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New Advances Reconstructing the Y Chromosome Haplotype of Napoléon the First Based on Three of his Living Descendants

Gérard Lucotte[1] & Peter Hrechdakian[2]

[1] Institute of Molecular Anthropology, 44 Monge Street, Paris 75 005, France

[2] Unifert Group S.A., 54 Louise Avenue, Immeuble Stéphanie, Bruxelles 1050, Belgium

Correspondence: Gérard Lucotte, Institute of Molecular Anthropology, 44 Monge Street, Paris 75 005, France. E-mail: lucotte@hotmail.com

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Abstract

This paper describes the findings of the complete reconstruction of the lineage Y chromosome haplotype of the French Emperor Napoléon I. In a previous study (Lucotte et al., 2013) we reconstructed, for more than one hundred Y-STRs (Y–short tandem repeats), the Y-chromosome haplotype of Napoléon I based on data comparing STR allelic values obtained from the DNA of two of his living descendants: Charles Napoléon (C.N.) and Alexandre Colonna Walewski (A.C.W.); in the present study we compare STR allelic values of C.N. and A.C.W. to those of Mike Clovis (M.C.), a living fifth generation descendant of Lucien (one of Napoléon's brothers). When compared between M.C., C.N. and A.C.W., STR allelic values are identical for a total of 93 STRs; that permits us to propose those values, for which the three living descendants are identical, as expected allelic values of Napoléon I's Y-chromosome haplotype. For seven STRs, allele values are variable between M.C., C.N. and A.C.W.; we propose for three of them (DYS442, DYS454 and DYS712) expected allelic values, based on data concerning the allele distributions of these STRs in the population.

Keywords: Napoléon the First, lineage reconstruction, Y-chromosome haplotype

1. Introduction

The French Emperor Napoléon the First (1769-1821), was the son of Charles Bonaparte (1746-1785) and Letizia Ramolino (1750-1836). He had four brothers: Joseph (1768-1844), Lucien (1775-1840), Louis (1778-1846) and Jérôme (1784-1860).

In a first study (Lucotte et al., 2011) we determined the Y-chromosome non-recombinant part (NRY) haplogroup of Napoléon, based on genomic DNA extracted from two islands of follicular sheats associated with his beard hairs conserved in the Vivant-Denon reliquary (Lucotte, 2010). This haplogroup, established by the study of 10 NRY-SNPs (single nucleotide polymorphisms), is E1b1b1c1*; an "oriental" haplogroup of origin, as shown by the frequency map of M34 in contemporary European populations (Lucotte and Diéterlen, 2014), the antepenultimate SNP of the E1b1b1c1* differentiation.

In this same first study (Lucotte et al., 2011) we studied the buccal smear DNA of Charles Napoléon (C.N.), the living fourth generation of male descent from Jérôme, for the first 37 NRY-STRs (short tandem repeats) of the Family Tree DNA (FT DNA) kit; that permits us to establish a first Y-STR profile of C.N. This profile is highly indicative of the E1b1b1 haplogroup, because of STR allelic values at the discriminant (from Athey, 2006) Y-markers DYS19 (allele *13*) and at DYS464.a, .b,.c and .d (alleles *13*, *14*, *15* and *16* respectively); moreover allele values (of *13*) at DYS19 and at YCaII.a and .b (*19* and *22*) are the same for Napoléon (N) and for C.N.

In a second study (Lucotte et al., 2013) we established a more complete (because based on the FTDNA-111STRs kit) Y-STR profile of C.N., and the 111-Y-STRs profile of Alexandre Colonna Walewski (A.C.W.), the fifth generation descendant of Alexandre Walewski (1810-1868) who was the son born of the union between Napoléon I and Countess Maria Walewska (1786-1817). Comparisons at the time between the two STRs profiles were realized for a total number of 130 STRs, six of them (DYS454; DYS481; DYS635 = Y-GATA-C4; DYS712; DYS724 = CDY.a and DYF397.2) having different allelic values between C.N. and A.C.W. At that time we only had three direct determinations available on real allele values of Napoléon (for DYS19 = *13*, and for the palindromic YCAII.a= *19* and .b = *22*).

We then proposed (Lucotte et al., 2013) a first reconstruction of the Y-chromosome haplotype of Napoléon, based on the expected STR allelic values obtained from the 124 identical STRs between C.N. and A.C.W.

