

Matching multicopy Y-STR markers in closely related individuals - Multicopy Y. STR
markers are located on the symmetrical armsof palindromes. The DNA sequences on the
Matching multicopy $\boldsymbol{Y}$-STR markers in closely related individuals - Multicopy Y-STR
markers are located on the symmetricalarmsof palindromes. The DNA sequences on the palindrom ic arms are nearly identical and therefore highly prone to intrachromosomal recombination events. The talk willdemonstrate how the recombination mechanismswillaffect apparent $m$ ismatches in closely related individuals and it will present new tools that can help to understand the inrachromosomal re-arrangements in the Yall palindromicregion.

## What's a palindrome?

## Palindromic word phrases

RADAR

Madam, I'm Adam.
So many dynamos. Cleveland DNA: Level C
 Red rum, sir, is murder.
Too bad, I hid a boot.
Sat in a taxi, left Felix at Anita's
Emil asleep, Hannah peels a lime.
Anne, I stay a day at Sienna.
Was it a car or a cat I saw?

A dognt in a pagodal
A palic
Max, I stay away at six a.m.
Go hang a salami! I'm a lasagna hog!
Yawn a more Roman way!

## What's a palindrome?

Palindromic word phrases:
Forward = Backward RADAR

Nucleic acids:

# Forward = Reverse Complement (Forward) 

## AGCTTCTAGTCGACTAGAAGCT

## What's a palindrome?

Nucleic acids:

> Forward = Reverse Complement (Forward)

## AGCTTCTAGTCGACTAGAAGCT

Reverse Complement (AGCTTCTAGTCGACTAGAAGCT)
= AGCTTCTAGTCGACTAGAAGCT

## What's a palindrome?

Nucleic acids:

# Forward = Reverse Complement (Forward) 

## AGCTTCTAGTCGACTAGAAGCT || |||||||||| ||||| || ||| || ||||||||||||| ||||||||||||||||| 

AGCTTCTAGTCGACTAGAAGCT

## Biological Relevance of Palindromes

Restriction enzymes cut DNA at palindromic recognition sequences

```
\[
5^{\prime}-\mathbf{G}^{\wedge} \mathrm{A} A \text { T T C-3' }
\]
\[
3_{4}^{\prime-C} \text { T T A A^G-5' }
\]
```

Palindrome

$$
\begin{aligned}
& 5^{\prime}-\mathbf{G} \wedge A ~ A ~ T ~ T ~ C-3 ' ~ \\
& 3^{\prime}-\mathbf{C} \text { T T A A^G-5' }
\end{aligned}
$$

EcoRI


## Biological Relevance of Palindromes

## Formation of hairpins

Single stranded DNA with partial palindromic sequence GAACTAGACTTAATGTGAGCTTATAAATTATAATGCTCTCACATTAAGTCTAGTTC


## Biological Relevance of Palindromes

## Hairpins regulate RNA translation

High temperature / low ionic concentration


Low temperature / high ionic concentration


No translation No protein

## Palindromes in the ds Human Genome



Double stranded DNA
Chromosome


## Palindromes in the ds Human Genome

E
E
E
E
E
E
E
Chromosome
But unexpected things happen...


Hydrogen bonding between palindromic arms

Possible base differences will be repaired by the cell's mutation repair system

## Recombinational Loss Of Heterozygosity (recLOH)

If we have a palindromic region (that means, that the DNA sequence has a loop and the ends of the loop can be put parallel next to each other and the parallel ends have nearly exatly the same DNA sequence, in other words an inverted repeat) we can model a simple structure like this:


## Recombinational Loss Of Heterozygosity (recLOH)

Palindromic sequences develop independently on each arm, so after some time they acquire mismatches (M) that could be STR mutations or SNPs on both arms. If it comes to a hairpin conformation, base pairing is not perfect and the cell tries to repair the apparent mutations.


## Recombinational Loss Of Heterozygosity (recLOH)

Depending on the direction of the repair enzyme complex, some mutations get duplicated on the other arm and some mutations disappear.


