QTL detection by multi-parent linkage mapping in oil palm (*Elaeis guineensis* Jacq.), Theoretical and Applied Genetics,

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Online Resource 1 Positions and effects of the QTL identified by the within-family or across-family analyses. at the risk genome-wide threshold α of 4% per cross

A. QTL identified by the within-family analyses

Trait	QTL	Within family analyses									
	code [a]	Estimation system [a]	Linkage group	Position [b] (cM)	Confidence intervalle		F [c] value	R^2 (%)	Estimated effects		
									Genetic background [d]	Parent [e]	
					from	to			Africa x Deli	Deli	Africa
Average bunch number/palm/year at 3-5 years (kg):	Bn3_5_4C	4	1	71.4	69.5	76.6	9.2	24.5	21.2	3.0	5.0
	Bn3_5_1C	1	4	207.9	188.3	218.2	9.3	14.7	30.0	-1.5	0.6
	Bn3_5_3-	3	15	10.9	0.0	23.0	11.5	28.7	24.0	-3.0	1.8
Average bunch weigth at 3-5 years (kg):	Bwt3_5_3-	3	4	197.0	195.0	209.1	10.5	28.0	6.2	0.5	0.0
	Bwt3_5_3-	3	7	90.8	82.1	111.3	15.1	35.9	6.2	0.5	0.5
	Bwt3_5_4C	4	8	126.1	111.3	152.5	8.8	25.0	8.2	0.9	1.1
	Bwt3_5_2C	2	16	39.8	30.1	48.9	8.5	22.8	5.6	0.0	0.3
Fresh Fruit Bunch yield/palm/year at 3-5 years:	FFB3_5_3-	3	15	5.9	0.0	18.1	10.5	27.0	146.9	14.0	3.4
	FFB3_5_2-	2	16	34.8	12.4	44.2	8.8	23.3	155.9	1.1	9.3

Palm oil yield/palm/year at 3-5 years (ton/ha/year):	PO3_5_2C	2	16	39.8	31.6	48.1	11.4	31.0	5.3	2.2	0.2
Average bunch number/palm/year at 6-9 years (kg):	Bn6_9_3-	3	12	22.7	17.1	50.6	11.9	30.2	13.9	0.8	1.9
Average bunch weight at 6-9 years (kg):	Bwt6_9_3-	3	12	26.9	0.0	50.2	9.0	24.3	17.5	0.0	1.6
Fresh Fruit Bunch yield/palm/year at 3-5 years:	FFB6_9_3-	3	4	70.3	61.7	100.3	12.0	31.2	235.6	14.9	10.4
	FFB6_9_3-	3	12	66.9	49.4	82.2	10.2	27.7	13.9	0.8	1.9
Palm oil yield/palm/year at 6-9 years (ton/ha/year):	PO6_9_3-	3	9	68.0	54.5	74.1	17.4	40.5	8.1	0.6	0.8
	PO6_9_3-	3	16	14.3	1.7	24.9	10.2	28.5	8.1	0.2	0.6
Average weigth of the analysed bunch (kg):	aBwt_1-	1	1	118.6	114.9	125.6	10.3	18.2	14.6	0.1	0.7
	aBwt_3-	3	4	152.3	142.6	161.8	12.7	33.2	27.0	7.0	1.8
	aBwt_1-	1	4	233.3	214.4	236.5	9.2	16.7	14.6	0.5	0.5
	aBwt_1-	1	10	17.7	7.3	23.6	10.4	18.5	14.6	0.3	0.8
	aBwt_1-	1	12	168.3	124.8	176.5	8.8	16.1	14.6	0.4	0.5
Average number of fruits per bunch:	Fn_3C	3	6	106.0	99.2	111.4	8.9	25.1	1975.8	15.7	247.6
Average weight of the fruit (g):	Fwt_1C	1	3	13.4	6.1	28.0	8.8	16.0	7.6	0.1	0.4
	Fwt_1C	1	7	99.0	81.8	119.8	9.6	17.3	7.6	0.0	0.4
	Fwt_1-	1	8	133.4	125.8	137.1	11.2	19.5	7.6	0.1	0.4
	Fwt_1-	1	12	168.1	150.1	175.7	9.1	16.5	7.6	0.1	0.3
	Fwt_2C	2	16	34.8	28.4	45.1	16.1	37.8	7.3	0.7	0.4
Pulp to fruit ratio (%):	%PF_1-	1	1	145.8	136.0	152.8	12.4	21.2	78.1	0.0	1.3
	%PF_1-	1	10	36.1	0.0	44.5	9.2	16.6	78.1	0.3	1.0