We have obtained now (Lucotte & Bouin Wilkinson, 2014) sixteen supplementary allelic direct determinations (on a lock of hair dandruff dating from 1811) for Napoléon I STRs, in order; DYS 19 = *13*; palindromic DYS385.a and b. = *16*; DYS389.i = *14*, .ii = *31*; DYS390 = *24*; DYS391 = *10*; DYS392 = *11*; DYS393 = *14*; DYS438 = *10*; DYS439 = Y-GATA-A4 = *12*; DYS448 = *20*; DYS456 = *15*; DYS458 = *16*; Y-GATA-C4 = *23* and Y-GATA-H4 = *11*. These results confirm our previous ones for allele *13* at DYS19; moreover all these other direct determinations (except for Y-GATA-C4) are in accordance with our previous direct predictions (Lucotte et al., 2013) concerning the expected values for the corresponding STRs.

Mike Clovis (M.C.) is the fifth generation descendant (Figure 1) of Lucien; to visualize the generations of the two male descent from the Walewski and the Jérôme lines, see the first figure of the Lucotte et al., 2013 article. In order to realize a triangular comparison between three living males related to Napoléon I (a direct descendant: A.C.W.; an indirect descendant from his brother Jérôme: C.N.; and M.C., an indirect descendant from his brother Lucien), we study now in the present article the Y-STR profile of M.C. by means of the FT-DNA – 111 STRs kit; and we compare this STR profile to those of C.N. and A.C.W.

2. Methods

Mike Clovis (M.C.) is the *propositus* (Figure 1) for this study. Buccal swab samples for this DNA donor were collected with informed consent. DNA extraction and STRs typing ("upgrade" for 111 genetic markers) were done according to FTDNA recommendations.

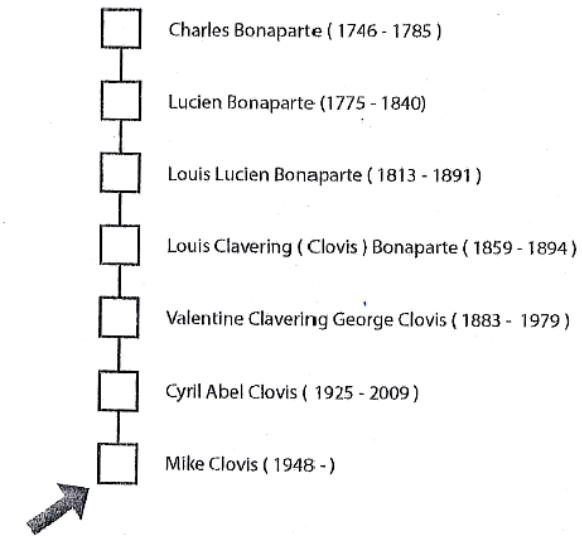

Figure 1. Chain of transmission (seven successive generations of paternal ancestry) from the ancestor Charles Bonaparte (Napoléon's father) to the *propositus* (arrow) Mike Clovis

3. Results

3.1 Comparisons of STR Allelic Values Between M.C. and C.N. – A.C.W.

Table 1 compares, for a total number of 106 STRs, allelic values obtained for M.C. to those of Charles Napoléon (C.N.) and Alexandre Colonna Walewsky (A.C.W.).

Seven STRs show different alleles between these three individuals, in order: DYS442 with an allele value = *11* for M.C. compared to *12* for both C.N. and A.C.W.; DYS447 with an allele value = *22* for M.C. compared to *21* for both C.N. and A.C.W.; for DYS454 the allele value = *11* for M.C. is identical to that of A.C.W., C.N. having an allele value = *7*; for DYS481 the allele value = *27* for M.C. is identical to that of C.N., A.C.W. having an allele value = *28*; for Y-GATA-C4 the allele value = *22* for M.C. is identical to that of C.N., A.C.W. having an allele value = *21*; for DYS712 the allele value = *23* for M.C. is identical to that of C.N., A.C.W. having an allele value = *25*; and for the palindromic CDY.a the allele value of M.C. = *34* is identical to that of A.C.W., C.N. having an allele value = *35*.

Table 1. Allelic values at 106 Y-STRs (numbers refer to the Y-markers of the FTDNA 111 "upgrade" for Mike Clovis (M.C.), Charles Napoléon (C.N.) and Alexandre Colonna Walewski (A.C.W.) NRY-DNAs. Asterisks indicate the seven differential markers (in italics) between M.C., and C.N. and A.C.W.

