal and external migrations? Genetic studies can also provide an answer to issues of social organisation. Several family grave clusters have been identified which could be associated with different social layers.

4. Small worlds and large realms: focusing on the social structure of the Carpathian Basin

4.1 The role of kinship in the formation of early Medieval societies: With the mapping of kinship relations in cemeteries, we can get a better understanding how communities were formed, what family actually meant at the time, and how kinship relations were represented through the burial customs. What was the structure of the mostly relatively small communities under Avar rule? Were they dominated by kin groups, were they otherwise genetically close, or rather mixed? Can we say something about exogamy or endogamy? A key question are the personal (blood) relations represented in cemeteries. In the pilot study, strong kindred ties between many community members emerged. However, it may be that the groups using burial grounds together (‘burial communities’) followed very different models. The comparison between neighbouring cemeteries can also show whether family relations were established between them.

4.2 Social hierarchies and the cohabitation between different groups: Social structure can be targeted from an interdisciplinary perspective. One feature that genetics may help to explore is to what extent cemeteries were composed of distinguishable genomic groups. How did biological origin correspond to social status? In Szólád and Collegno, there were two resp. three genetic clusters, with a clear cultural distinction (grave goods/few or no grave goods) and hierarchical structure (more/less protein consumption) between them (Amorim et al. 2018). Can similar models be found in Avar settlements? Did Avar warriors live in the same settlements (or at least, were they buried in the same cemeteries) as those whose productive labour supported them? What were the ways of

life that can be reconstructed on the basis of Avar period evidence, and how do they compare to those in neighbouring regions (for instance, Northern Italy, Bavaria or Eastern Europe)? There are as yet relatively few overviews on the social structure of the Carpathian Basin in the period and its changes, and HistoGenes provides a new basis for addressing this question.

4.3 Changing patterns of nutrition and status differences: Isotope evidence on diet already indicates that repeated transformations of nutrition came with the changes that took place in the Carpathian Basin in our study period. As the late Roman infrastructure was abandoned, people had to turn to new ways of subsistence. C and N isotope data suggest millet to have been a well-established staple crop during the 5th century (Hakenbeck et al. 2017), while its importance decreased in the 6th century (Alt et al. 2014). Ongoing research in the 'Mobility and Population Transformation' pilot project shows that average diet compositions changed repeatedly between the 5th and 7th centuries. We can learn more about this process by expanding the analysis to other parts of the Carpathian Basin and to neighbouring regions. This also entails a more comprehensive view of differences in diet between social groups in the same cemetery and among elites and lower status population, as deduced from grave goods and funerary architecture (Knipper et al. 2015).

4.4 Health and diseases: Anthropological analysis of the skeletons will routinely address traces of diseases or skeletal deformation and provide a huge wealth of data on health and frailty. A further line of research will be the genome wide analysis of pathogens conducted on 500 selected skeletons. Johannes Krause's team is one of the leading labs on ancient pathogen reconstruction, a field he pioneered and extended during his ERC-Starting grant APGREID (e.g. Bos et al. 2011, Schuenemann et al. 2013, Bos et al. 2014, Feldman et al. 2016, Spyrou et al. 2016, Spyrou et al. 2018). Not least, this regards the presence of *Yersinia pestis*, to be tested specifically in cases where more than one body is found in a grave. This may provide further evidence in the debated question of the impact of the Justinianic plague on early medieval societies in Europe. The combination of pathogen analysis and complete human genomes might further provide clues to the differing immunities in the various population groups.

