Supplementary Materials

Table S1 Distribution and frequency of the Y-chr subhaplogroups within the five contemporary provinces in Flanders. DNA-donors were attributed to provinces based on the birth place of their ORPA.

	West Flanders		**East Flanders**		**Flemish Brabant**		**Limburg**		**Antwerp**	
Y-chr subhaplogroups	**Distribution**	**Frequency**	**Distribution**	**Frequency**	**Distribution**	**Frequency**	**Distribution**	**Frequency**	**Distribution**	**Frequency**
Y*(xBT)	0	0.00%	0	0.00%	0	0.00%	1	1.61%	0	0.00%
E1b1b1* (E-M35*)	0	0.00%	0	0.00%	1	0.80%	0	0.00%	0	0.00%
E1b1b1a1 (E-V12)	0	0.00%	0	0.00%	0	0.00%	0	0.00%	1	0.55%
E1b1b1a2 (E-V13)	3	2.52%	1	0.91%	8	6.40%	1	1.61%	4	2.19%
E1b1b1a3 (E-V22)	1	0.84%	0	0.00%	1	0.80%	1	1.61%	0	0.00%
E1b1b1b (E-M81)	1	0.85%	0	0.00%	0	0.00%	0	0.00%	0	0.00%
E1b1b1c* (E-M123*)	0	0.00%	0	0.00%	1	0.80%	0	0.00%	0	0.00%
E1b1b1c1 (E-M34)	3	2.52%	1	0.91%	1	0.80%	1	1.61%	2	1.09%
G2a* (G-P15*)	0	0.00%	0	0.00%	0	0.00%	1	1.61%	0	0.00%
G2a3* (G-U8*)	3	2.52%	2	1.82%	5	4.00%	1	1.61%	6	3.28%
G2a3a (G-U16)	0	0.00%	0	0.00%	0	0.00%	1	1.61%	0	0.00%
G2a3b1 (G-U13)	0	0.00%	0	0.00%	0	0.00%	1	1.61%	0	0.00%
I1* (I-M253*)	16	13.46%	16	14.55%	14	11.20%	3	4.84%	22	12.02%
I1c (I-P109)	2	1.68%	0	0.00%	3	2.40%	0	0.00%	1	0.55%
I2* (I-P215*)	0	0.00%	2	1.82%	4	3.20%	1	1.61%	2	1.09%
I2a* (I-P37.2*)	2	1.68%	4	3.64%	1	0.80%	0	0.00%	2	1.09%
I2b* (I-M223*)	5	4.20%	6	5.45%	3	2.40%	1	1.61%	6	3.28%
I2b1 (I-M284)	0	0.00%	0	0.00%	0	0.00%	0	0.00%	2	1.09%
I2b3 (I-P78)	0	0.00%	0	0.00%	1	0.80%	0	0.00%	1	0.55%
I2b4 (I-P95)	0	0.00%	0	0.00%	1	0.80%	1	1.61%	0	0.00%
J1* (J-M267*)	0	0.00%	1	0.91%	1	0.80%	0	0.00%	0	0.00%
J1e* (J-P58*)	0	0.00%	1	0.91%	3	2.40%	0	0.00%	2	1.09%
J2a* (J-M410*)	4	3.36%	2	1.82%	1	0.80%	1	1.61%	5	2.73%
J2a2* (J-M67*)	0	0.00%	0	0.00%	1	0.80%	0	0.00%	1	0.55%
J2a2a* (J-M92*)	0	0.00%	0	0.00%	1	0.80%	0	0.00%	0	0.00%
J2a8 (J-M319)	0	0.00%	0	0.00%	1	0.80%	0	0.00%	1	0.55%
J2b2* (J-M241*)	0	0.00%	0	0.00%	1	0.80%	1	1.61%	2	1.09%
L1 (L-M27)	0	0.00%	0	0.00%	0	0.00%	0	0.00%	1	0.55%
L2 (L-M317)	0	0.00%	0	0.00%	1	0.80%	0	0.00%	0	0.00%
Q1* (Q-P36.1*)	0	0.00%	0	0.00%	0	0.00%	0	0.00%	3	1.64%
R1a* (R-SRY10831.2*)	0	0.00%	0	0.00%	0	0.00%	1	1.61%	0	0.00%
R1a1* (R-M17*)	2	1.68%	4	3.64%	4	3.20%	5	8.06%	11	6.01%
R1b1* (R-P25*)	0	0.00%	0	0.00%	1	0.80%	0	0.00%	0	0.00%
R1b1b* (R-P297*)	1	0.84%	0	0.00%	0	0.00%	0	0.00%	0	0.00%
R1b1b2* (R-M269*)	4	3.36%	1	0.91%	2	1.60%	1	1.61%	3	1.64%
R1b1b2a* (R-P310*)	2	1.68%	0	0.00%	2	1.60%	0	0.00%	1	0.55%
R1b1b2a1 (R-U106)	32	26.89%	33	30.00%	25	20.00%	15	24.16%	48	26.23%
R1b1b2a2* (R-P312*)	26	21.85%	18	16.36%	25	20.00%	18	29.03%	34	18.58%
R1b1b2a2d (R-SRY2627)	0	0.00%	0	0.00%	1	0.80%	0	0.00%	0	0.00%
R1b1b2a2g (R-U152)	12	10.08%	16	14.55%	11	8.80%	6	9.68%	21	11.48%
T* (T-M70*)	0	0.00%	2	1.82%	0	0.00%	0	0.00%	1	0.55%
Total	119		110		125		62		183	

R-Script Script written for R (The R Foundation for Statistical Computing, 2011), implementing a permutation test for population genetic differentiation using weighted average of the haplotype diversity H_S as a test statistic.

```
#R-script 'In the name of the migrant father'
#allele counts should be imported as a matrix or a table in the variable 'tab', with the alleles as rows and the populations as columns

tab <- as.matrix(tab)
tab <- tab[rowSums(tab)!=0,]

batches <- 20
permutations <- 500

pwHs <- rep(NA,batches)

sums <- colSums(tab)
tot <- sum(sums)

square.probs <- (tab/(rep(1,nrow(tab))%*%t(sums)))^2
hs <- (1-colSums(square.probs))*sums/(sums-1)
wHs <- sum(hs*(sums-2)/(tot-4))

expanded.s <- rep(1:nrow(tab), rowSums(tab))
perm <- factor(sample(expanded.s))

subs <- matrix(0, nrow=nrow(tab), ncol=ncol(tab))
starts <- cumsum(c(0,sums[-length(sums)]))+1
stops <- cumsum(sums)

for(b in 1:batches)
{
  pwhs <- 0
  for (p in 1:permutations)
  {
    perm <- sample(perm)
    subs[] <- mapply(function(x,y) table(perm[x:y]),starts,stops)
    sub.sums <- colSums(subs)
    sub.square.probs <- (subs/(rep(1,nrow(subs))%*%t(sub.sums)))^2
    sub.hs <- (1-colSums(sub.square.probs))*sub.sums/(sub.sums-1)
    sub.wHs <- sum(sub.hs*(sub.sums-2)/(tot-4))
    if (sub.wHs <= wHs)
      pwhs <- pwhs + 1
```

```
    }
    pwHs[b] <- pwhs/permutations
}

m <- mean(pwHs)
se <- sd(pwHs)/sqrt(batches)
print(paste('p =', m, '+-', round(se, 5), 'se'))
```

References

The R Foundation for Statistical Computing (2011) *R version 2.13.0*