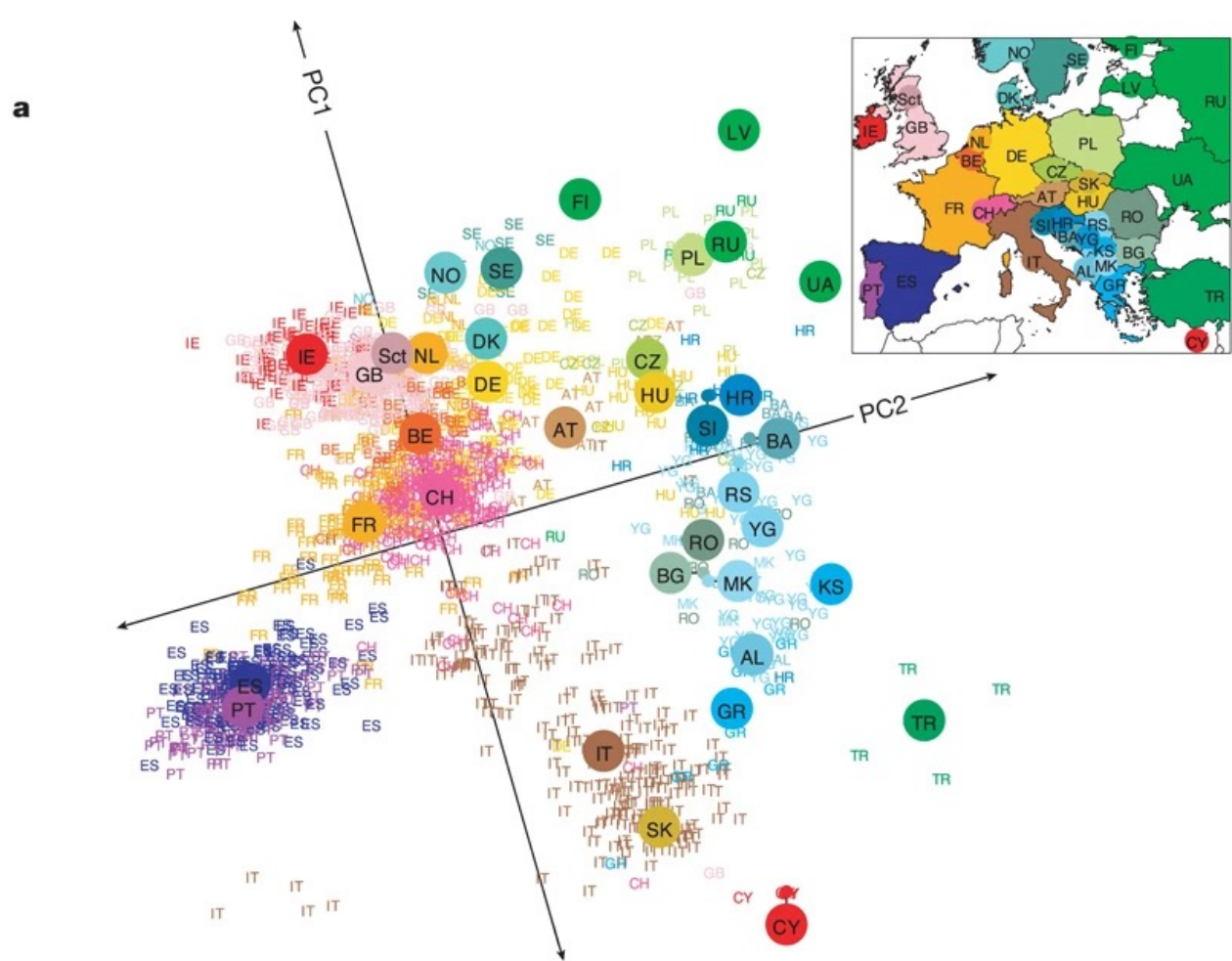
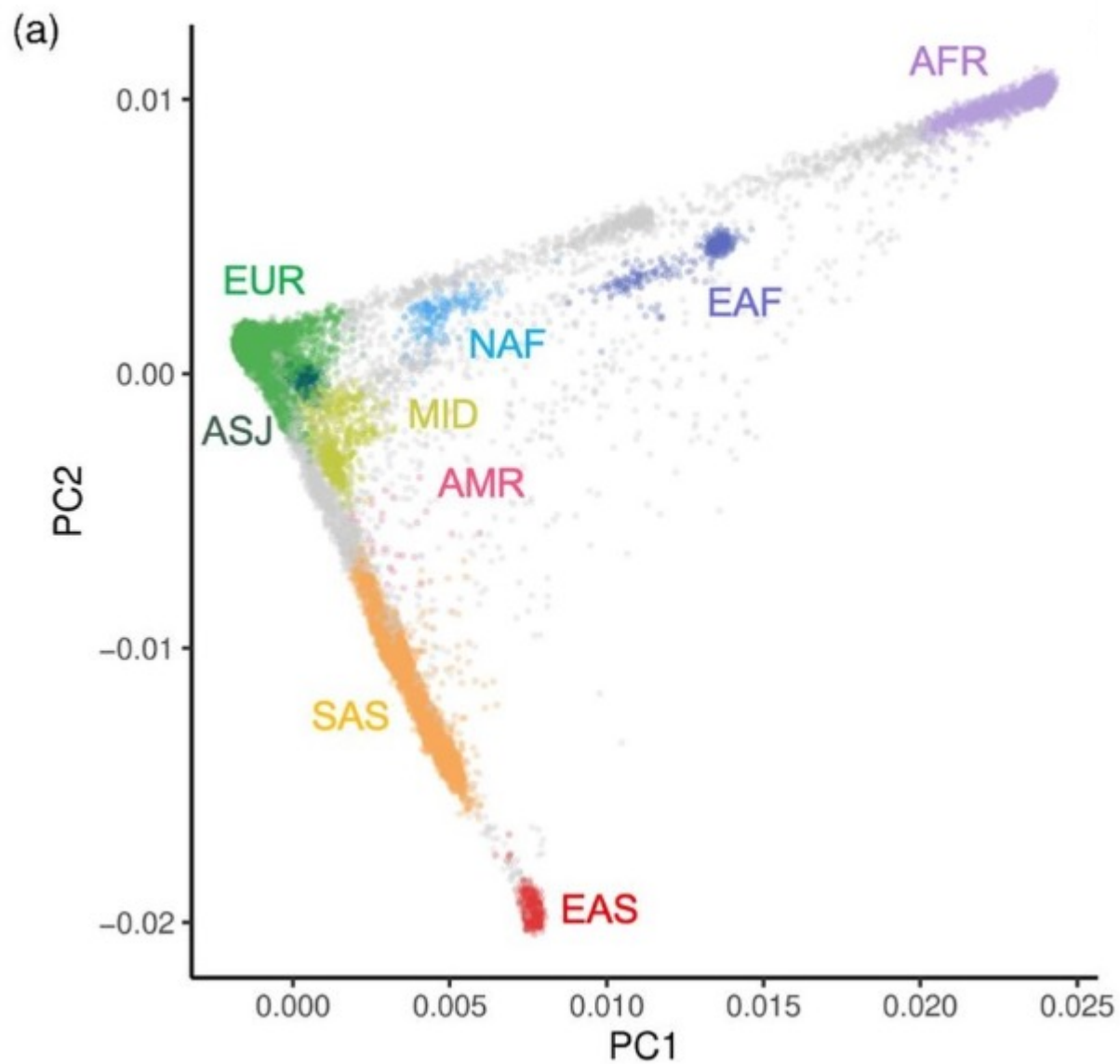