4.5 The impact of climate: Within several fields in the humanities and the natural sciences, there is an ongoing debate on the impact of climate change on human migration. Abrupt climatic changes possibly contributed to major socio-economic transformations. However, in recent years the growing body of evidence challenges the power of such claims (Hulme 2011; Flohr et al. 2016; Izdebski et al. 2016; Pinke et al. 2017; Büntgen and Di Cosmo 2017; Haldon et al. 2018). So far, evidence from the Carpathian Basin has not confirmed assumptions that the fall of the Avar khaganate was prompted by climate, but indicates long- term changes in living conditions, which surely had an impact, and may provide a further angle for understanding the transformations of the period (Preiser-Kapeller 2018). A research group based at Jena, headed by a collaborator, will use both the existing climatological data and produce an own dataset that will complement the available records. In the longer run, he will develop his own

larger project on the relation of climate change and Slavic expansion, with which we will closely collaborate.

4.6 Gendered and kin-based forms of representation: While representation is already one of the most researched topics of burial archaeology, with the help of genetic analysis, some new questions could be raised and answered. Did representation really work on a family level or was it based on the individuals' social persona? What is the meaning behind richly furnished child burials – were they used as a tool in the social competition between families? Were there only two gender models, or was the picture more diverse? Roman observers repeatedly reported about barbarian warrior women whom they called 'Amazons' (Pohl 2004; Geary 2006), for instance, in the Avar siege of Constantinople – can systematic anthropological sexing of skeletons revise previous gender distinctions made on the basis of the grave apparel (Effros 2000)? Do we find only one model of warrior masculinity, or was there more variation? This research will be accompanied by a historical study on 'barbarian' femininity/masculinity.

5. From data to history: integrating disciplinary results

5.1 The art of interpretation – monitoring the workflow: HistoGenes will not only collect and interpret data on the transformations in Eastern Central Europe in order to arrive at a substantially refined picture of the period. A key feature in the project is the systematic reflection of the epistemological process and of its methodological implications (see methodology section). The ambition is to create a reliable precedent for further interdisciplinary studies involving scientific archaeology and population genetics. This will mainly be achieved by a close collaboration between team members, and by an open network involving many other scholars in the field (see 'connective structure'). We will look for interpretations that match the complexity of the historical process, rather than straightforward historical narratives. We will reflect on the scholarly language in which we can communicate results, and seek to avoid misunderstandings and reifications that terms such as ethnicity, community, or migration, or the use of specific ethnonyms may entail – without abandoning 'loaded terms' that are often hard to replace. And we will experiment with translating the results from the paradigmatic structure of one discipline into another.

5.2 New approaches to the historical interpretation of archaeological evidence: Most historians still have problems integrating the results of mortuary archaeology into their narrative (cf. Halsall 1995). Therefore, archaeologists, scientists and historians will discuss the cemetery evidence and its implications for the history of migrations, cultural and social history in detail, analyse comparable cases and assess pertinent written evidence. In which contexts is community, ethnic affiliation or migration a plausible hypothesis of interpretation? Theoretical and methodological reflection on issues of early medieval identity will blend with rather pragmatic interpretation of the material traces of communities on the ground. HistoGenes will also contribute to discussions about the 'transformation of the Roman World', and about the divergent developments in Eastern Europe (and specifically, in the former Roman province of Pannonia) and the West – among them, the former Roman core area Italy (cf. Halsall 2007; Wickham 2005).

5.3 Community, migration and identity in the textual record: Building on the new data from genetic and isotope analyses and on the stunning progress in the archaeological record, migration narratives and perceptions of difference as documented in the written sources can be reassessed. How is migration framed in the historical record? In what ways did successive scholarship and modern national master narratives develop that picture? How do these perceptions relate to the scientific/archaeological record? This line of research will be complemented with a historical enquiry about perceptions of smaller communities and their collective agency in the sources. It will also address the Latin, Greek and Germanic terminology for small communities such as the ones that can be traced in the cemetery evidence. For instance, the pilot study has already shed light on the much-discussed term 'fara' for the basic migration and settlement units of the Longobards. How were local communities shown to act in narrative and documentary texts? This research can build on the results of the Austrian SFB 'Visions of Community' (2011-19) headed by the cPI (Pohl et al. 2016); and use a tool already established in his ERC Advanced Grant 'SCIRE' and augmented since, namely, the data-base GENS (Group terminology and Ethnic Nomenclature: a Semantic database, c. 400- 1200, <http://www.oeaw.ac.at/imafo/gens>). We can also rely on the results of the working group on 'Local Identities', also in the context of the SCIRE project (Patzold et al. 2016).