## Recombinational Loss Of Heterozygosity (recLOH)

DYS459, DYS724 (CDY) and DYS464 are on the same palindrome called P1


## Recombinational Loss Of Heterozygosity (recLOH)

In this example the haplotype has different alleles at all marker pairs
After the recombination event the heterozygosity is lost => recLOH


## Typical recLOH Patterns In Genetic Genealogy

A classical DYS459, CDY, DYS464 recLOH

| DYS459 | DYS724 (CDY) | DYS464 | Genetic distance? |
| :--- | :--- | :--- | :--- |
| $9-10$ | $37-38$ | $14-14-16-18$ |  |
| $9-10$ | $37-38$ | $14-15-16-18$ | 1 |
| $9-10$ | $37-38$ | $14-14-16-18$ | 0 |
| $9-10$ | $37-39$ | $14-14-16-18$ | 1 |
| $9-10$ | $37-38$ | $14-14-16-18$ | 0 |
| $10-10$ | $38-38$ | $14-14-18-18$ | 1 |
| $9-9$ | $37-37$ | $14-16-18-18$ | 1 |

Similar recLOH events happen at all palindromic multicopy markers

FamilyTreeDNA

| DYS385 | YCAII |
| :--- | :--- |
| $11-14$ | $19-23$ |
| $11-14$ | $19-23$ |
| $11-14$ | $19-19$ |
| $11-11$ | $19-23$ |

```
DYS385
11-14
11-14
11-11
```



## Highest Density of Palindromes in the Human Genome

Segmental Duplications in the Human Genome

| Chr | Length (bp) | Intrachromosomal |  | Interchromosomal |  | Total |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Length | \% | Length | \% | Length | \% |
| 1 | 245,203,898 | 6,431,462 | 2.6 | 3,964,057 | 1.6 | 8,678,912 | 3.5 |
| 2 | 243,315,028 | 6,380,301 | 2.6 | 3,757,634 | 1.5 | 8,935,221 | 3.7 |
| 3 | 199,411,731 | 1,646,046 | 0.8 | 1,870,056 | 0.9 | 2,671,459 | 1.3 |
| 4 | 191,610,523 | 2,323,764 | 1.2 | 2,547,466 | 1.3 | 3,927,792 | 2.0 |
| 5 | 180,967,295 | 4,066,897 | 2.2 | 2,083,920 | 1.2 | 5,208,550 | 2.9 |
| 6 | 170,740,541 | 2,048,892 | 1.2 | 1,123,050 | 0.7 | 2,854,222 | 1.7 |
| 7 | 158,431,299 | 9,629,716 | 6.1 | 3,734,503 | 2.4 | 11,722,991 | 7.4 |
| 8 | 145,908,738 | 1,576,863 | 1.1 | 1,694,593 | 1.2 | 2,153,612 | 1.5 |
| 9 | 134,505,819 | 8,451,476 | 6.3 | 4,371,262 | 3.2 | 9,403,888 | 7.0 |
| 10 | 135,480,874 | 6,460,047 | 4.8 | 1,919,342 | 1.4 | 7,741,228 | 5.7 |
| 11 | 134,978,784 | 4,223,832 | 3.1 | 2,147,666 | 1.6 | 5,382,256 | 4.0 |
| 12 | 133,464,434 | 1,616,743 | 1.2 | 1,134,900 | 0.9 | 2,582,114 | 1.9 |
| 13 | 114,151,656 | 1,451,225 | 1.3 | 1,655,399 | 1.5 | 2,700,321 | 2.4 |
| 14 | 105,311,216 | 282,478 | 0.3 | 849,400 | 0.8 | 1,116,676 | 1.1 |
| 15 | 100,114,055 | 5,520,203 | 5.5 | 3,339,498 | 3.3 | 7,091,918 | 7.1 |
| 16 | 89,995,999 | 7,378,691 | 8.2 | 3,456,338 | 3.8 | 8,247,312 | 9.2 |
| 17 | 81,691,216 | 5,505,106 | 6.7 | 1,217,149 | 1.5 | 6,432,722 | 7.9 |
| 18 | 77,753,510 | 230,844 | 0.3 | 1,400,896 | 1.8 | 1,627,497 | 2.1 |
| 19 | 63,790,860 | 1,763,189 | 2.8 | 918,571 | 1.4 | 2,531,577 | 4.0 |
| 20 | 63,644,868 | 772,190 | 1.2 | 1,068,246 | 1.7 | 1,369,456 | 2.2 |
| 21 | 46,976,537 | 431,633 | 0.9 | 1,714,574 | 3.6 | 1,734,567 | 3.7 |
| 22 | 49,476,972 | 2,303,175 | 4.7 | 1,633,388 | 3.3 | 3,481,523 | 7.0 |
|  | 152,634,166 | 3,579,325 |  | 4,550,908 | 3.0 | 8,047,172 | 5.3 |
| Y | 50,961,097 | 6,651,452 |  | 1,462,582 | 2.9 | 7,353,078 | 14.4 |
| Total | 3,070,521,116 | 90,725,550 | 3.0 | 53,615,398 | 1.7 | 122,996,064 | 4.0 |