# Ancient DNA unveils a thousand years of history in Sint-Truiden

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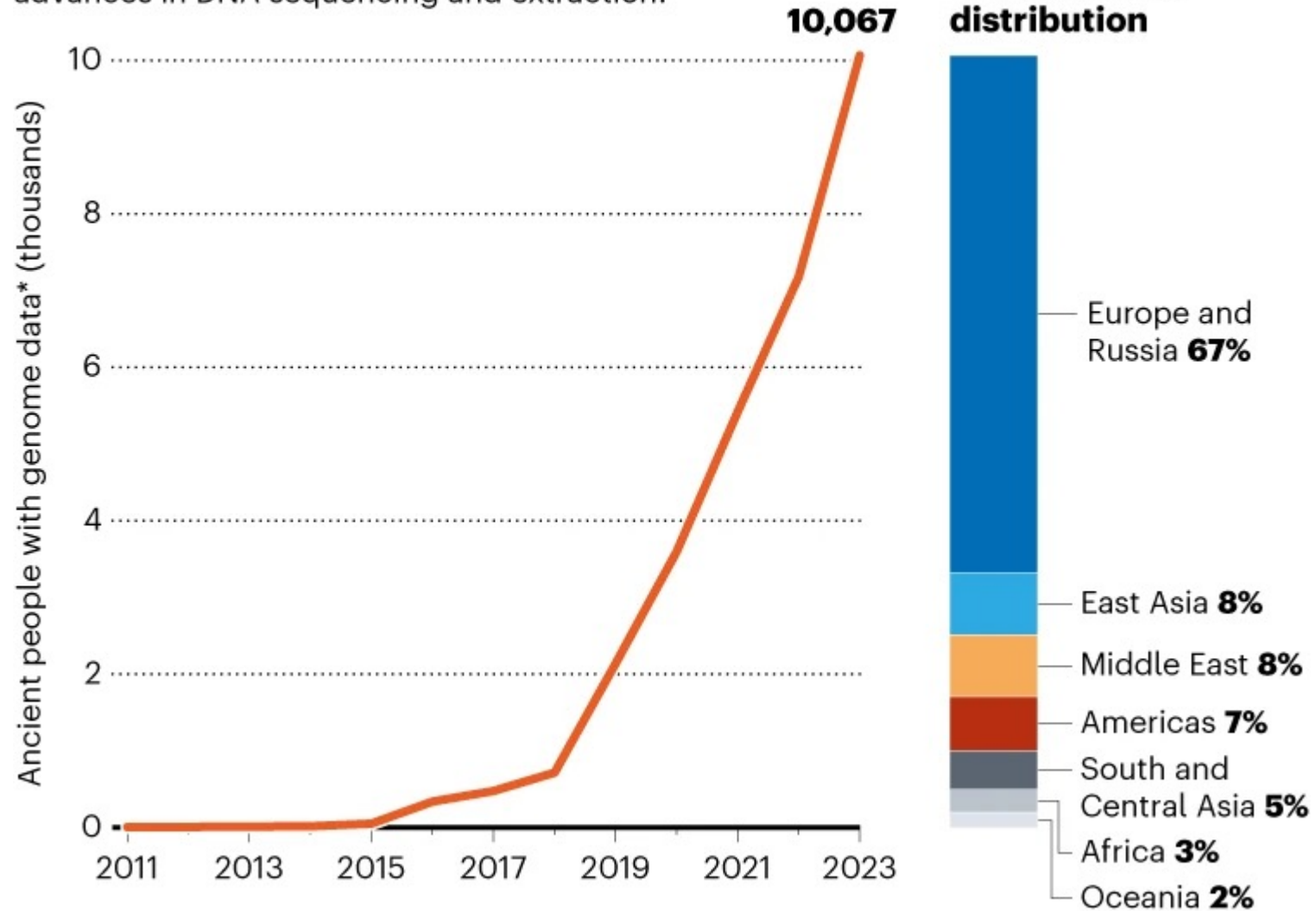
Noah Gaens





# ANCIENT-DNA GOLDRUSH

The quantity of genome data from ancient-human remains has grown rapidly since 2018, owing to advances in DNA sequencing and extraction.



©nature

\*Includes genome sequences and genome-wide data.



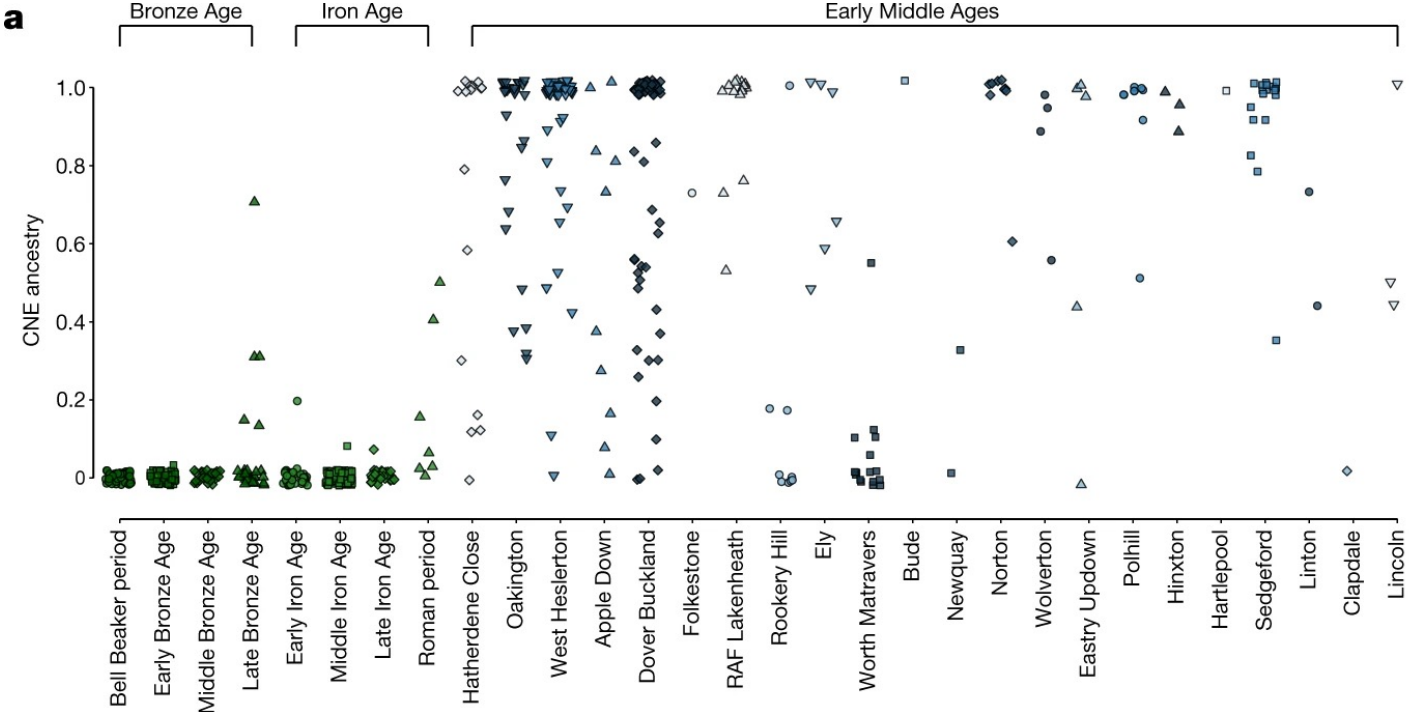
**Mesolithic hunter-gatherer populations (14,500 BP - 8,000 BP)**

**Early farmer expansions from Anatolia (8,500 BP)**

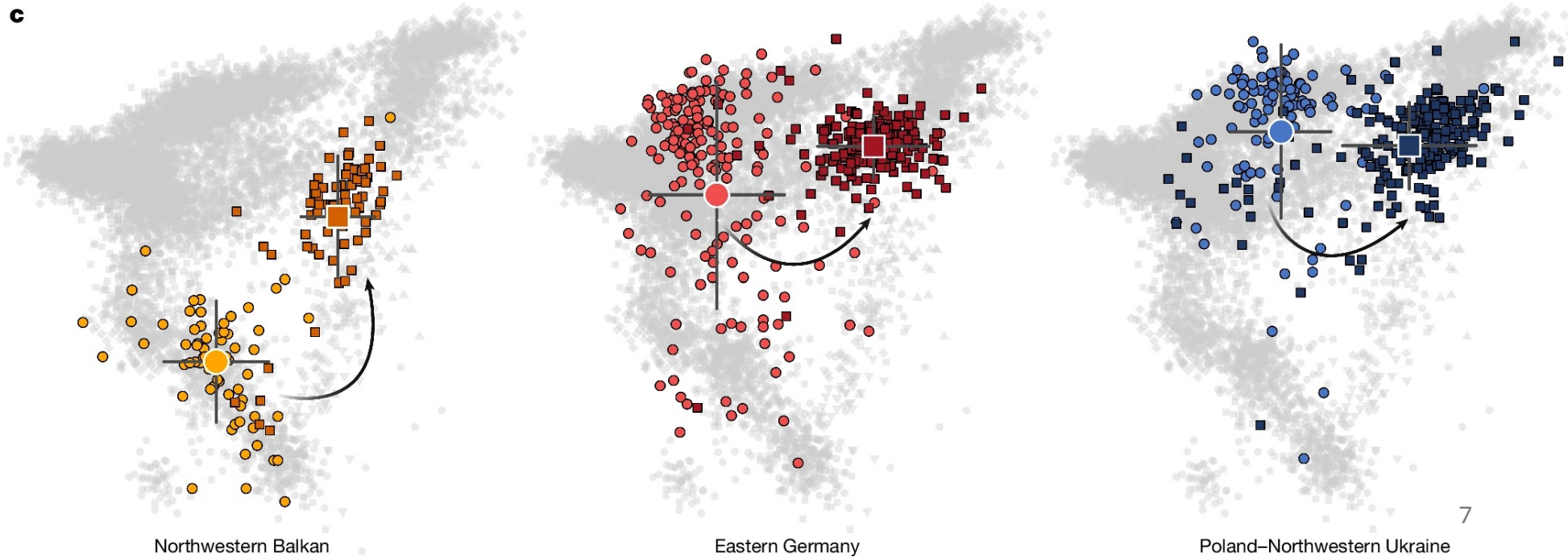
**Bronze Age migrations from the Ponthic-Caspian steppe (5,000 BP)**