5.4 The impact of steppe culture in Europe: The Central Asian steppe background and the eastern connections of the Avars will also be explored combining archaeological and historical evidence. This will require cooperation with specialists on early medieval central Asian history and archaeology. The steppe heritage of Eastern Central Europe and its Central Asian background will also be a topic for two major knowledge transfer activities by the Vienna team. 'Visualising the early medieval steppe peoples' will be a digital humanities format designed to make the controversial perceptions of the Eurasian steppes in Europe and the complex research on steppe identities more accessible both to scholars and to an interested public, using recent methods of digital visualization, story maps and interactive dissemination of knowledge.

Furthermore, Falko Daim prepares an exhibition on early medieval mounted steppe warriors in 2023 at the Schallaburg, one of Austria's main centres for large historical exhibitions, and at Halle/Saale. This exhibition is fully financed and will not receive support from the present project. Yet it gives an opportunity to present results from HistoGenes, and to conduct accompanying research on some objects to be exhibited and their significance for an overarching historical narrative.

Section b. Methodology

b1. Scientific methodology

HistoGenes is an ambitious attempt to draw together some of the leading specialists in their fields to integrate textual history, archaeology, biomolecular archaeology and population genetics, and to create new perspectives on a formative period of a core area

of Europe. We note that this is primarily a paleogenetic project driven by historical questions, and it aims not only at ground-breaking results in the well-circumscribed research field under scrutiny, but also at methodological reflection and innovation. In its project design, it is, to the knowledge of the applicants, unparalleled. It strives not only to integrate scientific archaeology fully as a method in the study of historical periods, but also to calibrate genomics of prehistoric periods by cross-checking its results through the anthropological, archaeological and written evidence.

The two major tasks will be a) the careful implementation of disparate methodologies, historical, philological, archaeological, anthropological, and scientific methods such as population genetics and isotope analysis, on c. 6000 burials from the region and their historical context, and b), the process of combining the results of these methodologies to respond to the specific historical questions posed above. Each PI and senior associate has extensive experience both in his or her specific discipline, but also in collaboration across disciplines. One of the key novel aspects of our study will be the comprehensive scientific analysis of all burials from entire cemeteries within the core areas of the Carpathian Basin, while we will take carefully determined samples from different groups within the peripheral cemeteries.

After careful archaeological, anthropological and historical surveying of specific cemeteries of interest (WP 1-2), petrous bone will be collected for the purpose of genomic characterization, while teeth (Sr) and ribs (C and N) will be collected for isotope analysis (WP 3). Following DNA extraction (Dabney et al. 2013) and UDG library preparation (Rohland et al. 2015), each sample will undergo Illumina shotgun screening for the level of endogenous DNA and levels of exogenous contamination (WP 4-6). Approximately ~750 samples with high endogenous content (>80%) and low library complexity will undergo whole genome sequencing (WGS), while the remaining 5,250 samples will be sequenced after targeted capture of 1.2 million known single nucleotide polymorphisms (SNPs) (Fu et al. 2013, Haak et al. 2015; Mathieson et al. 2015) (WP 7).

After basic data quality assessment (WP 8) there will be two strands of genomic analysis. First we will conduct an in-depth analysis of individual cemeteries or locales, focusing on disentangling levels of close biological relatedness to the level of at least three degrees of relatedness as well as broader patterns of genomic ancestry and population genetic structure (WP 9). Such analysis will also allow us to potentially identify individuals whose parents have distinct genomic ancestry profiles (i.e. admixture), and even resolve the ancestry of parents who are not even buried in the same cemetery as their children. We will also be able to use a combination of rare variants from WGS data and common SNP variation to identify connections between individuals for cemeteries that span multiple centuries. In addition, Sr isotope analysis can show whether individuals were indigenous or not, and to some extent indicate possible locations of their early lives (Knipper et al. 2017). C and N isotope data will inform us about diet as a proxy for social status (Knipper et al. 2015) (WP 12). Further, beyond the initial surveys, in-depth archaeological and anthropological analysis of sites will continue throughout the project (WP 15-16). As in our previous pilot study, we will

