

PIAST STATE SOCIETY – HISTORY DECIPHERED FROM DNA

Exploring the history of our ancestors – from written records to DNA – can reveal our deeper roots. Modern genomic research on ancient human remains is now challenging long-held assumptions and reshaping our understanding of Poland's past.

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Knowing the history of one's ancestors – learning where they came from, how they lived, and what relations they had with others – has always been important, both on the individual and family level and on the broader scale of entire communities or nations. Until recently, the main way to uncover this history was through the analysis of written records and the study of material remains – the products of the cultural and economic activities humans have engaged in over the centuries. However, technological advances in recent years, especially in molecular biology, have opened up entirely new possibilities for exploring the biological history of humankind through the study of genetic material preserved in ancient human remains. Thanks to these innovative approaches, we have gained access to information that in many cases reaches far deeper into the past than what can be learned from the analysis of material culture. As a result, *archaeogenomic research* – as this

field is known – has rapidly contributed to verifying or refuting many hypotheses and ideas about the history of the human species.¹

Recognizing the vast potential inherent in the emerging field of archaeogenomics, we undertook a project bold for its time: to study the genetic structure of populations inhabiting what is now Poland during the early centuries CE (the Iron Age) and the formative period of the Polish state (the early Middle Ages). It was indeed an ambitious decision, especially considering that in the early 2010s – when we began the project – only a dozen ancient genomes from humans and Neanderthals were known. Our interdisciplinary research on these two populations was conducted as part of a SYMFONIA project funded by Poland's National Science Centre, entitled "Dynasty and society of the Piast state in the light of integrated historical, anthropological, and genomic research."

Several years of intensive work have produced over 25 scientific articles, published in leading journals in the fields of history, archaeology, and biology. One of the most important, entitled "Genetic history of East-Central Europe in the first millennium CE," appeared in *Genome Biology* in 2023.² In our view, this article marks a significant turning point in a debate that has continued for over 200 years, regarding the



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origins of the West Slavs, including the society of the Piast state. The interdisciplinary research team that authored this groundbreaking publication included biologists, anthropologists, archaeologists, and historians. Without doubt, only such cross-disciplinary collaborations, where diverse scientific approaches can complement one another, have the potential to bring real progress in understanding the complex demographic processes that shaped East-Central Europe in the first millennium CE.

Europe before the Piast state’s formation

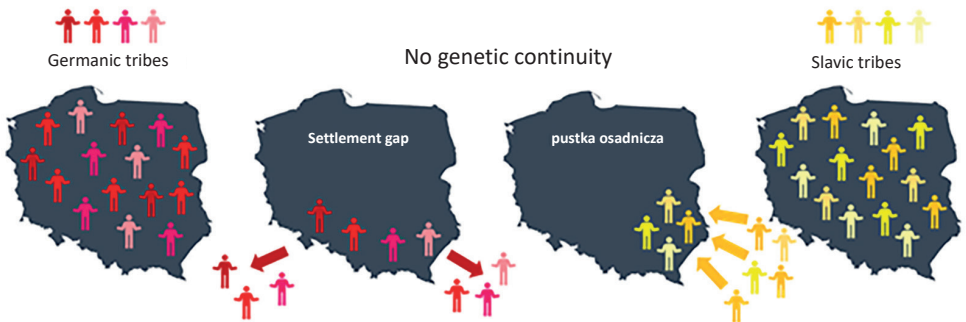
One of the most dramatic periods of the first millennium CE was undoubtedly the second half of the fifth century, when the Western Roman Empire finally collapsed under pressure from barbarian tribes. As a result, entirely new political and ethnic structures emerged across Europe.³ While the historical events and processes behind the transformation from antiquity to Christianity in the former Roman territories are relatively well understood, we still know little about the changes that took place in areas outside the newly formed Christian world. One such controversial issue is the appearance of the Slavs in Central Europe. Seeking to explain it, two opposing hypotheses were formulated many years ago. The first, known as the

allochthonous hypothesis, posits that the Slavs arrived in this part of Europe no earlier than the sixth century CE.⁴ The second, the *autochthonous* hypothesis, assumes that the Slavs had already inhabited the lands between the Oder and Vistula rivers long before the so-called Migration Period,⁵ traditionally dated from 375 CE (the Hunnic invasion of Europe) to 568 CE (the Lombard conquest of Italy) (Fig. 1).