- Since **Iron Age** (ca. 800 BCE): more **stable population structure** in Europe
  - Less gene flow from outside Europe
  
- Middle Ages (500-1500 CE):
  - Large-scale **intracontinental migration**, e.g. **Migration Period** (400-600 CE)
  - Major **regional genetic ancestry** reshuffling

# British Isles



# Central-Europe

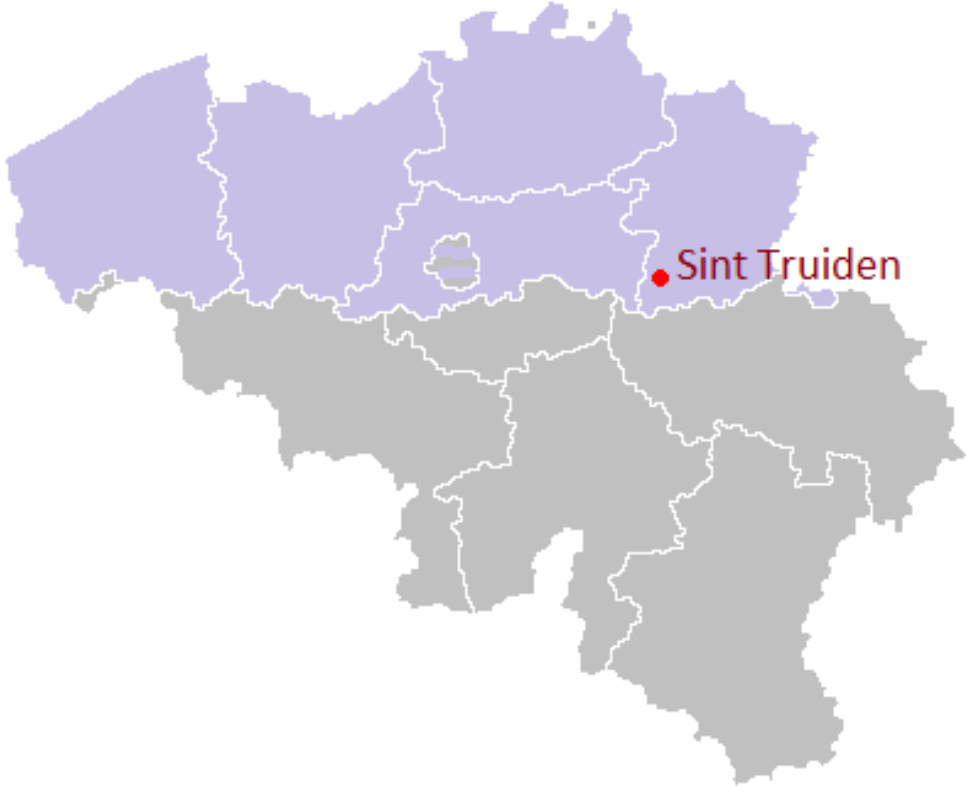


- Historical era: **major political and social transformation**
- **Genetically highly dynamic**
- **Impact** of these demographic changes in Western Europe during the last **two millennia**?
- Need for **long-time transect** studies

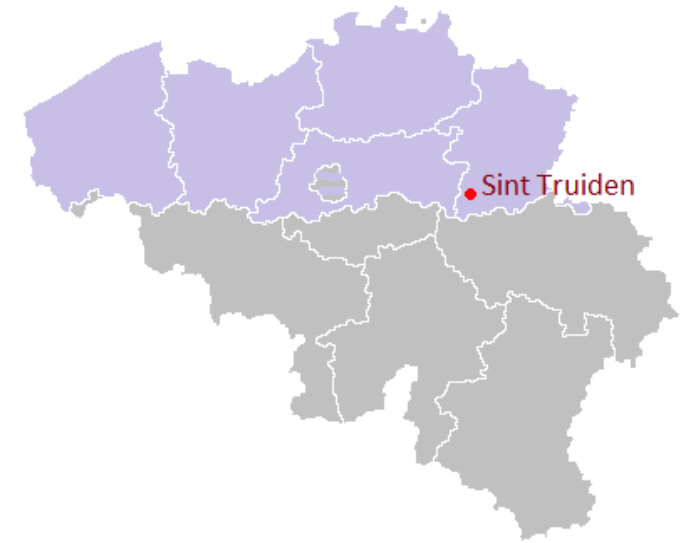
# Sint-Truiden

- Archaeological **excavations** (2018-2020)
  - Cemetery with **3,000** graves
  - **8th – 18th c.**
- **Low Countries:** high population density and urbanisation during Middle Ages
- Archaeo-historically **well-documented**