Liqing Zhang et al. "Patterns of Segmental Duplication in the Human Genome", Mol. Biol. Evol. 22(1):135-141. 2005

## Symbolic Map of the Yq11



FamilyTreeDNA

Ghr":
1 E9EEGEl
EGEEGED
EGEEEED
4 GEGEGEG1
EGEEGEEl
E: =rำ.
'T'F11, ヨ Crormosome



| DYS459 | $\mathbf{6}$ | $\mathbf{7}$ | $\mathbf{8}$ | $\mathbf{9}$ | $\mathbf{1 0}$ | $\mathbf{1 1}$ | $\mathbf{1 2}$ | $\mathbf{1 3}$ |
| ---: | ---: | ---: | ---: | ---: | ---: | ---: | ---: | ---: |
| $\mathbf{6}$ | 4 |  |  |  |  |  |  |  |
| $\mathbf{7}$ | 0 | 2 |  |  |  |  |  |  |
| $\mathbf{8}$ | 3 | 9 | 404 |  |  |  |  |  |
| $\mathbf{9}$ | 2 | 174 | 6467 | 7676 |  |  |  |  |
| $\mathbf{1 0}$ | 2 | 120 | 2540 | 20908 | 554 |  |  |  |
| $\mathbf{1 1}$ | 0 | 0 | 16 | 300 | 9 | 0 |  |  |
| $\mathbf{1 2}$ | 0 | 0 | 0 | 4 | 0 | 0 | 0 |  |
| $\mathbf{1 3}$ | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |

$\begin{array}{llllllllll}\text { Scale：} & 0 & 1 & 10 & 100 & 1000 & 10000 & 100000\end{array}$

正

都
12xulpat baserfly ver I
$\qquad$

－
$\qquad$ $1-2$ Sce電都
 2



Scale： |  | 0 | 1 | 10 | 100 | 1000 | 10000 | 100000 |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- |