Numbers	Y-STRs	Allelic values					
		Napoléon I	M.C.	C.N.	A.C.W.	Napoléon I	expected
3	DYS19 = DYS394	13	13	13	13	13	(direct determination)
5	DYS385.a (palindromic)	16	16	16	16	16	(direct determination)
6	.b	16	16	16	16	16	(direct determination)
8	DYS388		12	12	12	12	
10	DYS389.i	14	14	14	14	14	(direct determination)
12	.ii	31	31	31	31	31	(direct determination)
2	DYS390 = DYS708	24	24	24	24	24	(direct determination)
4	DYS391	10	10	10	10	10	(direct determination)
11	DYS392 (located in the untranslated region of the transcription unit TTTY10)	11	11	11	11	11	
1	DYS393= DYS395	14	14	14	14	14	(direct determination)
49	DYS413.a (palindromic)		22	22	22	22	
50	.b		22	22	22	22	
48	DYS425 (one copy of DYF371)		0	0	0	0	
7	DYS426 = DYS483		11	11	11	11	
105	DYS434		9	9	9	9	
53	DYS436		12	12	12	12	
19	DYS437= DYS457		14	14	14	14	
37	DYS438 (located in the untranslated region of the USP9 Y gene)	10	10	10	10	10	(direct determination)
9	DYS439 = Y-GATA-A4		12	12	12	12	(direct determination)
89	DYS441		14	14	14	14	
36	DYS442*		*11*	12	12	12	
57	DYS444= DYS542		11	11	11	11	
86	DYS445		11	11	11	11	
60	DYS446		12	12	12	12	
18	DYS447*		*22*	21	21	21?	
20	DYS448 (located in the P3 loop)	20	20	20	20	20	(direct determination)
21	DYS449		28	28	28	28	
56	DYS450		7	7	7	7	
85	DYS452		30	30	30	30	
17	DYS454*= DYS639		11	7	11	11	
16	DYS455 (located in the intron 2 of the TBL1 Y gene)		11	11	11	11	
30	DYS456	15	15	15	15	15	(direct determination)
13	DYS458	16	16	16	16	16	(direct determination)

14	DYS459.a (palindromic)	9	9	9	9
15	.b	9	9	9	9
26	DYS460= Y-GATA-A7.1	10	10	10	10
106	DYS461= Y-GATA-A7.2	11	11	11	11
84	DYS462	12	12	12	12
88	DYS463	18	18	18	18
22	DYS464.a (palindromic)	14	14	14	14
23	.b	15	15	15	15
24	.c	16	16	16	16
25	.d	17	17	17	17
45	DYS472	8	8	8	8
58	DYS481*	*27*	*27*	*28*	*28* or 27?
69	DYS485	15	15	15	15
63	DYS487= DYS698	14	14	14	14
54	DYS490	12	12	12	12
66	DYS492= DYS604	10	10	10	10
80	DYS494	9	9	9	9
71	DYS495	15	15	15	15
103	DYS497	14	14	14	14
96	DYS504= DYS660	16	16	16	16
75	DYS505	13	13	13	13
104	DYS510	17	17	17	17
47	DYS511	10	10	10	10
97	DYS513= DYS605	12	12	12	12
59	DYS520= DYS654	18	18	18	18
79	DYS522	12	12	12	12
38	DYS531= DYS600	10	10	10	10
94	DYS532	11	11	11	11
81	DYS533	11	11	11	11
55	DYS534	15	15	15	15
43	DYS537	12	12	12	12
72	DYS540	11	11	11	11
77	DYS549	12	12	12	12
76	DYS556	12	12	12	12
51	DYS557	21	21	21	21
98	DYS561	15	15	15	15
67	DYS565	11	11	11	11
62	DYS568	12	12	12	12
33	DYS570 (located in the untranslated region of the TBL1 Y gene)	19	19	19	19
64	DYS572	11	11	11	11