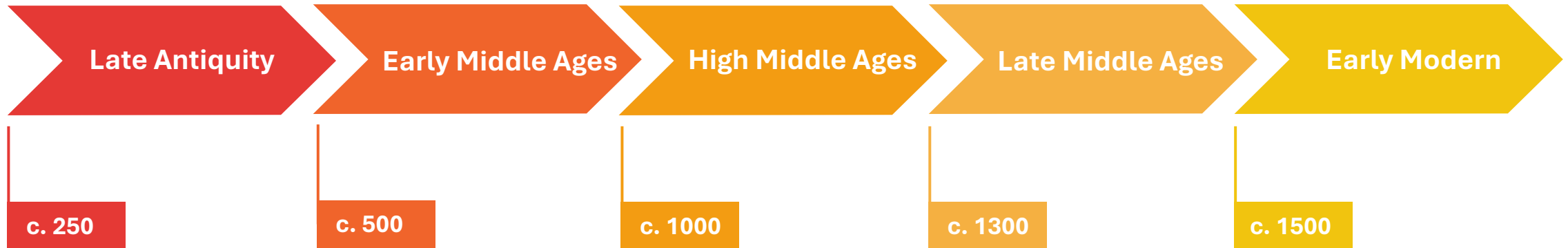
# Sint-Truiden



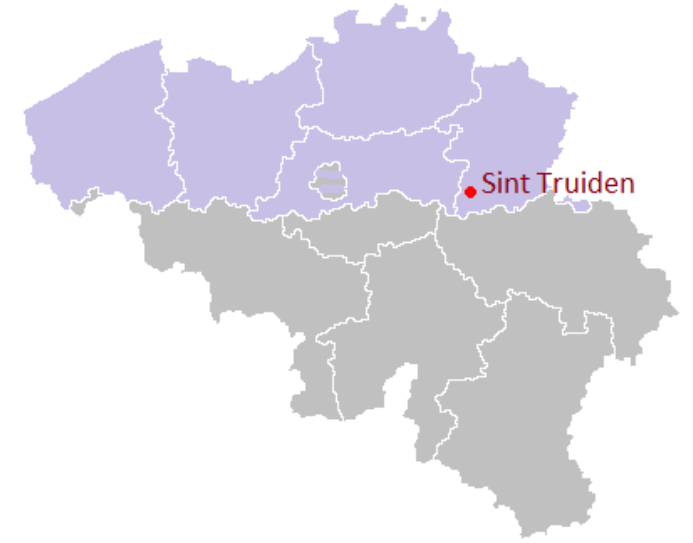
# Sint-Truiden



**Sarchinium:** Roman settlement

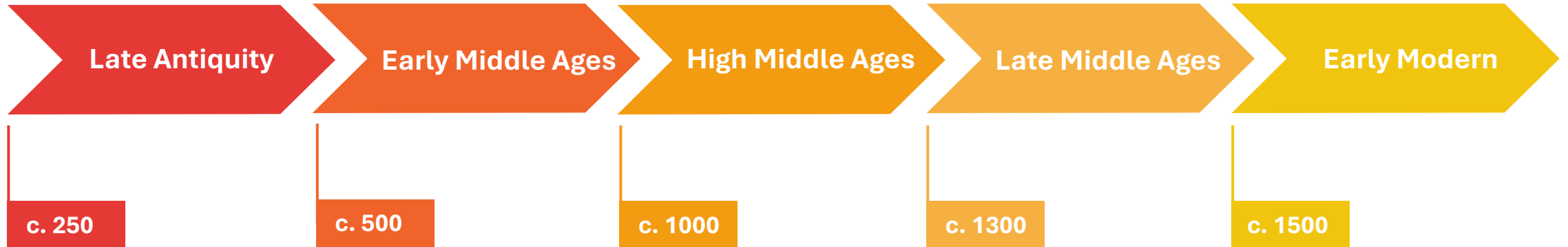


# Sint-Truiden

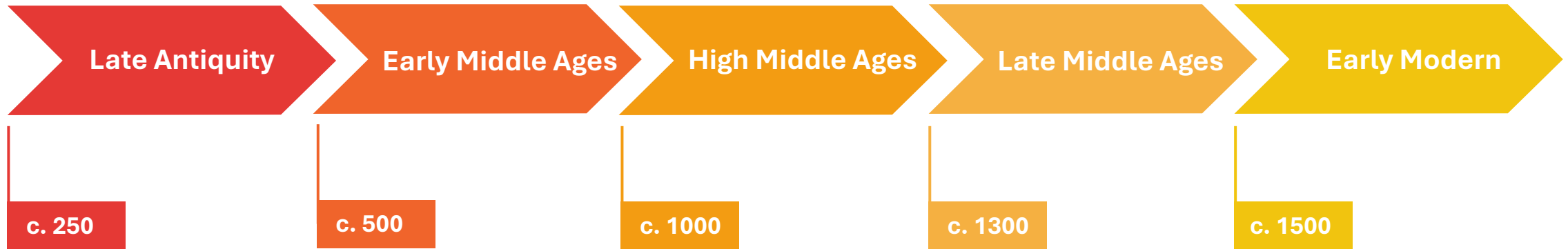
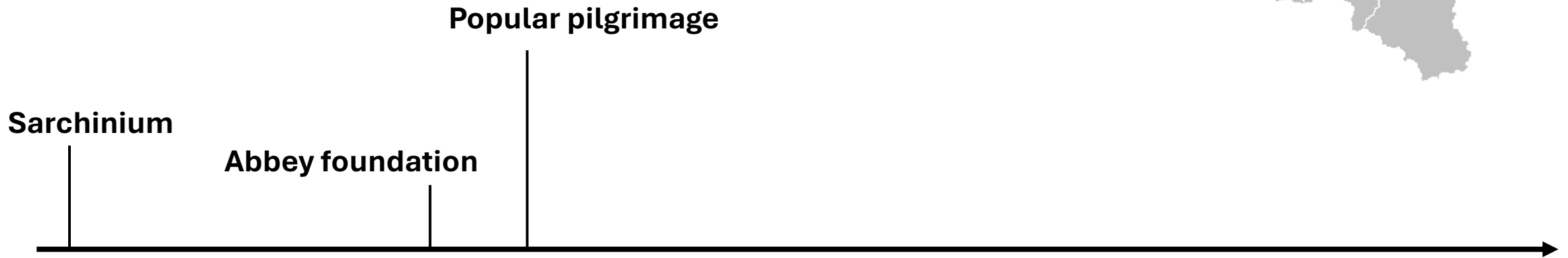
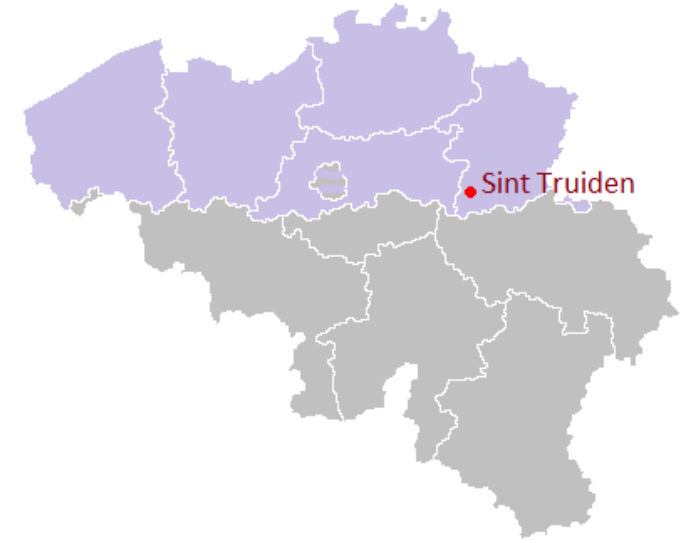


Sarchinium

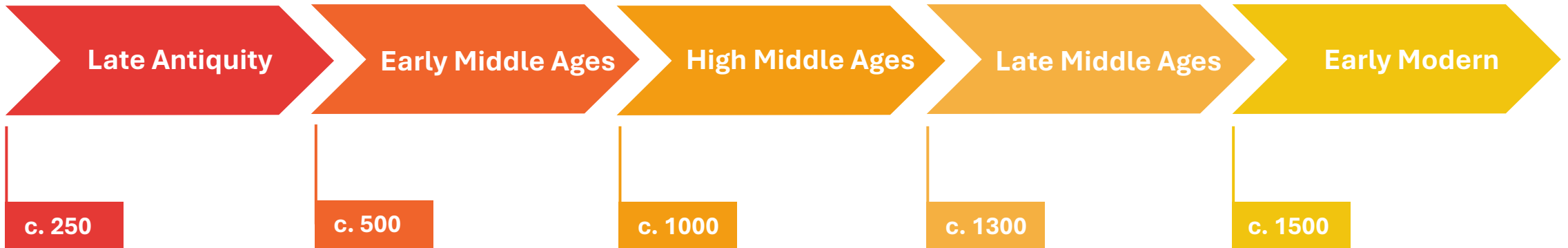
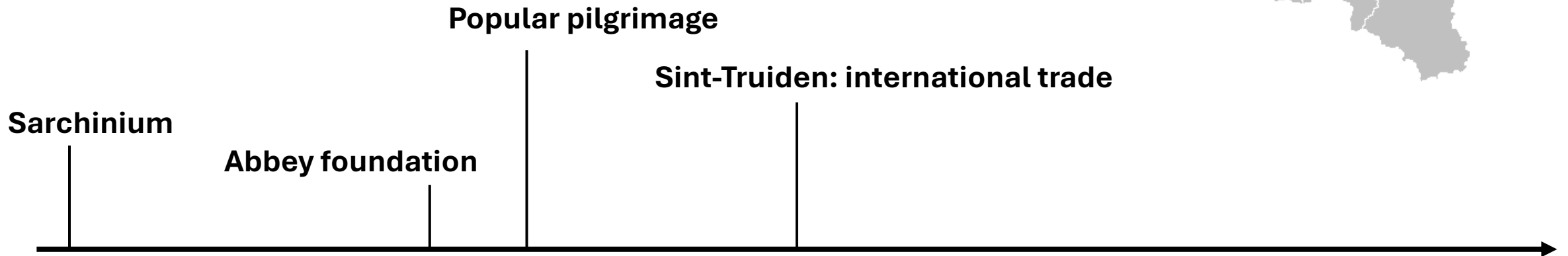
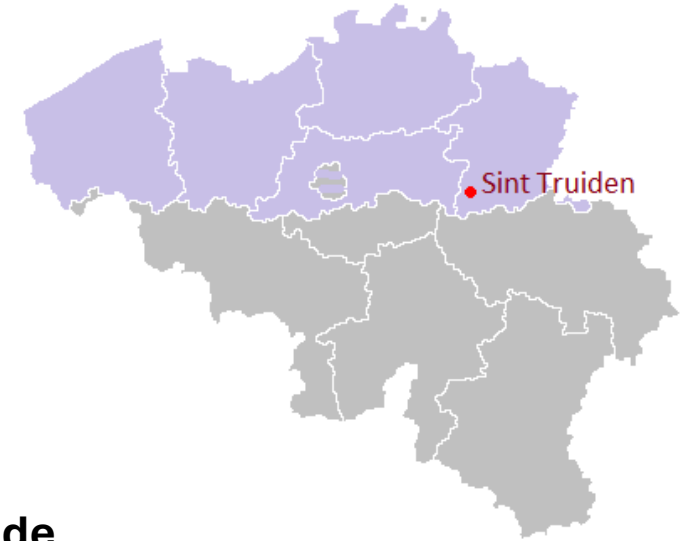
Abbey foundation by Saint-Trudo