The data collected so far indicate that by the end of the Late Neolithic period (3700–1800 BCE), the genetic structure of populations living in Central Europe had stabilized and remained largely unchanged through the end of the Bronze Age (1800–700 BCE).⁶ At that time, the genomes of people in the region consisted of three main components: the first linked to Western Mesolithic hunter-gatherers who had arrived in Europe around 14,000 years ago, the second to Neolithic Anatolian farmers who migrated into Europe 7,000–8,000 years ago, and the third to steppe pastoralists from the Caspian and Black Sea regions (the Yamnaya culture), who spread into Europe 4,000–5,000 years ago.

Questions about the later development of the genetic history of East-Central Europe remained unresolved for many years, largely due to a lack of suitable material for archaeogenomic research. This shortage of remains is primarily the result of the widespread cremation of the dead in the region, practiced from roughly 1700 BCE through the Middle Ages.

Allochthonous hypothesis



Autochthonous hypothesis

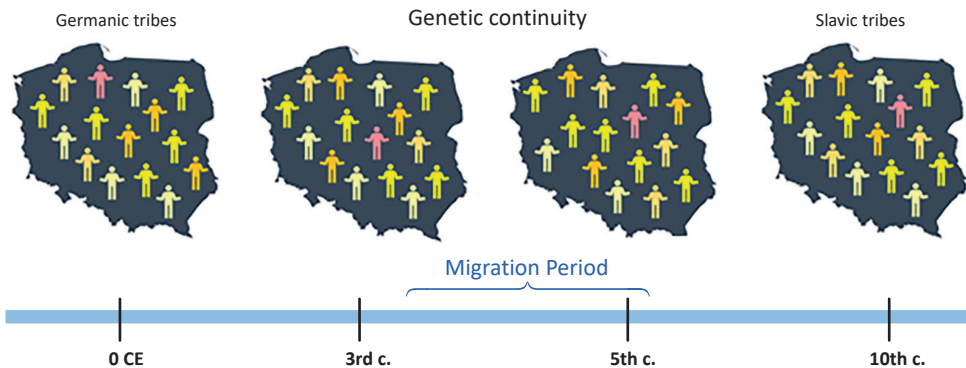


Fig. 1 Hypotheses tested in our study. The allochthonous hypothesis assumes the presence in present-day Poland of two genetically distinct populations: Germanic and Slavic. According to this view, the Germanic population lived in the area until the Migration Period, when it was replaced by Slavs arriving in the sixth century CE. The autochthonous hypothesis also posits two genetically distinct groups – Germanic and Slavic – but holds that exclusively the Slavs, not the Germanic peoples, had inhabited the region since at least the Iron Age

subsequent generations, by the second generation, the average local genomic component would rise to about 75%, and by the fourth generation, it would exceed 90%. This means that by analyzing the DNA of individuals from a population formed in the 1st century CE by northern immigrants and local women – and later drawing mainly from local genetic resources – we were, in effect, examining the genetic structure of the local population.

Interestingly, our analyses also showed that during the Roman period, the populations inhabiting what is now Denmark, northern Germany, Poland, and likely Lithuania and Latvia shared a similar genetic structure. Their genomes were composed of the same elements, with only the proportions differing between regions.

Moreover, we demonstrated that the genomes of Wielbark culture individuals living in the third-fourth centuries CE near present-day Hrubieszów contained nearly all the genetic components identified in the genomes of the later population that formed the Piast state society. This finding suggests that the major demographic processes shaping the genetic structure of the population inhabiting modern-day Poland in the tenth–eleventh centuries CE had already concluded by the fourth–fifth centuries CE. In other words, our results indicate that no further significant migration after the fifth century was needed to shape the genetic structure of the Piast state’s population.

