

DNA Matches to the main Plant family

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In the following table, the "Plant ID code" is a label for each volunteer for the DNA test. In the codes in this column, P denotes the spelling Plant whereas PT is for Plantt.

For each volunteer, the column "GD in 12" gives the Genetic Distance from the PMH (Plant Modal Haplotype) of the main English Plant family when only the first 12 loci are considered; the two values separated by a comma represent calculations in respectively the stepwise and infinite-alleles models. The testing company FTDNA (Family Tree DNA) uses intermediate calculations between these two bounds and the company quite obtusely changed the model used for their calculations in December 2012; the rather arbitrary FTDNA values remain bounded by those of our two standard types of calculation. Similarly, "GD in 25" gives the values when only 25 loci are considered. For 37 loci and above, we first give the pair of values excluding three fast changing markers and then the pair when we include them. The two pairs of values are separated by a '/'.

The column "GD in most" summarises the situation for the most FTDNA loci measured. The column "Related to main family" gives summary conclusions based on this preceding column with such a designation "poss,prob" denoting possible or probable for being intactly related to the main family. These designations are taken from the FTDNA FAQ. These designations ignore other supplementary evidence such as that from: control samples; Deep Clade testing; close matching to other Plants in the Y-STR cluster; and, documentary evidence of genealogical kinships.

In particular, the large control sample of everyone tested worldwide shows no-one even remotely matches the Plant cluster at the 37-marker level and above. False positive matches to the PMH (Plant Modal Haplotype) are not impossible but extremely unlikely even at the 12-loci level: the chance is 0.056 and very much lower when more loci are tested.

Even when this strong control sample consideration is ignored, the 6,6 match of P33a at the 37-loci level reduces to 3,3 when the three fast-changing markers are omitted. Such omissions at the 111-loci level also reduce the 9,9 of PT3a to 6,6 and the 10,7 of P29a to 6,5.

P1a, P19a and P29a have obtained Deep Clade enhancement of their "probable" (or "poss,prob") status; this enhancement is due to their sharing a quite rare haplogroup despite having rather marginal GDs from the PMH. As already mentioned, they are very distant anyway from any non-Plant, without even considering their rare Plant haplogroup.

Plant ID code	FTDNA kit code	GD in 12	GD in 25	GD in 37	GD in 67	GD in 111	GD in most loci yet measured	Related to main family	Deep-Clade check
P1a	11830	1,1	1,1	2,2/4,4	2,2/4,4	5,5/6,6	6,6 in 111	probable	yes
P1b	18329	0,0	0,0				0,0 in 25	related	
P1c	141186	1,1	1,1	2,2/4,4			4,4 in 37	probable	
P2a	277384	1,1	1,1	1,1/3,2			3,2 in 37	related	
P5a	11858	0,0	2,2				2,2 in 25	probable	
P7a	7818	0,0	0,0				0,0 in 25	related	
P7b	105871	0,0	0,0	0,0/5,3	0,0/5,3	3,3/7,6	7,6 in 111	probable	
P12a	22939	0,0					0,0 in 12	related	
P14a	43911	0,0					0,0 in 12	related	
P19a	96105	1,1	4,4	5,5/5,5	5,5/5,5	6,6/7,7	7,7 in 111	probable	yes
P20a	119000	0,0	0,0	0,0/1,1	1,1/2,2		2,2 in 67	related	
P23a	144948	0,0	0,0	1,1/2,2			2,2 in 37	related	
P25a	N83079	0,0	0,0	0,0/0,0	1,1/1,1		1,1 in 67	related	
P26a	182593	0,0	1,1	1,1/2,2	2,2/3,3		3,3 in 67	related	
P28a	230023	1,1	1,1	1,1/3,3	1,1/3,3	3,2/4,3	4,3 in 111	related	
P28b	248032	1,1	1,1	1,1/3,3			3,3 in 37	related	
P29a	232765	0,0	1,1	2,2/7,5	2,2/7,5	6,5/10,7	10,7 in 111	poss,prob	yes
P30a	273914	1,1	1,1	2,2/6,4	2,2/6,4		6,4 in 67	related	
P31a	280105	0,0					0,0 in 12	related	
P32a	280384	0,0					0,0 in 12	related	
P33a	295512	1,1	1,1	3,3/6,6			6,6 in 37	not	
P36a	372698	0,0	2,2	0,0/2,1	3,2/5,3	5,5/6,6	6,6 in 111	probable	
PT1a	18227	0,0	1,1	1,1/1,1	2,2/2,2		2,2 in 67	related	
PT2a	60092	0,0					0,0 in 12	related	
PT3a	235642	0,0	0,0	0,0/2,2	2,2/4,4	6,6/9,9	9,9 in 111	possible	