	%PF_1-	1	12	81.9	40.2	91.1	10.2	18.1	78.1	0.1	1.1
	%PF_1-	1	15	29.3	13.4	54.4	9.7	17.4	78.1	0.9	0.6
	%PF_1C	1	16	0.0	0.0	8.3	10.8	19.1	78.1	0.7	0.9
Palm oil to pulp ratio (%):	%POP_1C	1	1	136.3	131.0	141.8	25.2	33.5	54.5	0.1	0.7
Palm oil industrial extraction rate (%):	IER_1C	1	1	136.3	129.0	143.4	19.2	27.7	23.1	0.1	1.5
	IER_3C	3	4	207.9	172.2	220.1	10.0	27.3	26.0	0.8	0.4
Iodine value:	I_1-	1	1	83.5	74.4	91.2	10.4	19.3	55.5	0.2	0.7
	I_1C	1	15	29.3	27.8	30.1	20.2	31.7	56.0	0.8	0.8
%KF	%KF_1-	1	1	145.8	135.5	153.2	12.7	20.6	9.3	0.5	0.5
	%KF_1C	1	16	2.7	0.0	7.4	12.7	20.5	9.4	0.1	0.6
Stem height (m):	Ht_1C	1	4	157.3	141.1	181.5	10.6	17.9	654.5	14.4	35.3
	Ht_1C	1	8	64.3	54.9	67.3	21.3	30.3	654.5	6.5	34.4
	Ht_2C	2	11	45.0	0.0	86.7	11.9	31.0	652.5	1.8	56.7
	Ht_3C	3	15	69.0	59.6	74.6	10.9	29.2	673.8	14.8	28.3
Average number of leaves per crown:	Leaf_n_3-	3	4	197.0	194.7	208.8	11.3	29.9	36.0	2.7	1.5
	Leaf_n_4C	4	13	33.0	19.0	104.3	14.2	34.4	37.8	2.2	3.1
Average length of the leaf L17 (cm):	L17_L_1C	1	4	94.2	79.7	111.1	12.2	20.5	638.6	15.1	11.6
	L17_L_3C	3	4	221.8	212.6	228.6	12.6	32.3	643.6	2.0	21.7
	L17_L_1-	1	5	55.9	33.6	64.3	8.6	15.3	636.1	4.2	10.6

	L17_L_1C	1	10	139.2	125.2	143.7	11.0	18.8	638.6	11.4	11.3
Petiole average width of the leaf L17 (cm):	P_W_134C	1	3	59.5	49.0	63.3	8.2	12.7	9.1	0.2	0.2
	P_W_134C	3	3	59.5	54.3	67.3	11.4	30.5	10.4	0.4	0.0
	P_W_134C	4	3	57.3	56.2	58.5	12.8	32.5	10.1	0.1	1.0
	P_W_1-	1	5	55.9	41.0	64.3	15.8	25.1	9.1	0.2	0.2
	P_W_1-	1	15	83.6	81.3	85.1	9.4	16.6	9.1	0.0	0.2
Petiole average thickness of the leaf L17 (cm):	P_T_3-	3	13	72.8	55.1	91.5	13.5	33.7	4.8	0.1	0.2
Average number of leaflets per leaf L17:	Lt_n_4C	4	4	175.7	17.9	188.6	13.0	32.5	170.1	7.0	0.5
	Lt_n_1C	1	4	230.5	224.3	234.0	12.9	20.5	170.8	4.1	2.9
	Lt_n_2-	2	8	83.6	66.4	119.0	8.9	25.2	174.1	10.7	1.8
	Lt_n_2-	2	10	34.5	0.0	42.7	11.9	31.0	174.1	4.8	0.1
Leaflet average length of the leaf L17 (cm):	Lt_L_3C	3	10	64.6	55.8	77.0	10.0	27.4	114.1	3.3	0.0
Leaflet average width of the leaf L17 (cm):	Lt_W_2-	2	4	202.7	196.1	210.2	10.3	27.9	7.1	0.8	0.1
	Lt_W_2C	2	8	189.0	184.6	189.0	9.7	26.8	7.1	0.3	0.1

Note : [a]: QTL_**i**-: QTL detected by the within-family analysis on the single cross **i** with 1 = LM2T x DA10D; 2 = LM2T x LM269D; 3 = LM718T x DA10D; 4 = LM718T x LM269D. QTL_i**C**: QTL also detected by the across-family analysis on the multiple cross design **C**. [b]: From the first marker of the group. [c]: Significant F threshold of 8.6 (LOD of 3.7). [d]: Compared to the general mean of the cross. [e]: Additive substitution allelic effect (two allele of opposite effects by model).