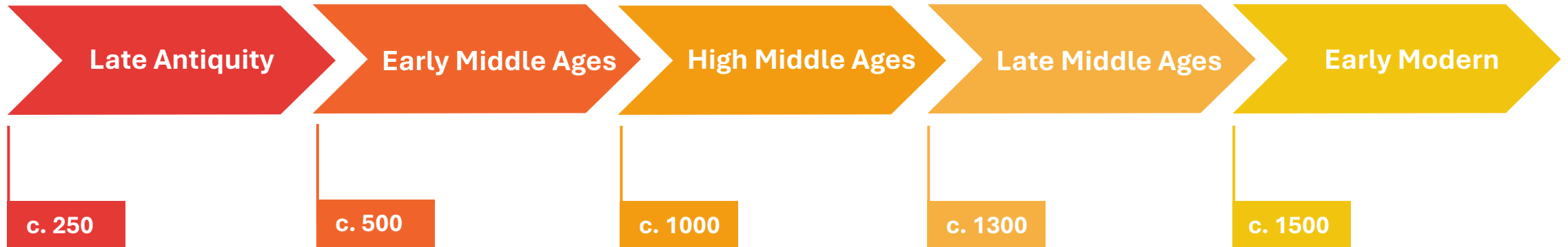
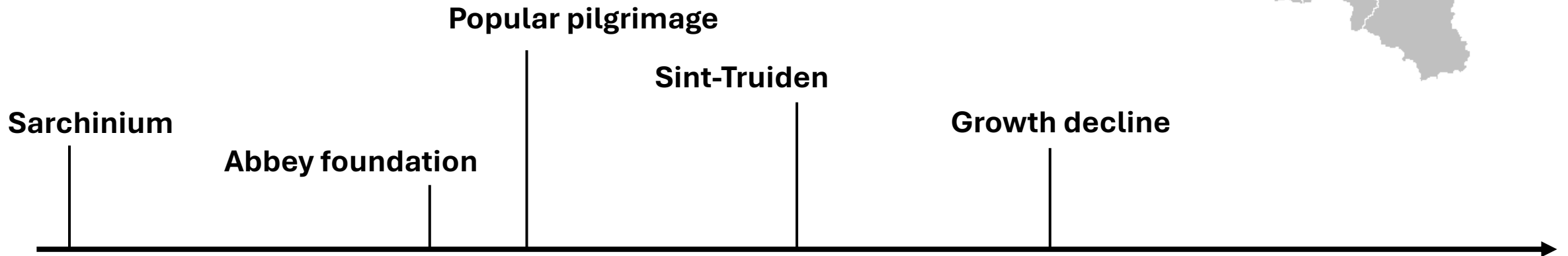
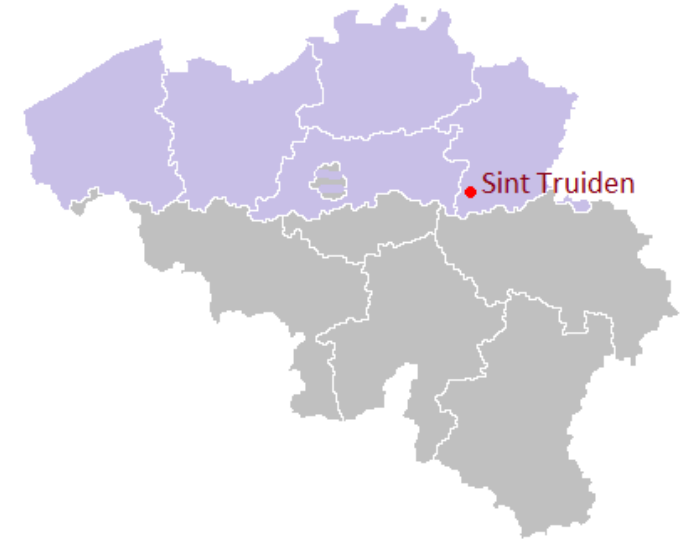
# Sint-Truiden

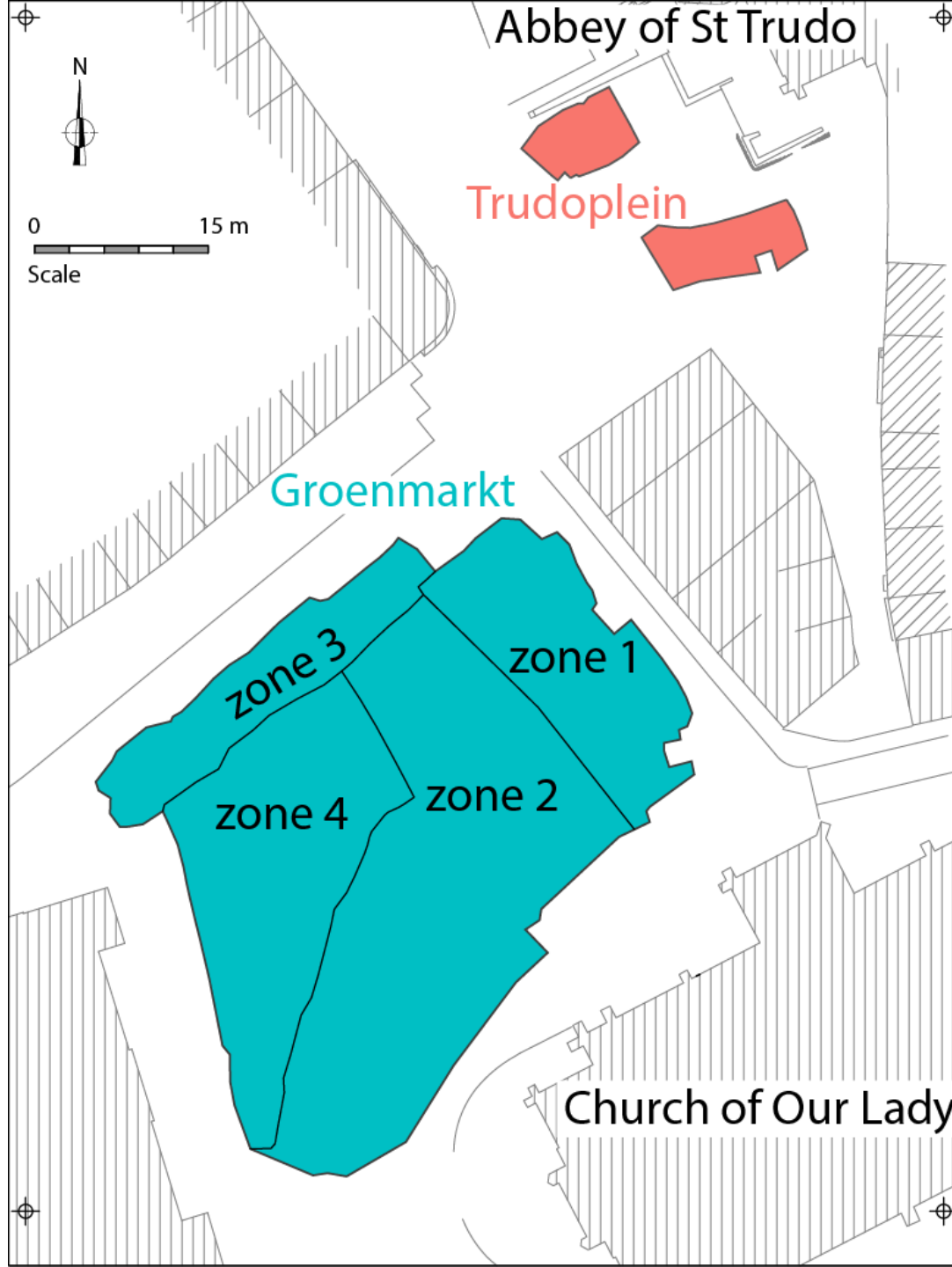


# Sint-Truiden



# Sint-Truiden





## Trudoplein

Outside Abbey walls  
7th – 14th c.

## Groenmarkt

7th – 18th c.