83	DYS575		8	8	8	8	
32	DYS576		18	18	18	18	
39	DYS578		8	8	8	8	
101	DYS587		22	22	22	22	
78	DYS589		11	11	11	11	
42	DYS589		7	7	7	7	
92	DYS593		16	16	16	16	
52	DYS594		11	11	11	11	
31	DYS607		12	12	12	12	
61	DYS617		13	13	13	13	
70	DYS632		8	8	8	8	
100	DYS635*= Y-GATA-C4	23	22	22	21	23	(direct determination)
82	DYS636		11	11	11	11	
65	DYS640= DYS606		13	13	13	13	
44	DYS641		11	11	11	11	
102	DYS643		12	12	12	12	
93	DYS650		18	18	18	18	
68	DYS710		31	31	31	31	
91	DYS712*		23	23	*25*	23	
73	DYS714		24	24	24	24	
95	DYS715		23	23	23	23	
74	DYS716		28	28	28	28	
34	DYS724 = CDY.a* (palindromic) = gene		34	35	34	35 ?	
35	.b		36	36	36	36	
99	DYSS726		15	15	15	15	
87	Y-GATA-A10		12	12	12	12	
27	Y-GATA-H4	11	11	11	11	11	(direct determination)
90	Y-GGATT-1B07		13	13	13	13	
28	YCAII.a (palindromic)	19	19	19	19	19	(direct determination)
29	.b		22	22	22	22	(direct determination)
40	DYF395S1.a (palindromic)	22	15	15	15	15	
41	.b		15	15	15	15	
46	DYF406S1		10	10	10	10	

Because you know exactly how many generations ago the ancestor lived (Figure 1), it is interesting to see how statistics / probabilities compare with reality. In this particular case: Mike > Cyril > Valentine-Louis Clavering > Louis > Lucien > Charles Bonaparte (= Carlo Buonaparte), the probabilities based on the calculations of the time of the most recent common ancestor (the TMRCA) calculations (from Walsh, 2001) are incorrect: comparing the STRs showing only 6 mismatches, it only estimates the probability that Mike Clovis (328303) and Alexandre Colonna Walewski (218983) shared a common ancestor within the last 1 generation = 0.07%, 2 generations = 1.13%, 3 generations = 4.93%, 4 generations = 12.48%, 5 generations = 23.38%, 6 generations = 36.19%, 7 generations = 49.27%,…; so, about 36 to 50% probability six generations back.

3.2. STRs with Identical Values

A total number of 82 STRs have identical allelic values between M.C., C.N. and A.C.W.: in order, the 71 non-palindromic STRs DYS388 = *12*; DYS425 = *0*; DYS426 = *11*; DYS434 = *9*; DYS436 = *12*; DYS437 = *14*; DYS441 = *14*; DYS444 = *11*; DYS445 = *11*; DYS446 = *12*; DYS449 = *28*; DYS450 = *7*; DYS452 = *30*; DYS455 = *11*; DYS460 = *10*; DYS461 = *11*; DYS462 = *12*; DYS463 = *18*; DYS472=*8*; DYS485 = *15*; DYS487 =*14*; DYS490 = *12*; DYS492 = *10*;DYS494 = *9*;DYS495 = *15*;DYS497 = *14*; DYS504 = *16*; DYS505 = *13*; DYS510 = *17*;DYS511 = *10*; DYS513 = *12*; DYS520 = *18*; DYS522 = *12*; DYS531 = *10*; DYS532 = *11*; DYS533 = *11*; DYS534 = *15*; DYS537 = *12*; DYS540 = *11*; DYS549 = *12*; DYS556 = *12*; DYS557 = *21*; DYS561 = *15*; DYS565 = *11*; DYS568 = *12*; DYS570 = *19*; DYS572 = *11*; DYS575 = *8*;DYS576 = *18*; DYS578 = *8*; DYS587 = *22*; DYS589 = *11*; DYS590 = *7*; DYS593 = *16*; DYS594 = *11*; DYS607 = *12*; DYS617 = *13*; DYS632 = *8*; DYS636 = *11*; DYS640 = *13*; DYS641 = *11*; DYS643 = *12*; DYS650 = *18*; DYS710 = *31*; DYS714 = *24*; DYS715 = *23*; DYS716 = *28*; DYS726 = *15*; Y-GATA-A10 = *12*; Y-GGAAT-1B07 = *13* and DYF40651=*10*.

Likewise for the 11 palindromic STRs: DYS413.a = *22*,.b = *22*; DYS459.a = *9*,.b=*9*; DYS464.a=*14*,.b=*15*,. c=*16*,. d=*17*, CDY.b=*36* and DYF395S1.a=*15*,.b =*15*,which have identical values between M.C., C.N. and A.C.W.

Because of this identity, we can reasonably infer that the 93 allelic values of the above genetic markers correspond to those expected for Napoléon I (because they have remained unchanged for 5/6 generations of remote ancestry).

3.3 Differential STRs

Table 2 lists and characterizes the seven STRs that differentiate between M.C., C.N., and A.C.W. Only one of them (CDY.a) is palindromic. The mutation rates, when known (Burgarella & Navascués, 2011), of these differential alleles are in the 10^{-3} range (except for DYS447). These rates are impossible to evaluate for the palindromic STR CDY. a, and unknown for the moment for DYS712.