implement a series of Fisher's exact tests to examine possible associations between genetic ancestry, material culture, anthropological characteristics, and isotopic profile at each individual site (Amorim et al. 2018). We will also expand this approach to incorporate greater variation and continuity in both the genetic and as well as the archaeological data using regression analysis approaches. This approach, carried out on the micro level considering each site as a unit, will build a comprehensive and unparalleled picture of local social organization and hierarchies.

Secondly, we will examine the genomic data (potentially in cohort with the strontium isotope data) for evidence of connections among regional sites. More specifically we will attempt to parameterize variable or punctuated episodes of migration and admixture that arise on top of background levels of gene flow (WP 10). Though inference of migration is a rich and active area of study in population genetics (e.g. Patterson et al. 2012, Petkova et al. 2015), we are particularly interested in developing methods that capitalize on rare variants in our WGS data, as pioneered by Jena senior researcher Stephan Schiffels (Schiffels et al. 2015), in order to infer fine-scale migratory contacts at regional and even intra-regional levels. Combining such information with inferences that extend our micro level approach to more regional levels (i.e. comparing the individual units described above) will allow for a differentiated, diachronic image of genetic groups, cultural and kinship patterns, and migratory processes across the Carpathian basin and beyond.

To tap into further evidence for the conditions of life and their changes, HistoGenes will also confront the roles of climate change and pathology in population movements. To determine the extent of plague within the populations in our sample, we will also sequence a subset teeth from multiple graves in our data set to attempt to identify the presence of this disease in the Carpathian basin (WP 11). In addition, using autumn/winter precipitation data for the period 400 to 900 CE already analysed from SW Romania supplemented by similar data to be collected from Moravia, we will seek correlations between population movements and settlements across the region and climatic patterns (WP 14).

Interpreting the patterns of the various data sets produced in HistoGenes in their archaeological and historical context will be a key interdisciplinary activity to arrive at significant conclusions (WP 18). This requires close archaeological analysis of many sites and of relations between them (WP 15). A set of textual studies will accompany the project, for instance, on the perception and terminology of local communities, identities and migrations (WP 17). The result will be an integrated analysis of human social organization, cultural forms, mobility, and change in Eastern Central Europe in the period, developed in extensive discussion between all four teams and documented in comprehensive publications and web resources (WP 19).

Risk/gain, feasibility: On the technical level, there is always a risk that some of the samples will not yield sufficient results, but with 6000 samples a significant amount of data will surely be produced. Access to material of c. 20,000 burials has already been secured; the samples will be selected according to bone preservation and availability of the necessary archaeological data (which in many cases has already been checked).

Close cooperation with excavators and museums and their commitment have been ascertained. The pilot studies have tested both sample quality and the feasibility of the workflow, and the team has already collaborated successfully. There is a slight risk of bureaucratic obstacles and of political intervention into academic procedures in Hungary, but all the more important is HistoGenes right now to secure independent funding. At present, institutional support has been secured; the flexible international project structure always allows to focus more on neighbouring countries. The second risk is that the interpretation of the data may be unclear or contradictory. Given the size of the project, that can hardly be due to a lack of data, but to the complexity of past populations – which would constitute a challenge to established models and narratives, an important result in itself. Even if only some of the many research questions and methodological issues can be resolved, this would still be a high-gain project that will set new standards.

b2. Work Packages and the organisation of the workflow

HistoGenes is designed in a double structure: on the one hand, there are the research questions as set out in the first section (a 3). On the other hand, the integrated interdisciplinary work flow to tackle all these questions will be structured into successive stages, which are set out as work packages below.