Parish cemetery (11th c.)  
1286 CE: zone 1 – zone 2

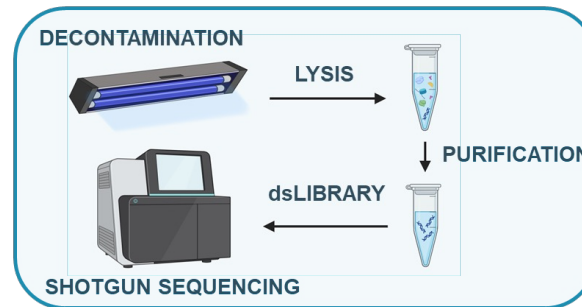
# Research design

- 3,000 skeletons
- 404 selected for ancient DNA analysis

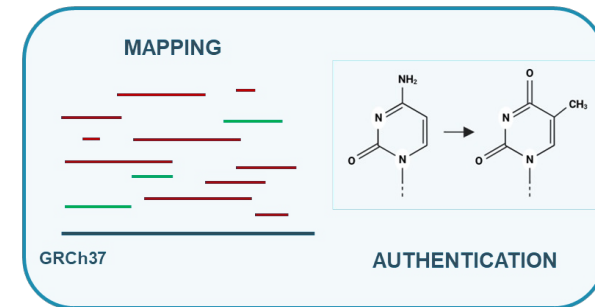
## 1. SAMPLING SKELETAL REMAINS



## 2. WET LAB PROCESSING



## 3. DRY LAB PROCESSING



- 332 high-quality DNA data



## **Patterns of ancestry and mobility**



## **Relatedness and inbreeding**



## **Population size dynamics and demographic recovery**

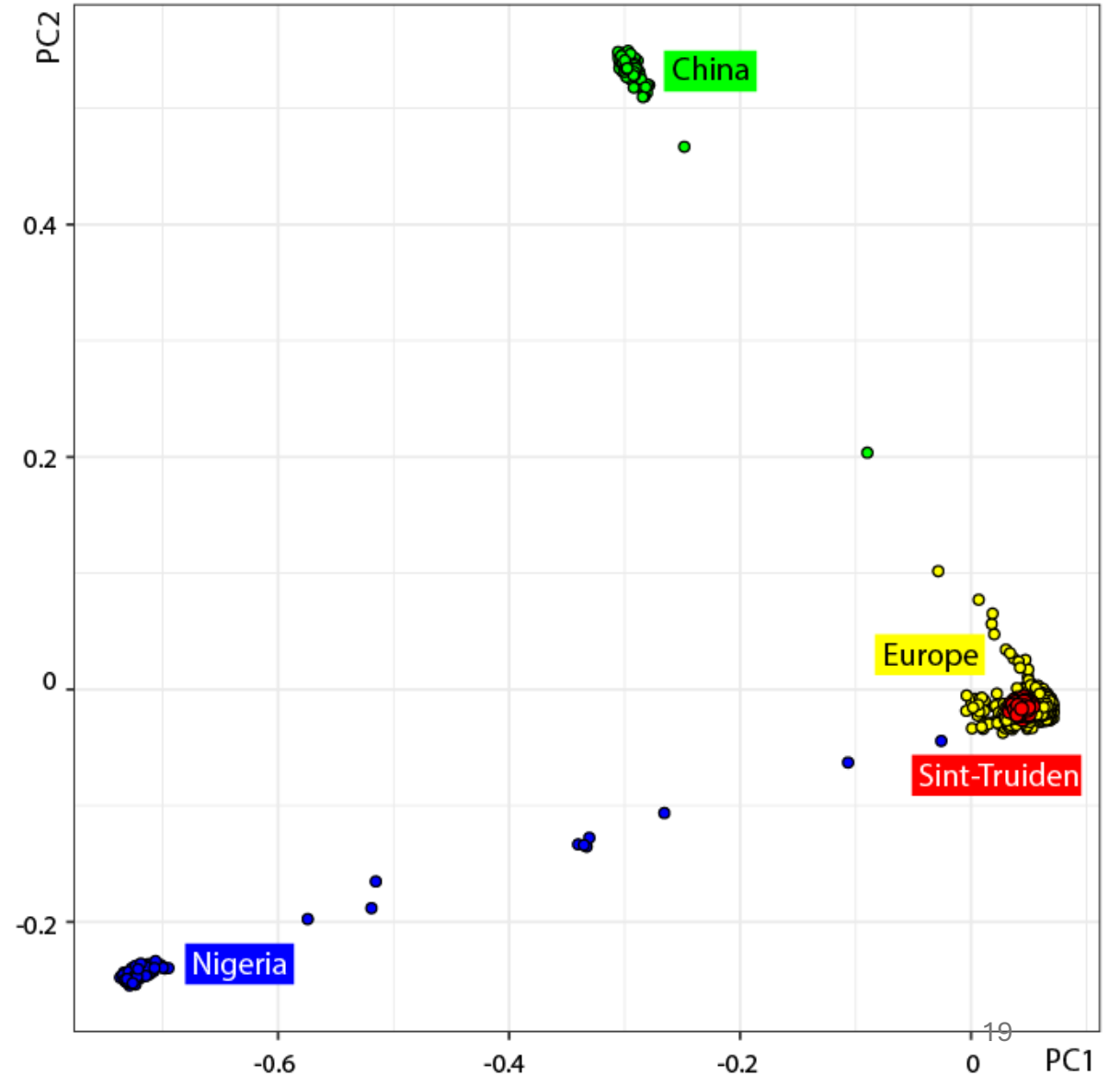