B. QTL identified by the across-family analysis

Trait	QTL	Across family analysis														
	code [f]	Estimation system [f]	Linkage group	Position [g] (cM)	Confidence Intervalle		F [h] value	R^2 (%)	Estimated effects							
									Genetic background of the cross i				Parent Deli j		Parent Africa j	
					from	to			1	2	3	4	DA10D	LM269D	LM2T	LM718T
Bn3_5	Bn3_5_4C	C	1	76.3	69.8	79.6	8.2	10.5	29.7	29.3	24.5	21.7	1.0	1.6	0.5	2.2
	Bn3_5_1C	C	4	207.9	204.1	219.9	5.1	6.8	29.7	29.3	24.5	21.7	1.7	0.4	0.2	0.4
Bwt3_5	Bwt3_5_-C	C	1	78.5	70.9	84.5	5.0	6.8	4.6	5.6	6.2	8.0	0.2	0.1	0.1	0.4
	Bwt3_5_4C	C	8	138.4	129.9	163.6	6.2	8.2	4.6	5.6	6.2	8.1	0.2	0.1	0.1	0.5
FFB3_5	FFB3_5_-C	C	1	71.4	56.7	86.1	6.9	9.1	136.3	156.3	148.7	148.5	6.9	11.3	3.5	12.4
PO3_5	PO3_5_-C	C	1	71.4	58.8	75.7	6.0	8.6	4.3	5.4	5.0	5.6	0.5	0.5	0.0	0.4
	PO3_5_2C	C	16	34.8	12.0	38.0	4.7	6.9	4.3	5.4	5.0	5.6	0.2	0.1	0.2	0.4
Bn6_9	Bn6_9_-C	C	15	75.7	69.1	88.8	7.3	9.2	21.7	16.3	14.1	9.2	0.9	0.3	0.6	0.9
Bwt6_9	Bwt6_9_-C	C	1	78.5	76.9	79.9	11.0	14.4	11.2	14.5	17.7	23.1	0.4	0.4	0.2	1.0
	Bwt6_9_-C	C	2	63.2	45.8	83.0	4.5	6.4	11.2	14.5	17.7	23.1	0.3	0.7	0.3	0.8
	Bwt6_9_-C	C	6	93.6	73.8	97.5	9.6	12.7	11.2	14.5	17.7	23.1	0.0	0.4	0.1	1.3

	Bwt6_9_-C	C	16	14.3	6.9	32.2	5.6	7.8	11.2	14.5	17.7	23.1	0.3	0.2	0.4	1.0
FFB6_9	FFB6_9_-C	C	1	88.5	58.5	102.2	5.4	7.1	235.4	222.0	232.1	198.9	7.1	1.2	7.3	11.5
Fn	Fn_3C	C	6	102.8	82.2	110.2	5.9	8.2	1276.9	1765.6	1958.1	2369.9	1.3	63.0	99.5	157.4
Fwt	Fwt_-C	C	1	129.6	123.2	141.6	7.8	11.0	7.5	7.2	9.1	9.0	0.5	0.4	0.1	0.2
	Fwt_1C	C	3	0.0	0.0	7.8	5.0	7.2	7.5	7.2	9.2	9.1	0.1	0.1	0.3	0.3
	Fwt_1C	C	7	33.0	26.7	53.6	4.5	6.6	7.5	7.2	9.2	9.1	0.0	0.0	0.4	0.0
	Fwt_2C	C	16	39.8	27.9	55.1	5.4	7.8	7.5	7.2	9.1	9.0	0.3	0.5	0.1	0.4
%PF	%PF_1C	C	16	7.7	0.0	13.1	5.9	8.2	77.8	80.5	80.9	82.3	0.6	0.4	1.1	0.7
%POP	%POP_1C	C	1	136.3	130.4	143.2	12.5	16.2	54.5	55.7	55.0	55.2	0.3	0.8	1.6	1.1
IER	IER_1C	C	1	136.3	130.0	144.4	9.1	12.6	23.2	25.3	25.8	26.9	0.0	0.1	1.1	0.9
	IER_3C	C	4	207.1	194.6	217.7	5.7	8.2	23.2	25.3	25.8	26.9	0.8	0.7	0.0	0.3
I	I_-C	C	13	50.7	41.1	60.8	5.4	9.2	55.7	55.7	53.4	52.5	0.2	0.5	0.5	0.6
	I_1C	C	15	29.2	28.2	32.4	17.0	24.2	55.7	55.7	53.4	52.5	0.5	0.8	0.7	1.2
%KF	%KF_1C	C	16	7.7	0.0	10.7	6.9	9.7	9.3	8.3	8.9	9.2	0.3	0.5	0.6	0.4
Ht	Ht_1C	C	4	165.6	152.1	197.6	6.3	9.0	647.9	645.8	674.3	706.0	3.4	0.2	32.3	0.0
	Ht_1C	C	8	71.3	62.6	77.0	9.0	12.5	647.9	645.8	674.3	706.0	3.1	54.0	26.6	0.7
	Ht_2C	C	11	131.6	92.6	140.9	9.6	13.1	647.9	645.8	674.3	706.0	3.4	0.2	32.3	0.0
	Ht_3C	C	15	64.4	56.9	78.6	9.4	12.8	647.9	645.8	674.3	706.0	10.2	50.6	2.5	23.3
Leaf_n	Leaf_n_4C	C	13	51.2	41.9	102.2	8.8	11.7	34.3	32.6	36.0	37.7	0.1	2.6	0.2	2.6