Table 2. Allele values for the seven differencial Y-STRs between Mike Clovis (M.C.), Charles Napoléon (C.N.) and Alexandre Colonna Walewski (A.C.W.). Expected allele values for **N** (Napoléon I) are established for the three Y-STRs DYS454 = *11*, DYS712 = *23* and DYS442 = *12*

Numbers	**Y-STRs**	**Palindromic**	**Mutation rates**	**N** (direct determination)	**Allele values**			**Racial background**	**N** (deduced / expected values)
					M.C.	C.N.	A.C.W.		
1	**Y-GATA-C4**		2.832x 10-3	23	22	22	21		
2	**DYS454**		$2.182x10^{-3}$		11	7	11		**11**
3	**DYS712**		?		23	23	25		**23**
4	**DYS442**		$1.926x10^{-3}$		11	12	12		**12**
5	**DYS447**		$7.414x10^{-4}$		22	21	21	+?	**21?**
6	**DYS481**		$6.937x10^{-3}$		27	27	28	+	**27-28?**
7	**CDY.a**	+			34	35	34		**35?**

We already know (Lucotte & Bouin-Wilkinson, 2014) the real allele value = *23* of Y-GATA-C4 for Napoléon I. Figure 2 shows the bimodal distribution of Y-GATA-C4 alleles in the population; Napoléon I (N) value corresponds to that of the second modal class. Allele values (=*22*) of Charles Napoléon (C.N.) and Mike Clovis (M.C.) can be explained admitting one-step (*minus* 1) mutations, and that (=*21*) of Alexandre Colonna Walewsky (A.C.W.) admitting a two-step (*minus* 2) mutation.

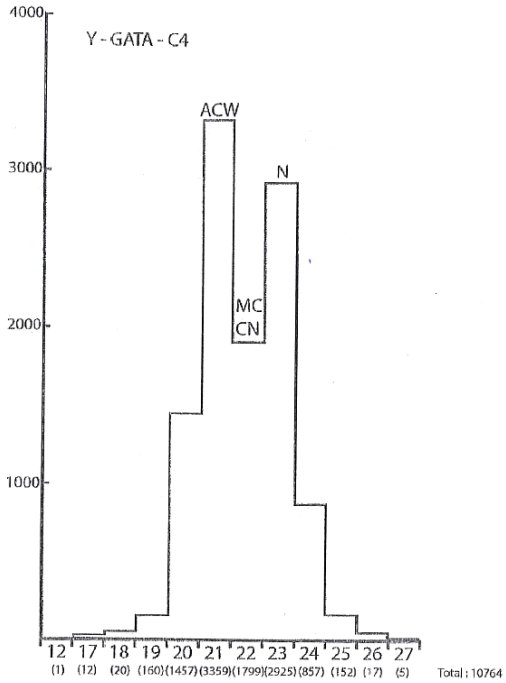

Figure 2. Y-GATA-C4 allelic distribution (www.genebase.com/in/dnaMarkerDetail.php?t=y&d=DYS635), based on values from 10 764 subjects

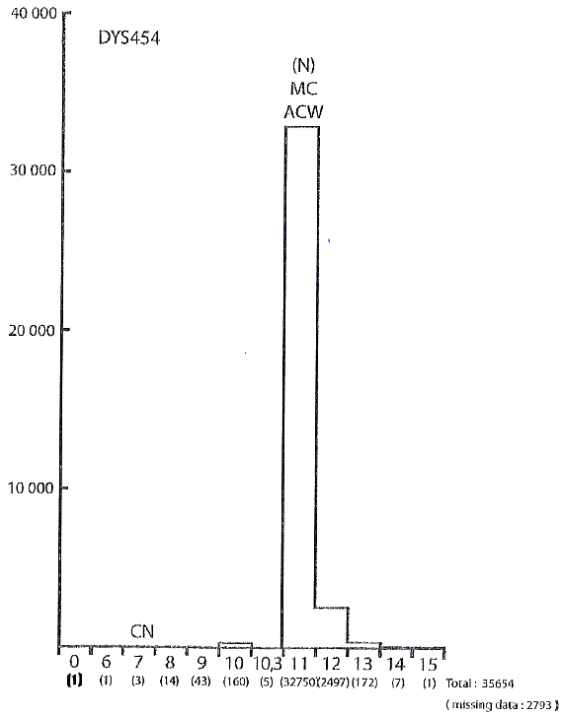

Figure 3. DYS454 allelic distribution (CEPH database), based on values from 35 654 subjects