## America's first genealogy

 driven DNA testing service| YCAII | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 11 | 0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 12 | 0 | 0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 13 | 0 | 0 | 0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 14 | 0 | 0 | 0 | 0 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 15 | 0 | 0 | 0 | 0 | 0 |  |  |  |  |  |  |  |  |  |  |  |  |
| 16 | 0 | 0 | 0 | 0 | 0 | 0 |  |  |  |  |  |  |  |  |  |  |  |
| 17 | 0 | 0 | 0 | 0 | 0 | 0 | 11 |  |  |  |  |  |  |  |  |  |  |
| 18 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 11 |  |  |  |  |  |  |  |  |  |
| 19 | 3 | 1 | 0 | 0 | 7 | 1 | 19 | 15 | 826 |  |  |  |  |  |  |  |  |
| 20 | 9 | 0 | 0 | 0 | 0 | 1 | 1 | 63 | 426 | 382 |  |  |  |  |  |  |  |
| 21 | 72 | 2 | 1 | 0 | 0 | 3 | 21 | 90 | 4180 | 196 | 418 |  |  |  |  |  |  |
| 22 | 11 | 0 | 0 | 0 | 0 | 0 | 3 | 45 | 2236 | 41 | 89 | 166 |  |  |  |  |  |
| 23 | 0 | 0 | 0 | 0 | 1 | 1 | 33 | 251 | 12245 | 145 | 89 | 46 | 123 |  |  |  |  |
| 24 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 2 | 748 | 8 | 7 | 7 | 40 | 0 |  |  |  |
| 25 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 23 | 0 | 0 | 3 | 10 | 0 | 0 |  |  |
| 26 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |  |
| 27 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

Scale:

## America's first genealogy

 driven DNA testing| DYS385 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 6 | 0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 7 | 0 | 0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 8 | 0 | 0 | 0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 9 | 0 | 1 | 0 | 6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 10 | 0 | 0 | 0 | 0 | 46 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 11 | 0 | 0 | 0 | 9 | 87 | 1092 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 12 | 0 | 0 | 1 | 14 | 36 | 817 | 720 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 13 | 0 | 0 | 0 | 19 | 95 | 5181 | 1032 | 1063 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 14 | 0 | 7 | 16 | 128 | 1143 | 27107 | 3455 | 4150 | 2976 |  |  |  |  |  |  |  |  |  |  |  |  |
| 15 | 0 | 1 | 3 | 42 | 222 | 6037 | 1399 | 1843 | 2531 | 1428 |  |  |  |  |  |  |  |  |  |  |  |
| 16 | 0 | 5 | 41 | 23 | 43 | 1128 | 511 | 1377 | 1161 | 1545 | 653 |  |  |  |  |  |  |  |  |  |  |
| 17 | 0 | 2 | 5 | 4 | 44 | 210 | 250 | 1147 | 782 | 641 | 863 | 365 |  |  |  |  |  |  |  |  |  |
| 18 | 0 | 0 | 1 | 3 | 67 | 107 | 172 | 600 | 417 | 404 | 990 | 892 | 216 |  |  |  |  |  |  |  |  |
| 19 | 0 | 1 | 0 | 5 | 60 | 31 | 124 | 397 | 136 | 255 | 302 | 249 | 84 | 29 |  |  |  |  |  |  |  |
| 20 | 0 | 0 | 0 | 1 | 43 | 13 | 83 | 131 | 88 | 91 | 104 | 40 | 25 | 9 | 1 |  |  |  |  |  |  |
| 21 | 0 | 0 | 0 | 0 | 13 | 6 | 10 | 108 | 16 | 31 | 12 | 12 | 2 | 2 | 0 | 0 |  |  |  |  |  |
| 22 | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 39 | 8 | 5 | 5 | 8 | 1 | 0 | 1 | 0 | 0 |  |  |  |  |
| 23 | 0 | 0 | 0 | 0 | 0 | 0 | 5 | 17 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |  |  |  |
| 24 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 3 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |  |  |
| 25 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |  |
| 26 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

Scale:
$\begin{array}{llllllll}0 & 1 & 10 & 100 & 1000 & 10000 & 100000\end{array}$