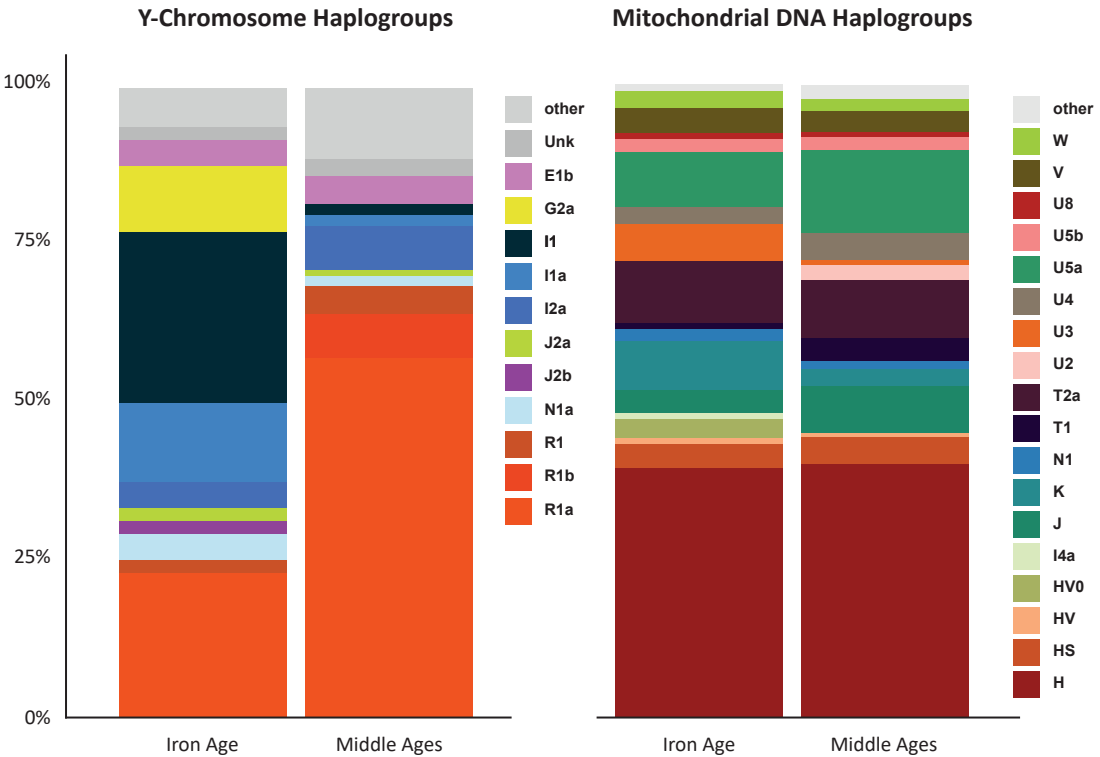
It is worth reiterating that, according to the scenario described above, individuals of the Wielbark culture living in the third century CE would have been the eighth- or ninth-generation descendants of northern immigrants and local women. Their genomes were thus nearly identical to those of the local population. The only significant difference was the Y chromosome, passed down exclusively through the male line. These results are consistent with the autochthonous hypothesis, which posits genetic continuity in Central-Eastern Europe throughout the first millennium CE.

Genetic continuity in the first millennium CE

Throughout the first millennium CE – from the Roman period to the emergence of the Piast state – a strong northern genetic component remained present among populations living in what is now Poland. This applied even to the local population that continued cremating their dead as the primary funerary practice up to the end of the millennium. In women, there were no significant genetic changes over this entire period: they did not arrive with the northern migrants and were consistently of local origin (see Fig. 3).

The situation with local men appears slightly more complex. In general, their genomes were very similar to those of the incoming northerners, with one

Fig. 3
Percentage prevalence of individual Y-chromosome and mitochondrial DNA haplogroups in Iron Age and medieval populations. Each Y-chromosome and mitochondrial haplogroup is represented by a different color. The results clearly show that the male lineages dominant among early immigrants to the area of present-day Poland differed from those found in the medieval population, while the frequency of female lineages remained virtually unchanged throughout the first millennium CE. This finding suggests that the migrants were primarily men, whereas the women were of local origin – supporting the hypothesis of admixture between newcomers and the indigenous population



