AFLP and SSR Polymorphism in a *Coffea* Interspecific Backcross Progeny ((*C. heterocalyx* x *C. canephora*) x *C. canephora*)

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SUMMARY

An interspecific cross (BC 1) involving a species with one of the biggest genomes in Coffea genus (*C. heterocalyx* (HET), qDNA = 1.74 pg) and a species with a medium genome size (*C. canephora* (CAN), qDNA = 1.43 pg) was studied using two types of molecular markers, AFLPTM and SSR. One hundred and eighty eight AFLP bands and 34 SSR primer pairs were suitable for the mapping. The total map length was 1360 cM with 190 loci distributed on 15 linkage groups.

The results were compared to the results obtained previously on an interspecific BC 1 progeny involving a species with a medium size genome (*C. liberica* var. *dewevrei*, DEW) and a species with one of the smallest size genome (*C. pseudozanguebariae*, PSE). They are discussed considering three main points: 1) the interest of the different markers type, 2) – the genomic distribution of AFLPs and SSR markers and 3) – the relation between AFLP polymorphism and the genome size.

INTRODUCTION

Within *Coffea* sub-genus, all species but one (*C. arabica*) are diploid (x = 11) and the 2C nuclear DNA content (qDNA) ranges from about 1 to 1.8 pg. Moreover F1 interspecific hybrid fertility increases as the qDNA difference decreases. The genome size difference between *C. pseudozanguebariae* (PSE, 1.13 pg) and *C. liberica* var dewevrei (DEW, 1.43 pg) concerns all chromosomes. The genome size of their BC 1 hybrids increased as the chromosome number from DEW increased. Species-specific AFLPs mapped using this interspecific BC1 progeny were either clustered or not and distributed throughout the genome. In this work we study an interspecific cross involving *C. heterocalyx* (HET, 1.74 pg) and *C. canephora* (CAN, 1.43 pg). AFLP and SSR bands were characterised according to polymorphism observed within-species and between-species.

MATERIAL & METHODS

The BC1 progeny (72 plants) was derived from [CAN x HET] x CAN.

Genomic DNA isolation, AFLP and SSR protocols, data analyses are described in Coulibaly et al. (in press).

For both SSRs and AFLPs, HET bands were scored 1 for presence and 0 for absence.

Table 1. AFLP primer combinations analysed and type and number of amplified bands produced per species.

Primers	Total CAN bands	Species-specific CAN/HET bands	Intra-CAN polymorphic bands (%)	Total HET bands	Specific HET/CAN bands
E1/M1	108	17	70 (64.8)	65	14
E1/M3	78	9	55(70.5)	50	19
E1/M4	84	9	53 (63.1)	67	18
E1/M5	85	14	44 (51.8)	53	15
E2/M1	141	12	87 (61.7)	102	21
E2/M2	103	16	61 (59.2)	77	25
E2/M3	95	9	63 (66.3)	66	22
E2/M7	84	10	57 (67.8)	50	21
E2/M8	130	20	78 (60)	86	11
E3/M1	107	12	70 (65.4)	72	13
E4/M8	90	10	65 (72.2)	44	14
E6/M1	75	9	49 (65.3)	48	13
total	1180	147 (12.5)	752 (63.7)	780	206 (26.5)

X/Y: species comparison —X relative to Y. E1: AAC, E2: AAG, E3: ACA, E4: ACC, E6: ACT, M1: CAA, M2: CAC, M3: CAG, M4: CAT, M5: CTA, M7: CTG, M8: CTT.