## **Health and immune responses to pandemics**



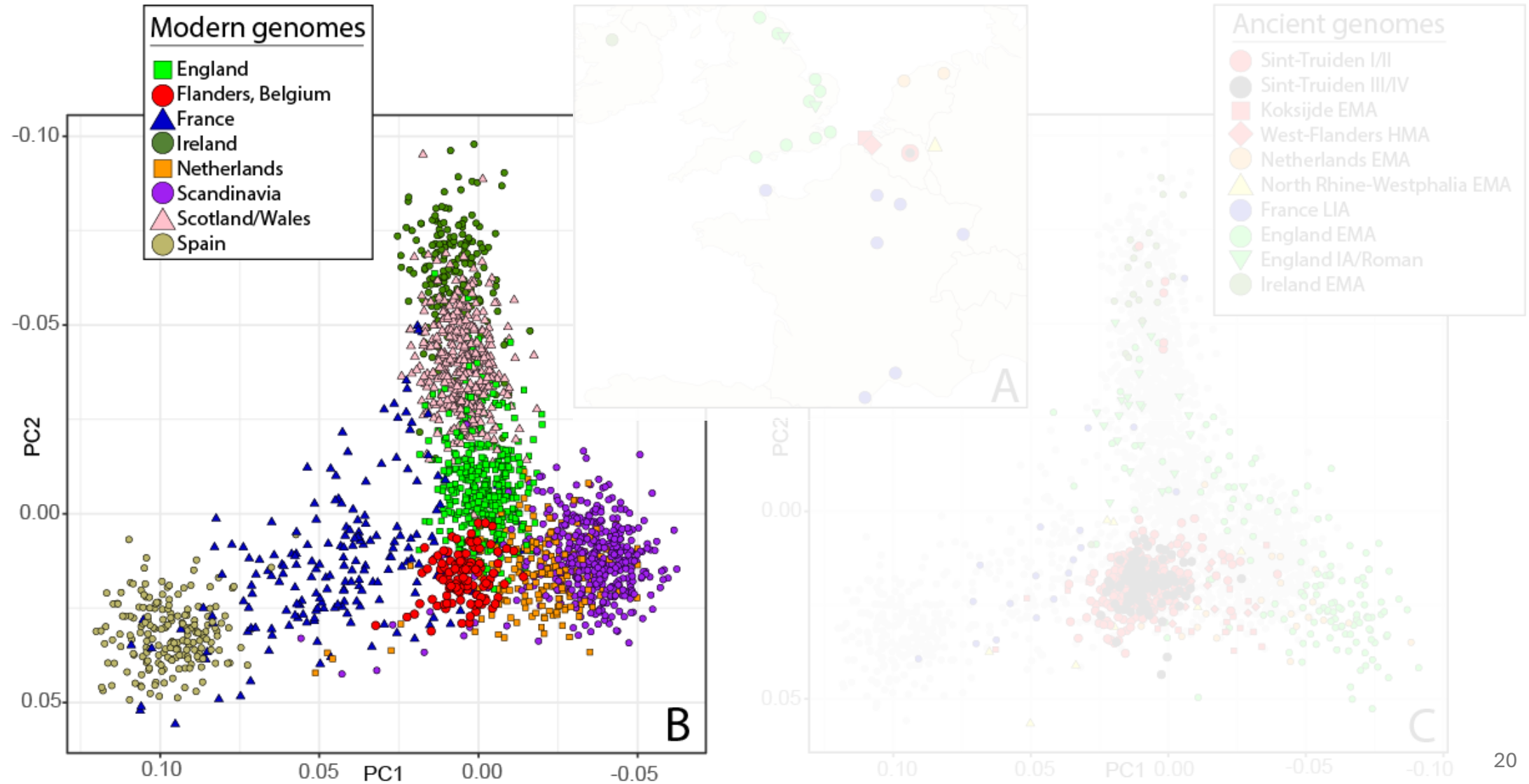
# Patterns of ancestry and mobility

- Genetic ancestry
  - No continental outliers



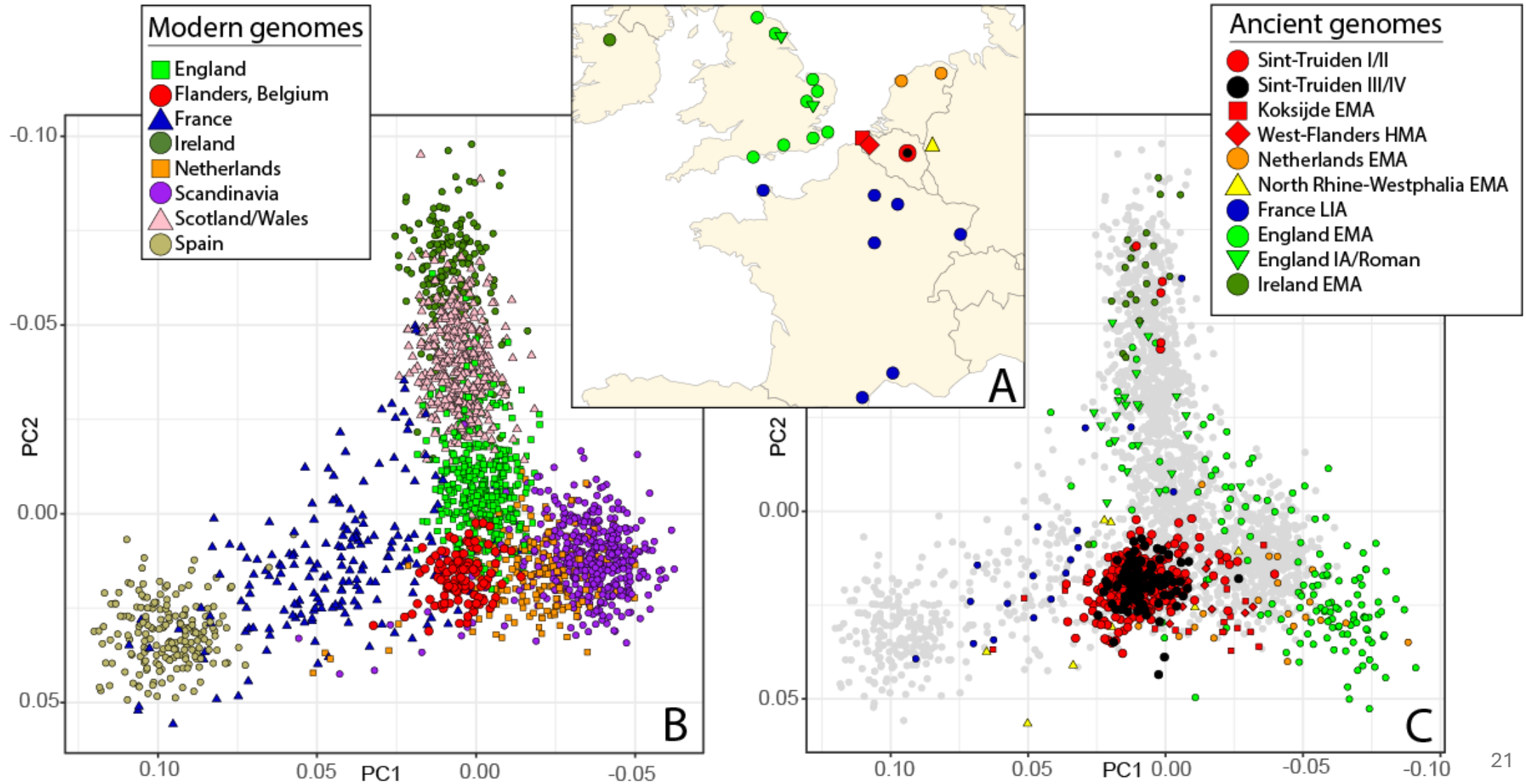


# Patterns of ancestry and mobility





# Patterns of ancestry and mobility





# Patterns of ancestry <sup>A</sup>

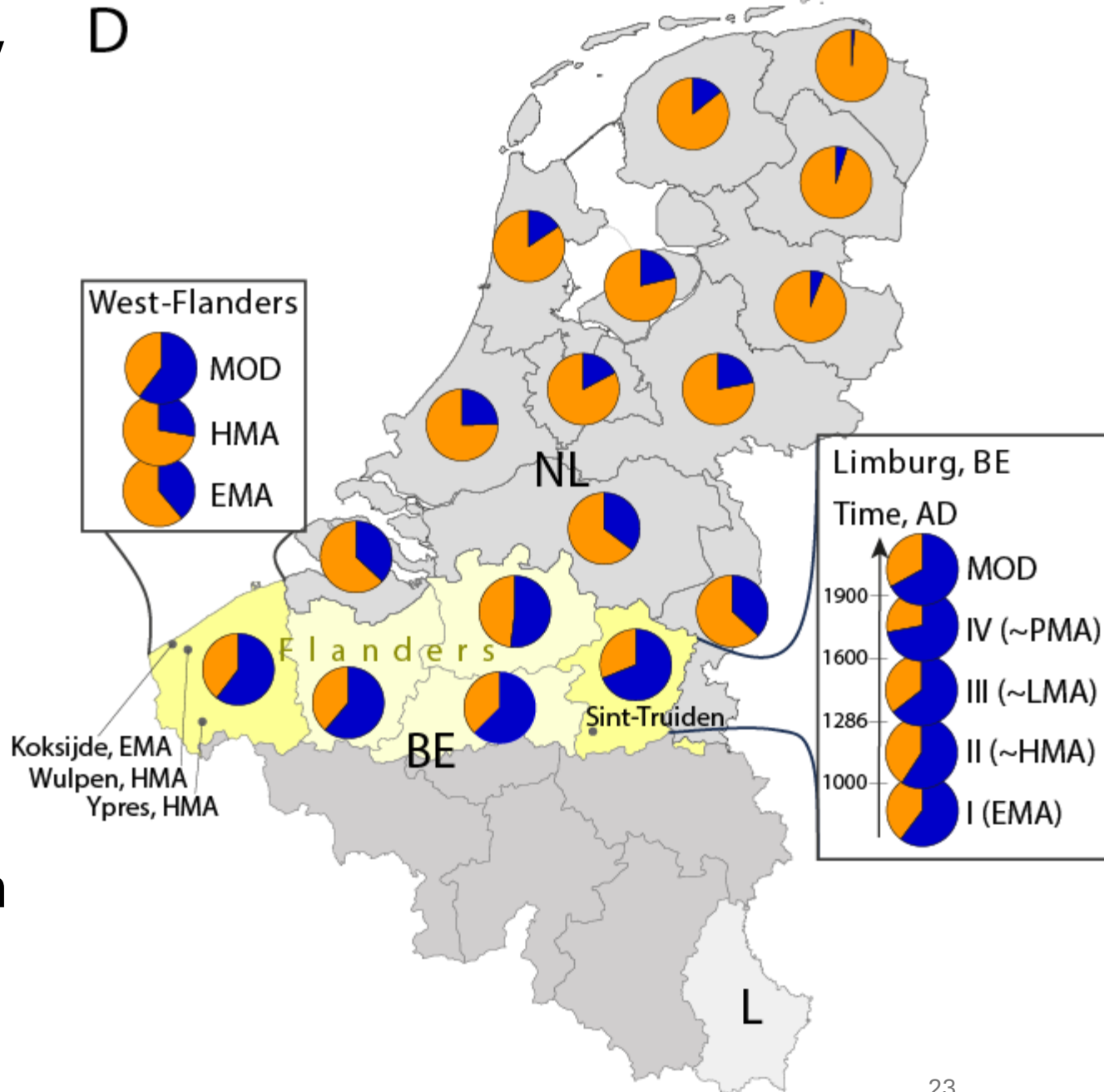
- Population connectedness
- Sharing of long genomic segments
- Outliers: highest affinity with Irish and Scottish individuals