| DYS724 | 9 | 26 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 9 | 0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 26 | 0 | 0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 28 | 0 | 0 | 0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 29 | 0 | 0 | 0 | 1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 30 | 0 | 0 | 0 | 6 | 5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 31 | 0 | 0 | 0 | 5 | 5 | 11 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 32 | 0 | 0 | 0 | 2 | 5 | 23 | 27 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 33 | 0 | 0 | 0 | 4 | 29 | 55 | 53 | 61 |  |  |  |  |  |  |  |  |  |  |  |  |
| 34 | 1 | 0 | 1 | 22 | 41 | 55 | 106 | 168 | 182 |  |  |  |  |  |  |  |  |  |  |  |
| 35 | 0 | 0 | 0 | 8 | 38 | 80 | 95 | 229 | 467 | 404 |  |  |  |  |  |  |  |  |  |  |
| 36 | 0 | 0 | 0 | 2 | 27 | 63 | 70 | 235 | 435 | 926 | 845 |  |  |  |  |  |  |  |  |  |
| 37 | 0 | 1 | 1 | 2 | 14 | 90 | 75 | 173 | 547 | 1057 | 1846 | 1051 |  |  |  |  |  |  |  |  |
| 38 | 0 | 0 | 0 | 1 | 17 | 46 | 45 | 199 | 433 | 939 | 1622 | 1963 | 935 |  |  |  |  |  |  |  |
| 39 | 0 | 0 | 0 | 0 | 5 | 6 | 33 | 153 | 294 | 524 | 808 | 1151 | 957 | 290 |  |  |  |  |  |  |
| 40 | 0 | 0 | 0 | 0 | 3 | 7 | 11 | 52 | 132 | 244 | 421 | 444 | 447 | 220 | 82 |  |  |  |  |  |
| 41 | 0 | 0 | 0 | 0 | 1 | 4 | 12 | 16 | 58 | 114 | 138 | 132 | 134 | 83 | 40 | 12 |  |  |  |  |
| 42 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 7 | 14 | 27 | 54 | 23 | 31 | 12 | 8 | 2 | 8 |  |  |  |
| 43 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 1 | 7 | 8 | 7 | 4 | 4 | 1 | 1 | 0 | 1 |  |  |
| 44 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 4 | 0 | 2 | 2 | 0 | 0 | 0 | 0 | 0 | 0 |  |
| 45 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

Scale:
$\begin{array}{llllll}0 & 1 & 10 & 100 & 1000 & 10000\end{array}$

FamilyTreeDNA

## DYS464 - A Complex Marker With (Usually) 4 Alleles



## DYS464 - A Complex Marker With (Usually) 4 Alleles



## DYS464 Extended PCR




g
g
JOE
G
TAMRA

## DYS464 Extended PCR

If the primer ending with G yields a peak, the allele is classed as a G-type.
If the primer ending with C yields a peak, the allele is classed as a C-type.

DYS464-forward
DYS464-reverse-G-Type DYS464-reverse-c-Type

FAM-ttacgagctttgggctatg (exactly like Redd paper)
JOE-cctgggtaacagagagactctttcag (ending with G)
邻-cctgggtaacagagagactcttcac (ending with C)

PCR parameters: $30 \times\left(90^{\circ}, 65^{\circ}, 70^{\circ}\right)$ and $60^{\circ}$ end-elongation $1 / 2 \mathrm{~h}$
Peaks with a green fluorescence (JOE) are called G-type.
Peaks with a yellow fluorescence ( $\mathrm{TM} / \mathrm{R}$ ) are called C-type.