The distribution of DYS454 alleles in the population is shown in Figure 3. According to Redd *et al.* (2002) DYS454 is one of the most stable (with a pre-eminent modal class = *11*) of the marker set. Because both A.C.W. and M.C. alleles belong to this modal class, the most parsimonious interpretation is that allele *11* at this marker is the ancestral form - that of Napoléon I (N) - and that the allele value = *7* for C.N. represents a derived one, which happened during one of the five generations separating C.N. from the common ancestor Carlo Buonaparte. It is probable that this variant *7* (characteristic of the Jérôme line) is due to a multistep deletion, a rare event which often results in a most stable allele (Lucotte et al., 2013).

Although based on a relatively low number of subjects studied, figure 4 shows a representative allele distribution for DYS712. The interest of this recently described marker is that it certainly represents one of the most variable STR of the panel (its modal class corresponds to allele *22*). Alleles of C.N. and M.C. = *23* and the A.C.W. allele = *25*. The expected N value is probably *23*, because this class corresponds to the second one in importance; and the A.C.W. value = *25* must be due to a two-step (*plus* 2) mutation.

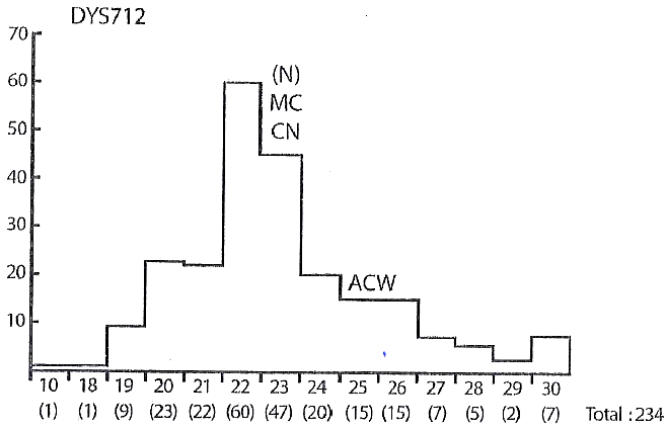

Figure 4. DYS712 allelic distribution (K. Norved, personal communication) of 234 American Caucasians

Figure 5 shows the modal distributions of alleles for DYS442 and DYS447, based on a sample of 1000 European subjects (English: 56, Germans: 59, French Parisians: 191, French Basques: 97, Corsicans: 328, North Italians: 46, Central-Italians: 112, Sardinians: 111; from Diéterlen and Lucotte, 2005). For DYS442 the allele value = *12* of C.N. and A.C.W. corresponds to the modal class; so it is probable that the expected N value is *12*. The value = *11* for M.C. must correspond to a one-step (*minus* 1) mutation.

The pattern of variations is more complicated to interpret for DYS447, because none of the allele values is located at the modal (=*25*) nor at the adjacents (*26* and *24*) classes: allele values for C.N. and A.C.W. = *21*, and *22* for M.C. We presume that the DYS447 distribution presents a small peak in frequencies (possibly due to racial background) at the left tail of the modal class. In this hypothesis, but it is highly speculative, the expected N value could be = *21* (because of the two *21* allelic values of C.N. and A.C.W.).

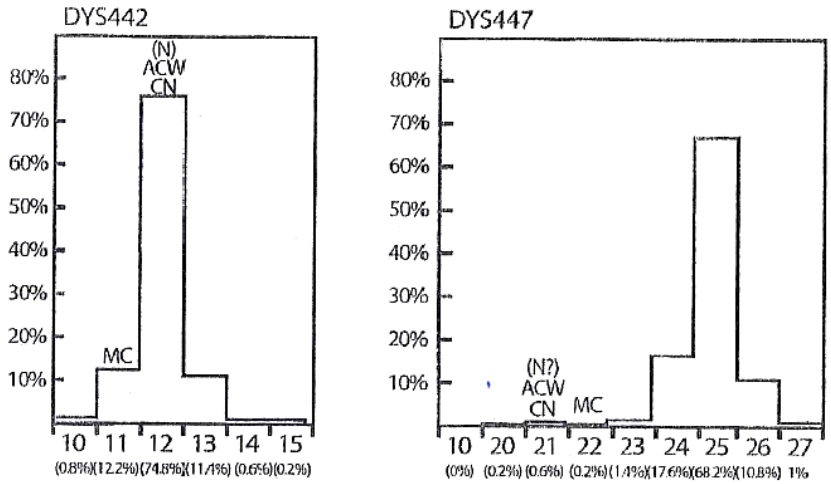

Figure 5. DYS442 and DYS447 allelic distributions, based on our sample of 1 000 unrelated European Caucasians