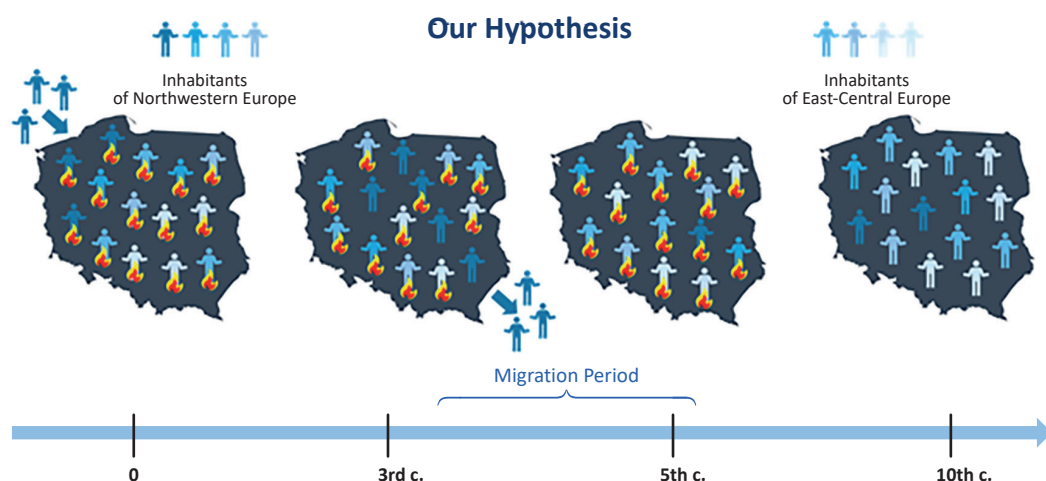


Fig. 4
The hypothesis emerging from our research assumes genetic continuity alongside cultural discontinuity. Our results contradict earlier assumptions that two genetically distinct populations – Germanic and Slavic – inhabited Northwestern and East-Central Europe in the first millennium CE. The analyses indicate genetic continuity among populations living in what is now Poland from at least the Iron Age through the Middle Ages. They also suggest that all populations along the Baltic coast during the first millennium shared a similar genetic structure. Fire symbols indicate that cremation was a common burial practice among the local population, but not among the migrants associated with the Wielbark culture

exception: the Y chromosome, which is carried only by males and passed exclusively from father to son. The Y-chromosomal lineages of the immigrants differed from those of the local population (see Fig. 3). Due to the highly patriarchal social structure at the time, these communities were largely closed to local men. It is thus unsurprising that the Roman-period males we studied – both immigrants and their descendants – displayed predominantly northern Y-chromosome haplogroups (I, II).

However, as the Wielbark culture gradually spread throughout the territory of modern Poland, we also begin to see the emergence of Y-chromosome haplogroups such as R1a, which likely originated from local men. This indicates that the previously mentioned exclusion of local males from these communities was not always effective. In this way, the typically northern Y chromosomes (I, II) – a clear genetic marker distinguishing the immigrants from the indigenous population – were gradually replaced by local Y chromosomes (R1a).

It is therefore not surprising that when the northern newcomers left the area in the 4th–5th centuries CE, the expansion of northern Y-chromosome haplogroups (I, II) came to an end. These haplogroups continued to exist within the population that later

formed the Piast state, but they were no longer dominant. For obvious reasons, such dominance could only be maintained within groups made up primarily of immigrants.

As previously noted, the prevalence of cremation as the dominant funerary custom makes it impossible to determine with certainty which Y-chromosome haplogroup prevailed among the local population in the early centuries CE. However, the appearance of R1a haplogroups—commonly associated with later populations generally considered Slavic—within Wielbark culture communities suggests that Y-chromosome continuity is also likely. Haplogroup R1a was dominant among the local population both at the beginning of the first millennium CE (i.e. before the arrival of immigrants who established the Wielbark culture) and at its end. In other words, the local men living in the early centuries CE on the territory of present-day Poland were the ancestors of those who, in the tenth–eleventh centuries CE, formed the society of the Piast state.

However, this does not mean that Slavs were already present in this region in the early centuries of the Common Era. The term “Slavs” refers to a culture that, according to archaeological evidence, did not begin to develop until around the 6th century CE (Fig. 4). ■

¹ G. Brandt et al., Ancient DNA reveals key stages in the formation of Central European mitochondrial genetic diversity, *Science* 2013, no. 342(6155), pp. 257–261; M.E. Allentoft et al., Population genomics of Bronze Age Eurasia, *Nature* 2015, no. 522(7555), pp. 167–172.

² I. Stolarek et al., Genetic history of East-Central Europe in the first millennium CE, *Genome Biology* 2023, no. 24, <https://doi.org/10.1186/s13059-023-03013-9>.

³ C.E.G. Amorim et al., Understanding 6th-century barbarian social organization and migration through paleogenomics, *Nature Communications* 2018, no. 9, <https://doi.org/10.1038/s41467-018-06024-4>.

⁴ K. Godłowski, Pierwotne siedziby Słowian [The Original Homelands of the Slavs], Kraków 2000.

⁵ J. Piontek, Etnogeneza Słowian w świetle najnowszych badań antropologicznych [Ethnogenesis of the Slavs in Light of Recent Anthropological Research], *Slavia Antiqua* 2006, no. 47, pp. 161–189.

⁶ I. Lazaridis et al., Ancient human genomes suggest three ancestral populations for present-day Europeans, *Nature* 2014, no. 513(7518), pp. 409–413.

⁷ A. Cieśliński, The society of Wielbark culture, AD 1–300. In: *The past societies, vol. 4: Polish lands from the first evidence of human presence to the Early Middle Ages: 500 BC – 500 AD*, ed. A. Rzeszotarska-Nowakiewicz, Warsaw 2016, pp. 217–256.