## DYS464 Extended PCR

## Electropherogram


5007.70-464a-05-05-07.tsa 24 Green DY $\$ 464.2 \mathrm{~g}$


## DYS464 Extended PCR

## Electropherogram


5022.70-464a-05-05-07.fsa 36 Green DYS464.2g


## DYS464 Extended PCR

## Haplogroup I


5082.90-464a-05-05-06.tsa 5 Yellow DYS464.2c

No C-type alleles!
6000
-4000
-2000


| Y hgroup | DYS 464 | $\cdots$ - -2 |
| :---: | :---: | :---: |
| A | 119-13g-13g-169 |  |
| E | 149-15.3g-17g-189 |  |
| E3b1 | 149-15.3g-17g-189 |  |
| $G$ | $13 \mathrm{~g}-14 \mathrm{~g}-15 \mathrm{~g}-15 \mathrm{~g}$ |  |
| 62* | $12 \mathrm{~g}-12 \mathrm{~g}-12 \mathrm{~g}$-13g |  |
| । | $12 \mathrm{~g}-14 \mathrm{~g}-15 \mathrm{~g}-16 \mathrm{~g}$ |  |
| 11 a | 129-14g-14g-169 |  |
| 11 a 3 | 12g-12g-14g-14g-15g-16g | Other haplogroups have |
| 11 b | $11 \mathrm{~g}-14 \mathrm{~g}-14 \mathrm{~g}-14 \mathrm{~g}$ | only G-type alleles |
| 11 b | 119.14g-14g-159 |  |
| 11 b 2 a | 119-14g-14g-15g |  |
| 11b2al | 119-119-14g-159 |  |
| 11 c | $14 \mathrm{~g}-15 \mathrm{~g}-15 \mathrm{~g}-16 \mathrm{~g}$ |  |
| J2a ${ }^{*}$ | 12g-13g-15g-16g-16g-16g |  |
| N | 14 g 14.3 g |  |
| R1a ${ }^{*}$ | 12g-15g-15g-16g |  |
| R1b | $16 \mathrm{c}-16 \mathrm{c}-16 \mathrm{~g}-16 \mathrm{~g}$ |  |
| R1b | 15 c 16 c |  |
| R1b | 15c-15c-17c-17g |  |
| R1b | 14c-16c-17c-17g |  |
| R1b | 14c-15c-16g-17c |  |
| R1b | 16 c 16 g |  |
| R1b | 15c-15c-16c-16g |  |
| R1b | 14c-15c-17c.17g | R1b has usually 3 C-type |
| R1b | 15c-16c-17g-17g | alleles and one G-type allele |
| R1b | $15 \mathrm{c}-16 \mathrm{c}$ | alles and one G-type allele |
| R1b | 15c-15c-15c-15c |  |
| R1b | 15c-15c-17c-17g |  |
| R1b | 15c-17c-17c-18g |  |
| R1b | 15c-15c-17c-18g |  |
| R1b | 15c-15c-16g-17c |  |
| R1b | 16c-16c-17c-17g |  |
| R1b | 14c-15c-15c-15g |  |
| R1b | 15c-15c-16c-18g |  |
| R1b | 15c-15c-16c-17.19 |  |
| R1b | 15c-15c-16g-17c |  |
| R1b | 13c-15c-17c-17g |  |
| $R 16$ | 15c-15c-17g-17g | Exceptions most likely |
| R1b | 15c-16c-16c-18g |  |
| R1b | 15c-15c-16c-17c | products of recLoH |

## Typing of DYS464X

119-139-13g-169
.39-119-18g
$13 \mathrm{~g}-14 \mathrm{~g}-15 \mathrm{~g}-15 \mathrm{~g}$
12 g -12g-12g-13g
$12 \mathrm{~g}-14 \mathrm{~g}-15 \mathrm{~g}-16 \mathrm{~g}$
$140-140 \cdot 16$
$11 \mathrm{~g}-14 \mathrm{~g}-14 \mathrm{~g}-14 \mathrm{~g}$
11g-14g-14g-15g
11g-14g-14g-15g
$11 \mathrm{~g}-11 \mathrm{~g}-14 \mathrm{~g}-15 \mathrm{~g}$
$12 \mathrm{~g}-13 \mathrm{~g}-15 \mathrm{~g}-16 \mathrm{~g}-16 \mathrm{~g}-16 \mathrm{~g}$
129-14.39
12g-15g-15g-16g

15c-15c-17c-17g
14c-16c-17c-179
$16 \mathrm{c} \cdot 16 \mathrm{~g}$
5c-15c-16c-16
(.17(.17
$15 \mathrm{c} \cdot 16 \mathrm{c}$
15c-15c-15c-15c
5c-15c-17c-179
15c-15(-1) -18
$15 \mathrm{c} \cdot 15 \mathrm{c} \cdot 16 \mathrm{~g} \cdot 17 \mathrm{c}$
16c-16c-17c-17g
14c-15c-15c-15g
5c-16c-18
15c-15c-169.17c
$15 c \cdot 15 c \cdot 11 \mathrm{l} \cdot 11 \mathrm{~g}$
5c-16c-16c-18
$15 c-15 c-16 c-17 c$