L17_L	L17_L_1C	C	4	99.2	82.4	117.0	5.5	8.1	634.9	652.6	644.3	650.6	9.2	6.7	13.5	1.9
	L17_L_3C	C	4	217.9	189.1	222.8	6.0	8.7	634.9	652.6	644.3	650.6	2.0	3.4	0.8	21.4
	L17_L_1C	C	10	133.5	125.2	143.6	8.0	11.3	634.9	652.6	644.3	650.6	10.6	16.8	6.2	8.5
	L17_L_-C	C	13	92.3	61.8	104.3	5.0	7.3	634.9	652.6	644.3	650.6	2.9	19.7	4.6	12.3
P_W	P_W_134C	C	3	59.5	49.0	63.3	9.4	12.7	8.9	9.0	10.4	10.1	0.3	0.0	0.0	0.2
	P_W_-C	C	16	7.7	0.0	13.8	5.6	8.0	8.9	9.0	10.4	10.1	0.1	0.1	0.2	0.2
P_T	P_T_-C	C	3	49.4	42.0	68.7	7.3	9.9	4.6	4.6	4.8	4.5	0.1	0.0	0.1	0.1
Lt_n	Lt_n_-C	C	2	16.1	0.0	35.3	6.4	9.1	171.1	175.3	171.6	170.5	0.1	0.4	4.2	0.6
	Lt_n_4C	C	4	160.4	59.5	205.7	4.8	7.1	171.1	175.3	171.6	170.5	0.6	2.9	1.7	0.4
	Lt_n_1C	C	4	230.5	226.3	233.4	10.8	14.5	171.1	175.3	171.6	170.5	3.1	1.9	1.9	2.6
	Lt_n_-C	C	14	116.5	103.6	116.5	4.8	7.0	171.7	175.6	171.8	170.4	0.1	0.1	2.2	0.9
Lt_L	Lt_L_3C	C	10	74.6	33.0	90.7	5.0	7.1	104.6	93.6	113.1	99.7	4.0	1.4	1.0	0.3
Lt_W	Lt_W_2C	C	8	149.9	52.7	189.0	4.5	6.4	6.4	7.2	5.8	6.3	0.1	0.3	0.1	0.1

Note: [f]: QTL_-**C**: QTL detected by the across-family analysis on the multiple cross design **C**. QTL_**i**C: QTL also detected by the within-family analysis on the single cross **i** with cross 1 = LM2T x DA10D; 2 = LM2T x LM269D; 3 = LM718T x DA10D; 4 = LM718T x LM269D. [g]: From the first marker of the group. [h]: Significant F threshold of 4.5 (equivalent LOD of 3.9). [i]: Compared to the global mean of the multiple cross design. with 1 = LM2T x DA10D; 2 = LM2T x LM269D; 3 = LM718T x DA10D; 4 = LM718T x LM269D. [j]: as [e]: additive substitution allelic effect (two allele of opposite effects by model).