WP 1. Archaeological and historical preparation of information and research questions regarding the specific sites (funerary contexts – structural deposits, funerary architecture; grave goods; spatial distribution). The information will be fed into an existing database of all major cemeteries from Austria (600-1100 CE), which will be extended to all sites studied in HistoGenes. The OpenAtlas database system (www.openatlas.eu) contains information on stratigraphy, typology, anthropology and chronology of graves, burials and artifacts along with GIS-geometries of their location and shape. It can then be extended with results of the scientific analyses. The data model is based on the CIDOC-CRM, an internationally established standard for cultural heritage documentation, and allows for a standardized data acquisition. Thus, the large amount of collected data will be internally and externally comparable as well as sustainable. Specialised software can then be used to carry out e.g. network analyses, statistical calculations, GIS-analyses, and much more. It offers furthermore a state of the art way and comprehensible method to visualize, present and publish archaeologically and anthropologically analysed burials digitally and if desired as online open data. Data management will be secured in collaboration with collaborating institutions; the genetic datasets will also be stored in the SRA data base (Budapest and Vienna, Princeton).

WP 2. Anthropological preparation of skeletons for sampling: sexing, age, conspicuous features (Budapest and Vienna anthropologists).

WP 3. Sample collection: Petrous bone (where available) and teeth (where necessary) will be collected by the Budapest team led by a collaborator. Petrous bone will preferentially be used for human DNA sequencing. Second permanent molars will be preferentially used for Sr and ribs for C and N isotope analysis. This procedure ensures

optimal comparability with ongoing pilot research. Teeth will also be used for pathogen screening. Animal teeth and bones provide comparative samples (Budapest).

WP 4. DNA extraction: DNA will be extracted from ~100mg of bone powder using a silica-based method specifically developed for fragmented DNA (Dabney et al. 2013) (Jena, Budapest).

WP 5. Illumina library preparation and screening shotgun sequencing Genomic libraries will be prepared using a custom double-indexing protocol (Kircher, Sawyer, and Meyer 2012; Gansauge et al. 2017) along with a partial UDG treatment (Rohland et al. 2015). This partial UDG treatment will allow us to use the same library to both test for ancient DNA authenticity and perform population genetic analysis by restricting damage to the terminal nucleotides of the fragment. Multiple equimolar libraries will then undergo single- ended shotgun sequencing on an Illumina NextSeq or HiSeq platform. In addition genomic libraries will be enriched for human mitochondrial DNA using a bead-capture methodology (Maricic, Whitten, and Pääbo 2010) and also undergo pooled sequencing. Over the six years approximately 6,000 samples will be prepared in the ancient DNA labs in Jena.

WP 6. Bioinformatic processing: Raw sequencing data will be transferred to Stony Brook University (SBU) for bioinformatic processing where sequencing reads will be trimmed, mapped, and filtered for PCR duplications according to a protocol optimized for ancient DNA (Kircher 2012; Peltzer et al. 2016). Post- mortem degradation effects will be assessed using MapDamage (Ginolhac et al. 2011) and sex will be estimated based on the relative autosomal to X and Y chromosome coverage (Mittnik et al. 2016). Schmutzi (Renaud et al. 2015) will be used to estimate contamination from the mtDNA capture sequences, and ANGSD will be used to estimate contamination for all male samples (Rasmussen et al. 2011). We note that this process is automated and will provide us for each sample with an assessment of the level of endogenous human DNA available, the library complexity, level of contamination and whether it contains signatures typical of ancient DNA post-mortem damage (IAS Princeton and Stony Brook).