The existence of this racial background is evident for DYS481 (English: 102, Indians: 83, Africa: 94; from D'Amato et al., 2010), where the three European, Asiatic and African distributions are superposed on the graph (Figure 6): the *27* (for C.N. and M.C.) and *28* (for A.C.W.) classes are relatively well represented at the right tail of the Asiatic distribution, but none (for *27*) or few (for *28*) for the European distribution; but in any case we cannot decide if the expected N value is *27* or *28*.

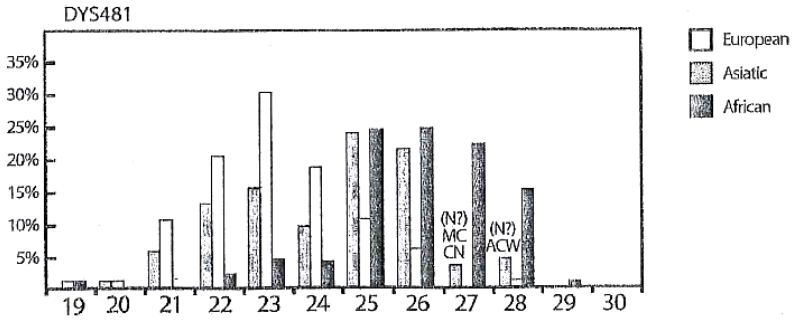

Figure 6. DYS481 allelic distribution (from d' Amato et al., based on samples of 102 European subjects (English), 83 Indians and 94 Xhosas

This sort of racial context intervening for some STR alleles determining the Y-haplotype is interesting to consider, because of the oriental origin (Lucotte & Diéterlen, 2014) of the E1b1b1 haplogroup of Napoléon I, more precisely known now (Lucotte et al., 2013) as E1b1b1b2a1 L792^{+} haplogroup.

Figure 7 shows the modal distributions – based on our sample of 1000 European subjects – of allelic classes for the palindromic markers CDY.a and CDY.b. It is because of the identity of allele values = *36* between C.N., A.C.W.

and M.C. that we proposed that the expected N value for CDY.b is *36*. (though it corresponds to the fourth frequency class in importance, located at the left tail of the modal class).

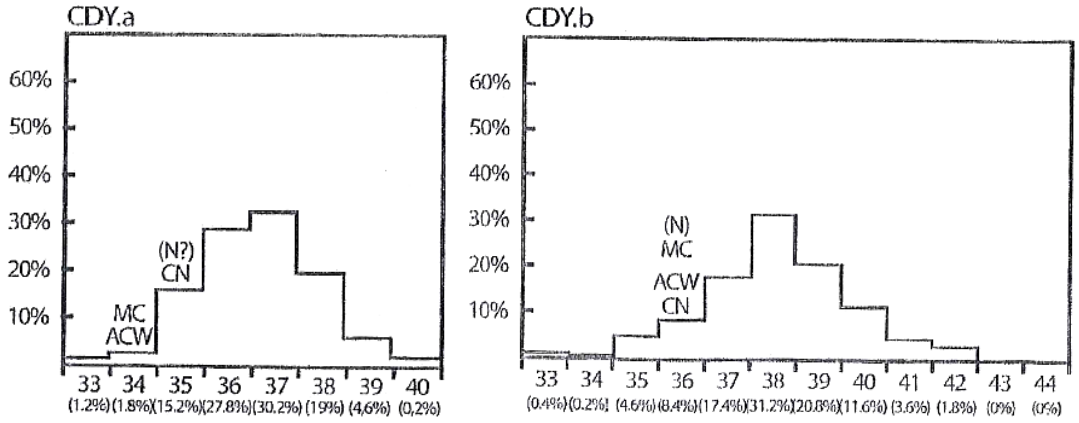

Figure 7. CDY.a and .b allelic distributions, based on the sample of 1 000 unrelated European Caucasians

Predictions about the variation of palindromic Y-STRs, even in the more simple situation of a two-copy marker like CDY, is a very hazardous matter (Lucotte et al., 2013) because we do not know exactly the precise mechanisms involved. For CDY.a the C.N. allelic value = *35*, and the A.C.W. and M.C. values = *34*. We retain here the possibility, but it is also highly speculative, that the expected N value could be = *37* (because, as for CDY.b, it corresponds to the third frequence class, located at the left tail of the modal one). Certainly the *35* alleles for A.C.W. and M.C. cannot be explained by such a simple mechanism as that of one-step (*minus* 1) mutation.