Table 2. Characterisation of AFLP bands obtained in different genome comparisons. The total numbers of bands were calculated from the sole HET genotype and 10 genotypes for CAN, PSE and DEW.

	total monomorphic bands (%)	species-specific bands (%)	Within-species polymorphic bands (%)
CAN/HET	428/1180 (36.3)	147/1180 (12.5)	752/1180 (63.7)
HET/CAN[a]		*188/780 (24.1)*	
PSE/DEW[b]	463/1259 (36.8)	112/1259 (8.9)	796/1259 (63.2)
DEW/PSE[b]	506/1296 (39)	123/1296 (9.5)	790/1296 (60.9)

[a]*: bands present in HET and absent in the 10 CAN genotypes are both species-specific and genotype-specific HET bands.*
[b]*: Unpublished data from Ky et al. (2000), calculated from the 12 primer combinations giving the highest species-specific PSE/DEW bands.*

RESULTS

87.4 and 80.5% of AFLPs and SSRs were mapped and distributed throughout the 15 linkage groups. The A/T content of +3/+3 selective nucleotides was neither correlated with the total number of bands nor with the number of polymorphic bands within-CAN species. When comparing species with the same mating system but different genome sizes, the total number

of bands was similar. The difference observed between CAN self-incompatible and HET self-fertile could more likely be explained by the heterozygosity level.

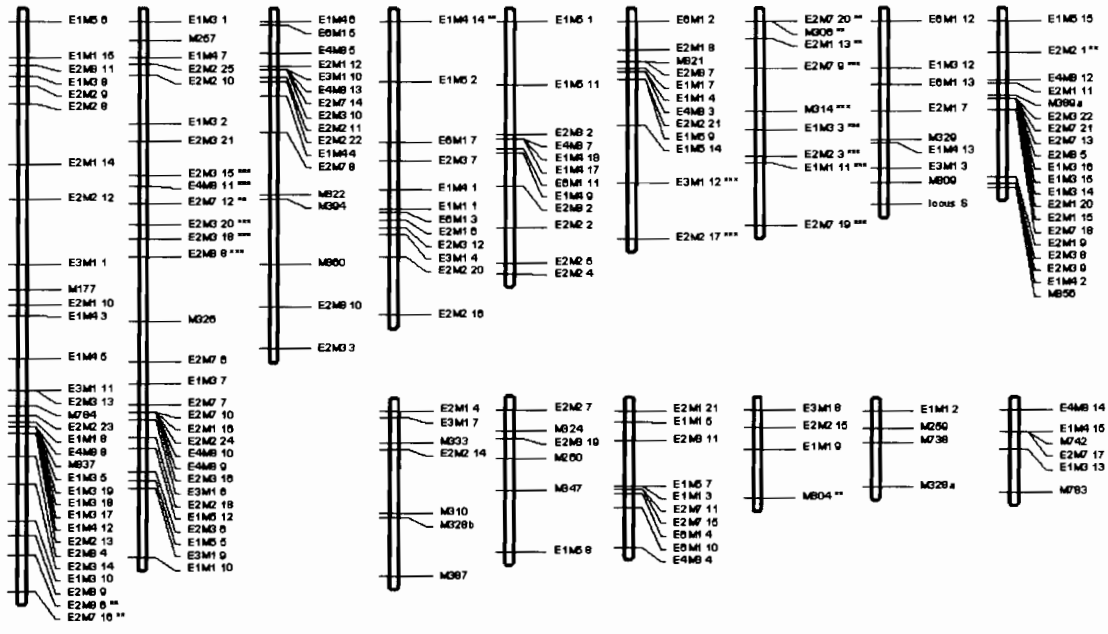

Figure 1.

CONCLUSION

The AFLP polymorphism we observed herein was not correlated with the proportion of repeated sequences or with their AT richness.

Species-specific bands seemed to be similar in number irrespective of the genome sizes considered and their phylogenetic relation. Our results suggest two independent mechanisms involved: genomic differentiation affecting all species simultaneously, and directional DNA expansion/contraction in genomes over an east-to-west geographical distribution gradient.

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In: ASIC 2004 : 20th international conference on coffee science = ASIC 2004 20ème colloque scientifique international sur le café = ASIC 2004 : 20 internationales wissenshaftliches kolloquim über kaffe = ASIC 2004 : 20° coloquio cientifica internacional sobre el café

Paris : ASIC, 699-701. ASIC 2004 : International Conference on Coffee Science, 20

ISBN 2-900212-19-7