WP 7. Whole Genome Sequencing and 1240k SNP capture: Samples with sufficiently low library complexity and high endogenous content (>80%) will undergo direct whole genome shotgun sequencing (WGS) to ~5-15x coverage via single ended 1x100bp sequencing on the Illumina NovaSeq platform at the New York Genome Center (NYGC). For samples with low to medium high endogenous content (>1%) we will target 1.2 million known SNPs (Haak et al. 2015; Mathieson et al. 2015) using an established in-solution enrichment protocol (Fu et al. 2013) followed by sequencing on the Illumina HiSeq platform in Jena. Based on past experience we anticipate ~10-25% of samples will reach the threshold for WGS and the vast majority of the remaining samples will be amenable to SNP capture. Occasionally, samples of particular interest that initially had undergone capture will undergo whole genome sequencing. Bioinformatic processing will again be as described in WP 6 (Princeton, Stony Brook and NYGC).

WP 8. Genomic Data quality assessment Genotypes, pseudo-haploid calls and genotype likelihoods will be generated using custom software to account for post-mortem damage

and partial UDG treatment (Amorim et al. 2018; Link et al. 2017). Principal Component Analysis (Patterson, Price, and Reich 2006) will be applied via a pseudo-haploid call approach, with our ancient samples examined within the context of various modern whole genome and SNP array reference datasets (1000 Genomes Project Consortium et al. 2015; Nelson et al. 2008; Mallick et al. 2016; Busby et al. 2015). This analysis will identify quality control problems in genotype calling while also helping to observe general patterns in the data that may motivate additional hypotheses (Stony Brook).

WP 9. Within cemetery/local genomic analysis: Within cemeteries biological kinship will be estimated using IcMLkin from genotype likelihoods (Lipatov et al. 2015). IcMLkin can accurately identify biological kinship down to at least three degrees of relatedness and we have recently modified it to account for admixed individuals and population structure. We will also develop an approach that uses a combination of rare variants from WGS and putative haplotype tracts from SNP capture data to infer more distant relatedness, for example for cemeteries or local regions that span multiple centuries. Genotype likelihoods will also be used to infer possible genetic structure amongst individuals and admixture within individuals using NGSadmix (Skotte, Korneliussen, and Albrechtsen 2013). We have also modified the program SPA (Yang et al. 2012) to utilize genotype likelihoods that will allow us to more precisely estimate the likely ancestry of missing parent (i.e. one not buried amongst another parent-child duo that we may genotype). Physical phenotypes of our individuals (hair, eye and skin pigmentation) will be inferred using the HlrisPlex system (Walsh et al. 2013), as our array contains SNPs associated with these traits, along with SNPs associated with lactase persistence and other traits (Mathieson et al. 2015) (IAS and Stony Brook).

WP 10. Genomic analysis modeling mobility and migration: Evidence of migration between burial communities will be inferred using a variety of approaches, including modeling of genetic drift via f -statistics (Patterson et al. 2012) and covariance matrices (Pickrell and Pritchard 2012), and model-based inference from simulations using Approximate Bayesian Computation (Beaumont, Zhang, and Balding 2002). However, a key novel aspect of our approach for identifying migrants and parameterizing population migration will be developing new methods that capitalize on the rare variants (Mathieson and McVean 2014; Schiffels et al. 2016; Brown and Pasaniuc 2014; Novembre and Peter 2016) found in our dense WGS data (~750 samples) to refine fine-scale spatial relationships even at regional levels (IAS, Stony Brook and Jena).

WP 11. DNA analysis of pathogens. Approximately 500 samples, using samples from teeth in burials with two or more individuals, will be extracted, DNA libraries prepared and about 5 million reads shot-gun sequenced for initial pathogen screen using a recently developed ancient pathogen screening pipeline (Vagene et al. 2018). Positive samples will be used for complete ancient pathogen reconstruction following in-depth bacterial genome analysis (e.g. Bos et al. 2011) (Jena).