Other haplogroups have only G-type alleles alleles and one G-type allele

Exceptions most likely products of recLOH
Dsulapen insenfingen I méf

## What Is The Use Of The DYS464X Test?

Most R1b males that we have tested show 3 C-types and 1 G-type. All other haplogroups (including R1a) show 4 G-types.
1.) The DYS464X method can verify, if a person is really R1b
2.) In many cases we can determine, if a single large peak really represents two different alleles
3.) Some DYS464 patterns look similar when the conventional test is used, but really consist of completely different alleles. For example:
$14 \mathrm{c}-15 \mathrm{c}-17 \mathrm{c}-17 \mathrm{~g}$ is completely different from $14 c-15 g-17 c-17 c$,
but this wouldn't be seen with the conventional typing method.
4.) DYS464X is a method that helps us observe recombinational loss of heterocygosity (recLOH)

## DYS464 Examples From An Arbitrary Surname Project:

```
(conventional results)
surname A, 1: 14-14-16-17
surname A, 2: 14-14-16-17
surname A, 3: 14-14-16-17
surname B, 1: 14-14-16-18
surname C, 1: 14-14-15-17
```

If all the 5 persons are R1b then they can be typed with an extended DYS464 test.
We might get the following results:
surname $A, 1: 14 \mathrm{c}-14 \mathrm{c}-16 \mathrm{~g}-17 \mathrm{c}$
surname A, 2: $14 \mathrm{c}-14 \mathrm{c}-16 \mathrm{~g}-17 \mathrm{c}$
surname $A, 3: 14 \mathrm{c}-14 \mathrm{c}-16 \mathrm{c}-17 \mathrm{~g}$
surname B, 1: $14 \mathrm{c}-14 \mathrm{c}-16 \mathrm{~g}-18 \mathrm{c}$
surname C, 1: $14 \mathrm{c}-14 \mathrm{c}-15 \mathrm{~g}-17 \mathrm{c}$
From that result we could say:

- A1 and A2 match completely
- A3 has at least a genetic distance of 2 from (A1 \& A2)
- B1 has a genetic distance of 1 from (A1 \& A2)
- C1 has a genetic distance of 1 from (A1 \& A2)

ins G
poly A

C-type and T-type reverse primers <br> \section*{DYF399 <br> \section*{DYF399 <br> <br> A Fast Moving, <br> <br> A Fast Moving, <br> <br> Asymmetrical Palindromic Y-STR} <br> <br> Asymmetrical Palindromic Y-STR}


## DYF399 - A Fast Moving, <br> Asymmetrical Palindromic Y-STR <br> 



4 为

## 








FamilyTreeDNA

## DYS425 I DYF371

## The HUGO sequence has also a Null allele at DYS425

ttggagagaagaagagagaaacaggctctagaatttagaaaaatgttgttgttgttgttgttgttgttgttgtt ttggagagaagaagagagaaacaggctctagaatttagaaaaatgttgttgttgttgttgttgttgttgttgtt

 TGGAGAGAAGAAGAGAGAAA

- TGGAGAGAAGAAGAGAGAAAT

TGGAGAGAAGAAGAGAGAAAC

10c-10c-13c-14c

Normally in R1b (and most other haplogroups):
$10 c-12 t-13 c-14 c$

FamilyTreeDNA

## How comes It To A Deletion?

## Symetry in the red/red (P1P2) region allows another irregular conformation:



## How comes It To A Deletion?

The circular DNA molecule can't replicate on its own and gets lost in the next cell cycle


## Famous People with a P1/P2 Deletion

$\qquad$ ,



FamilyTreeDNA