4. Discussion

In the goal to establish the Y-chromosome haplotype of Napoléon the First we determined initially, in his genomic DNA extracted from two islands of follicular sheats associated with his beard hairs conserved in the Vivant-Denon reliquary (Lucotte et al., 2011), allelic values for the three Y-STRs DYS19 and for two palindromic STRs YcaII.a and .b. Subsequently (Lucotte and Bouin-Wilkinson, 2014), based on genomic DNA of his hair dandruff dating from 1811, we determined allelic values for 16 STRs: DYS19 (for which we confirmed the first allelic value previously obtained), the palindromic STRs DYS385.a and .b, DYS389.i and ii, DYS390, DYS391, DYS392, DYS393, DYS438, the variable STR-Y-GATA-A4, DYS448, DYS456, DYS458, Y-GATA-C4 and Y-GATA-H4. The corresponding allele values for these 18 STRs correspond to the real allelic values of the Napoléon I Y-haplotype.

Because of the identity of allelic values of STRs between Charles Napoléon (the living fourth generation of male descent from Jérôme (Napoléon I's youngest brother) and Alexandre Colonna Walewski (a direct living sixth generation descendant from Napoléon I), we proposed (Lucotte et al., 2013) expected allelic values of Napoléon I for a total number of 109 STRs (33 of them being palindromics). For some of the six variables (between Charles and Alexandre) STRs: DYS454, DYS481, Y-GATA-C4, DYS712, CDY.a (palindromic) and DYF397.2 (palindromic), we proposed as expected allelic values for Napoléon I the most probable allelic forms according to STR distributions; the allele value of DYS454 = *7* for Charles Napoléon appeared then as a highly discordant one.

Mike Clovis is a living, previously unknown, fifth descendant of Lucien (another brother of Napoléon I). The objective of the present study is to compare, for a total number of 106 STRs, allelic values between him, Charles Napoléon and Alexandre Colonna Walewski. Identity of allelic values between the three was confirmed for 82 non-palindromic STRs and for 11 palindromic STRs; that confirms, in a triangular form, that these 93 STR allelic values are definitely those previously proposed as expected allele values of the Napoléon I Y-haplotype.

These comparisons between Mike Clovis, Charles Napoléon and Alexandre Colonna Walewsky permit us to clarify some of the questions asked by the variable values between them: for DYS454, the allele value = *11* for Mike Clovis is the expected allelic value of Napoléon I, as previously proposed. For DYS712, the allele value = *23* for Mike Clovis corresponds also to the expected allelic value of Napoléon I already proposed; however in this case it is not the modal class of distribution of DYS71 values that is concerned, but the nearest one of the right edge of this distribution.

Compared to Charles Napoléon and Alexandre Colonna Walewski, Mike Clovis had different allele values for DYS442 = *11* and DYS447 = *22*. For DYS442, as proposed previously, allele value = *12* is probably the expected allelic value of Napoléon I because it corresponds to the modal class of the distribution; and allele value = *11* for Mike Clovis results from a single mutational event (one-step, *minus* 1).

It is impossible to predict some expected allelic value of Napoléon I for DYS447, because the three obtained allele values (that of Mike Clovis = *22* could be the result of a one-step *plus* 1 mutational event) are all located at the left tail of the distribution. It is impossible also to predict some expected allelic value of Napoléon I for DYS481, even when interpreted in the context of the oriental origin of the E1b1b1c1 haplogroup (Lucotte and Diéterlen, 2014), because all the three obtained allele values are now located at the right tail of the distribution.

We ignore, for the moment, what is the Y-chromosome haplotype of Carlo Buonaparte; but it seems highly probable, because of the similarities between the Y-STR values presently obtained, that he was the biological father of Lucien, Napoléon and Jérôme (all these three having the same Y-haplogroup). As a by-product of such studies, we established that the allele value = *7* for DYS545 is highly characteristic of the Jérôme line; possibly, as shown here, the allele value = *11* for DYS442 could be characteristic of the Lucien line. It remains a possibility that allele values of *25* for DYS712 and of *28* for DYS481 could be characteristics of the direct Napoléon I line, at least for the Walewski descent.

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