WP 12. Isotope analysis for Sr and C/N isotopes: Sr isotope analysis of about 3000 samples of human teeth and comparative material (e. g. animal teeth or modern environmental samples [Maurer et al. 2012]) will identify non-local individuals coming

from areas with geological conditions differing from those at the location of the respective cemeteries. Sampling complete cemeteries informs on age and sex-based differentiated mobility patterns and identifies groups with similar isotopic backgrounds. Strontium will be separated from mechanically cleaned core enamel under clean-room conditions and the isotopic composition determined by a multi-collector ICP-MS (NuPlasma NR MC-ICP-MS). C and N isotope ratios of bone collagen reflect dietary proteins. They distinguish C3 and C4 plants as staple crops, differ along food chains (plant vs. meat-based diets), between terrestrial diets and fish, or reflect land-use practices, such as manuring. C and N isotope data will identify broad dietary changes over time, differences among regions, and within cemeteries regarding age, sex or possible social status. Collagen will be extracted from 1000 samples of human and animal bones for comparison. Sample preparation includes mechanical cleaning, demineralization, denaturation, filtering, and freeze-drying (Knipper et al. 2014). The collagen will be combusted in triplicates in a vario PYRO cube CNSOH elemental analyzer coupled to an Isoprime precisiON isotope ratio mass spectrometer. The data will be integrated with published and unpublished results from previous research, which will contribute significant baseline information and enhance data interpretation 3000 samples for Sr (subcontracted), 1000 samples for C/N (Curt-Engelhorn-Zentrum Archaeometrie, GmbH, Mannheim, in cooperation with Budapest).

WP 13. ¹⁴C dating will be performed from the bone or tooth collagen of 500 samples selected across all sites (Budapest in cooperation with radiocarbon lab of CEZA, Mannheim lab). For most of the period, there is a relatively detailed chronological grid derived from historical sources, coin finds and an elaborate relative chronology of material. Apart from validation by archeological analysis (WP 15), this will be systematically verified using ¹⁴C. In areas of good data density, ¹⁴C dates will be modeled with Bayesian statistics in order to set sharp absolute chronological boundaries for population changes and transitions as well as occurrences of pathogens, and can even be refined using genetic data from families spanning multiple generation. Sample material used for ¹⁴C dating can be used for isotope analysis (WP 12) and vice versa (Curt-Engelhorn- Zentrum Archaeometrie, GmbH, Mannheim, in cooperation with Budapest).

WP 14. Climatological considerations: The Jena group of Adam Izdebski will feed into HistoGenes data from a wide variety of climate archives and proxies, as all of them have their biases (e.g., dendrochronological data have a seasonal bias for the spring (for the dendroclimatological data relevant for the Pannonia region, see Popa and Kern 2009; Büntgen et al. 2011, 2013)). This will include palaeoclimate information for different parts of the Pannonian plain, in particular for rainfall and effective moisture, that can be highly regional, contrary to temperature (Labuhn et al. 2016). There is also one speleothems record for the eastern parts of the Carpathian Basin (Warken et al. 2018), which can provide high-resolved and well- dated reconstructions of cold-season or annual weather conditions. For the purposes of our project, it will be validated with an independent speleothem study for the western parts of the region. In cooperation with Dominik Fleitmann (Reading), Juerg Luterbacher and Elena Xoplaki (Giessen), we will study

different proxies in a speleothem from a cave in Moravia, which will allow us to gain insights into several aspects of past climates, such as precipitation and temperature (Haldon et al. 2014; Xoplaki et al. 2016, 2018) (Jena).

WP 15. Archaeological in-depth analysis of relevant cemeteries to supplement information collected in WP 1. There will be continuing interdisciplinary discussion and interpretation of the incoming data from archaeological and historical perspective. Groups distinguished by archaeological analysis (period of inhumation, sex, age, quality of dress and apparel etc.) will be considered separately in the scientific analysis, and fed back into the archaeological interpretation. On the basis of a detailed chronology, social-archaeological studies concentrating on one site and on regional comparisons will be conducted, and cultural contacts studied. Migrations will be analysed as complex social acts (Burmeister 2000, Furholt 2018) and in their impact on community-level patterns of cohabitation of locals and non-locals. Corresponding to the approach of archaeology of identity (Díaz et al. 2005, Insoll 2007, Amundsen et al. 2011), the funeral is seen as a complex social performance, where different identities (age, gender, kinship, social rank, profession, religion, ethnicity etc.) of the individual and the community could be expressed (Halsall 1995; Agarwal– Glencross 2011, Zvelebil–Pettitt 2013, Johnson 2018) (Budapest, Vienna).