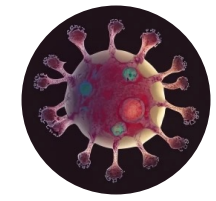
	Ancient										Flanders, Belgium								Modern								
	France-LIA	England-Roman	Ireland-EMA	Orkney-VA	Denmark-VA	Norway-VA	Netherlands-EMA	Germany-EMA	England-EMA	Kokijde, EMA	WYp-HMA	ST-main	ST-out	E&WFlanders	Antwerp	F-Brabant	Limburg	Netherlands	Denmark	Norway	Sweden	Irish	England	Scotland	Wales	France	Spain
France-LIA	7	14	14	0	9	21	25	0	11	6	23	12	0	5	11	7	6	9	9	7	8	8	8	9	9	8	6
England-Roman	14	35	22	6	16	10	12	13	14	8	20	17	33	12	14	14	10	12	14	13	12	13	13	16	14	10	8
Ireland-EMA	14	22	195	107	12	15	11	10	11	7	7	12	133	10	10	20	17	8	11	7	8	45	12	25	13	7	4
Orkney-VA	0	6	107	125	7	50	0	0	10	0	0	13	150	0	24	15	13	10	13	19	9	34	9	20	9	7	3
Denmark-VA	9	16	12	7	29	22	41	33	39	24	16	17	22	11	13	11	10	14	15	12	12	9	11	10	9	6	5
Norway-VA	21	10	15	50	22	112	15	27	28	18	22	17	16	9	16	14	10	9	13	19	17	13	12	12	12	5	4
Netherlands-EMA	25	12	11	0	41	15	77	38	53	45	22	19	29	11	9	6	2	24	10	12	16	8	13	10	12	7	6
Germany-EMA	0	13	10	0	33	27	38	127	43	39	32	23	0	14	12	15	13	21	15	11	10	7	13	13	11	7	7
England-EMA	11	14	11	10	39	28	53	43	78	54	25	22	10	17	16	14	14	17	15	13	12	11	15	12	13	8	5
Kokijde, EMA	6	8	7	0	24	18	45	39	54	260	88	17	20	9	13	15	8	16	15	9	9	11	13	15	12	7	3
WYp-HMA	23	20	7	0	16	22	22	32	25	88	213	21	15	27	8	14	12	15	14	10	9	11	10	14	11	10	9
ST-main	12	17	12	13	17	17	19	23	22	17	21	53	9	15	26	23	26	15	11	10	10	9	12	11	10	8	7
ST-out	0	33	133	150	22	16	29	0	10	20	15	9	80	12	10	0	0	10	16	10	12	43	20	37	24	7	9
E&WFlanders	5	12	10	0	11	9	11	14	17	9	27	15	12	55	20	14	15	11	9	10	8	6	9	9	8	8	5
Antwerp	11	14	10	24	13	16	9	12	16	13	8	26	10	20	113	36	27	16	9	11	9	6	9	9	9	7	5
F-Brabant	7	14	20	15	11	14	6	15	14	15	14	23	0	14	36	76	41	8	8	9	9	8	10	14	9	7	7
Limburg	6	10	17	13	10	10	2	13	14	8	12	26	0	15	27	41	105	17	8	8	5	7	8	8	7	9	6
Netherlands	9	12	8	10	14	9	24	21	17	16	15	15	10	11	16	8	17	27	9	9	8	7	8	9	9	6	4
Denmark	9	14	11	13	15	13	10	15	15	15	14	11	16	9	9	8	8	9	35	12	13	7	9	8	7	6	5
Norway	7	13	7	19	12	19	12	11	13	9	10	10	10	10	11	9	8	9	12	56	18	7	8	8	8	7	4
Sweden	8	12	8	9	12	17	16	10	12	9	9	10	12	8	9	9	5	8	13	18	30	7	8	8	6	5	4
Irish	8	13	45	34	9	13	8	7	11	11	11	9	43	6	6	8	7	7	7	7	7	38	10	20	12	5	5
England	8	13	12	9	11	12	13	13	15	13	10	12	20	9	9	10	8	8	9	8	8	10	15	13	16	7	4
Scotland	9	16	25	20	10	12	10	13	12	15	14	11	37	9	9	14	8	9	8	8	8	20	13	51	11	7	5
Wales	9	14	13	9	9	12	12	11	13	12	11	10	24	8	9	9	7	9	7	8	6	12	16	11	113	6	4
France	8	10	7	7	6	5	7	7	8	7	10	8	7	8	7	7	9	6	6	7	5	5	27	7	6	7	5
Spain	6	8	4	3	5	4	6	7	5	3	9	7	9	5	5	7	6	4	5	4	4	5	4	5	4	5	15



# Patterns of ancestry

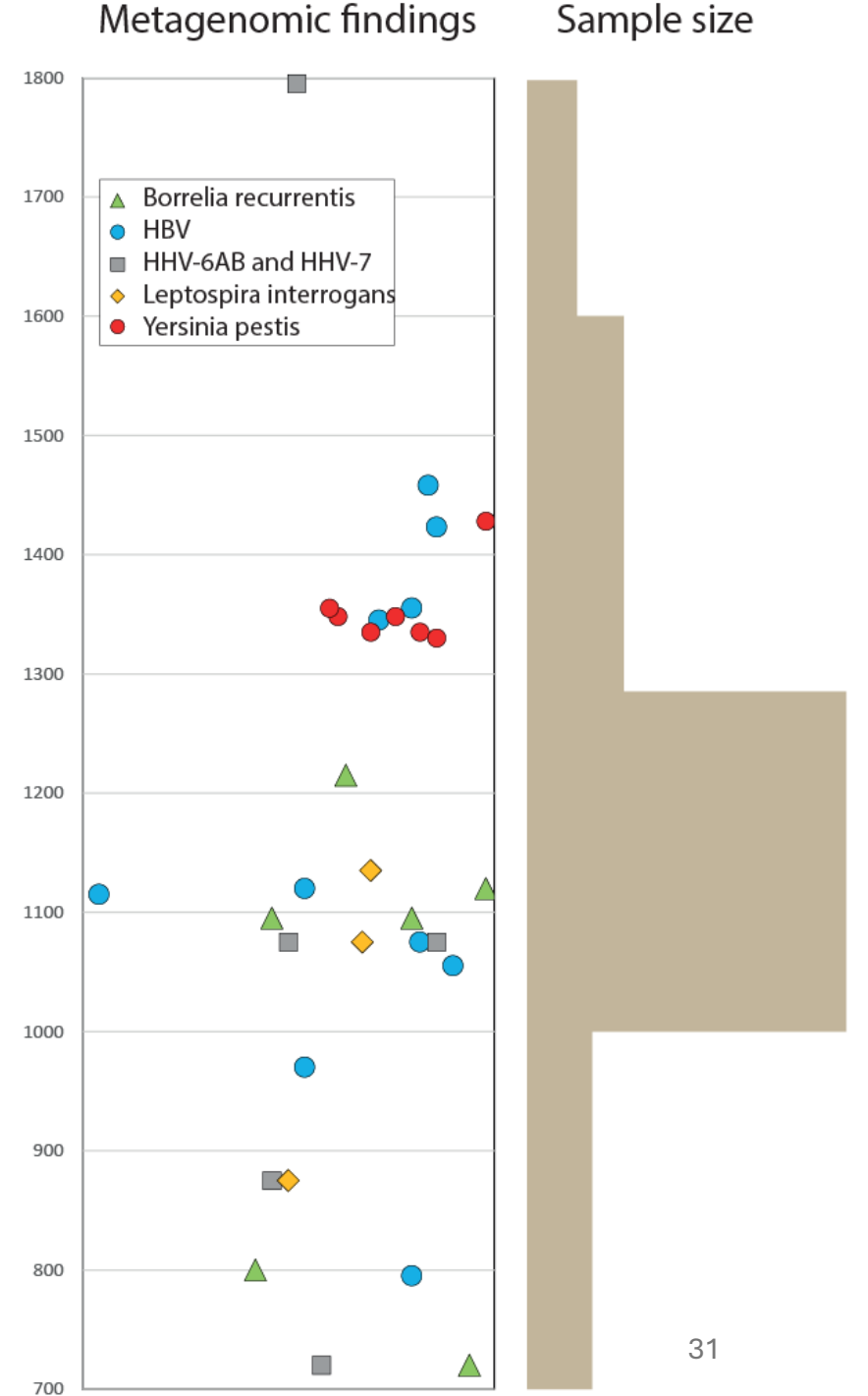
- Model with two sources
  - ‘Gaulish’ ancestry
  - ‘Germanic’ ancestry
- North-south cline
- Temporal continuity in Sint-Truiden





# Health and pandemics

- Pathogen screening
- *Yersinia pestis*
  - All dated to the 14th c. ( $\neq$  archival sources)
  - $\neq$  Light-touch theory
  - Individual graves
  - No plague-induced immune response



# Why Sint-Truiden needed the VSC?

## **PROBLEM: aDNA**

### **Massive genomic datasets**

- Ancient DNA samples + reference panels
- Millions of variants per individual

### **aDNA complexity**

- Fragmented
- Damaged

### **Computationally intensive analyses**

- Genotype imputation
- Population genetic modeling

## **SOLUTION: VSC**

### **High-performance computing**

- Parallel processing
- Massive memory availability

### **Efficient pipelines**

- Fast
- Scalable (e.g. imputation Tier1)

### **Large-scale storage**

- Handles TB-scale genomic datasets

# Acknowledgements

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Linde Braet

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Pieterjan Deckers

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