WP 16. Anthropological in-depth analysis of selected skeletons, mostly from Avar core area: traces of deficiencies, marks of violence, stress symptoms, exposure to hard work, strain on joints, morphology of teeth, epigenetic traits, rates of fertility and mortality in a cemetery (Vienna, Budapest).

WP 17. Accompanying historical studies: The key task is to relate the micro-studies of small communities, which result from the collected data and the archaeological evidence, to the broader narrative perspectives offered by historical accounts. On the agenda are source studies about local communities, migration and identity (see a3 5.3); methodological studies about the historical interpretation of archaeological and genetic evidence (e.g. a monograph by P. Geary), and a History of the Longobards (W. Pohl) (Vienna, Princeton).

WP 18. Integration of the results, presentation and discussion of the data and their interpretation at conferences and workshops (all four teams).

WP 19. Publication and dissemination activities: Scholarly output will include individual results, studies of sites, works of archaeological comparison and scientific papers. Overall project results will be published in joint conclusive papers in high ranking journals. Open access publication will be practice, where possible, in green open access. A broad overview of the uses of genetics for the study of early medieval history will be provided in a monograph by Patrick Geary. Walter Pohl will use the project results to find ways to write a history of the Longobards without framing it in notions of ethnic linearity. The history Postdoc will write a monograph about the transformations of Pannonia between the 5th and 7th centuries, an aspect of the ‘transformation of the Roman World’ that lacks a recent historical overview. Conference proceedings and themed issues in historical journals will reflect the discussions between the project team and invited

guests. Online tools will include the archaeological Open Atlas database (WP 1) and the historical GENS database (a3 5.3). For a broader public, the digital humanities tool 'Visualising the early medieval steppe peoples' and the 2023 exhibition on steppe warriors at the Schallaburg (a3 5.4) will be provided (all four teams).

b3. Project structure and connectivity

The PIs and many team members have already worked together in the pilot projects. The interdisciplinary and international workflow has been put in place and can be further developed in the HistoGenes.

Interdisciplinarity is not only practiced between PIs, but in each of the four teams. PIs will be supported by senior associates who will collaborate directly, by junior team members, and by senior advisory groups. The workflow and work packages usually involve more than one of the PI teams, which will also help to integrate the project. Of course, the distance between the four host institutions presents a challenge. The project design provides for regular communication and has established several instruments to further project cohesion: PI meetings via zoom, also involving senior team members, will be held at least monthly, but whenever necessary more frequent, to decide about strategic choices, the fine-tuning of the workflow, and issues of organisation. Yearly plenary meetings/workshops of all project teams will discuss procedure, problems, results, specific sites, and may include input from guests. Additionally, an interdisciplinary forum will unite the groups working on different sites, about issues of comparison and methodological problems, and allow

in-depth discussions about the interpretation of the archaeological evidence and the incoming data. These meetings will be particularly frequent in the first and the last project phase, will have a flexible format and will as a rule include non-team members familiar with the sites or issues. They will usually be held at Vienna, Budapest or on-site. Regular PI team and work package meetings will allow coordination between concerned team members, also between related work-packages. The writing process of joint articles and documents will be facilitated via google.docs. Public ventures will draw other scholars into the discussion process, and allow team members to meet: Open network workshops with invited guests will focus on specific issues. Three large conferences (start-up, mid-term and final conference) with distinguished guests will present the research agenda and results, supplement expertise lacking in the team, and allow communication with other projects in the field. Sessions at the International Medieval Congresses in Leeds and Kalamazoo and at other large venues will publicize HistoGenes, as will the project website and blog.

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