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Two large reciprocal translocations characterized in the disease resistance-rich burmannica genetic group of Musa acuminata

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INTRODUCTION

Bananas (Musa genus) provide staple food for millions of people in Asia, Africa, Latin America and Oceania, and represent a major cash crop around the world. Most current cultivars are derived from Musa acuminata (A genome, 2n = 2x = 22), sometimes combined with Musa balbisiana (B genome, 2n = 2x = 22). Musa acuminata diverged following the Pliocene geographical isolation in distinct South-east Asian continental regions and islands (Daniells et al., 2001; Perrier et al., 2009; Janssens et al., 2016; Rouard et al., 2018). It has been divided into 6–9 partially interfertile subspecies (M. a. ssp. burmannica, burmannicoides, siamea, malaccensis, truncata, errans, microcarpa, zebra and banksii) based on morphology and geographic distribution (Simmonds, 1962; Perrier et al., 2009). The current domestication scenario suggests that plants were transported during human migrations, leading to hybridization between Musa species and subspecies (Perrier et al., 2011). This resulted in the emergence of inter(sub)specific hybrids with reduced fertility (Dodds and Simmonds, 1948; Shepherd, 1999). Early farmers would then have selected parthenocarpic diploid and triploid hybrids producing edible fruits with high flesh and low seed content. These hybrids were then propagated clonally. The hundreds of current cultivars are thus products of centuries – in some cases millennia – of vegetative propagation. Only a few of them are cultivated at a large scale and one clonal cultivar group, i.e. Cavendish, accounts for >50 % of world banana production. These large-scale monocultures have favoured the emergence of diseases and extensive pesticide use (Lescot et al., 2008).
Observations of chromosomal pairing during meiosis showed irregularities in the *M. acuminata* and *M. balbisiana* interspecific hybrid and in *M. acuminata* intersubspecific hybrids, with the presence of univalents and multivalents (Shepherd, 1999; Jeridi et al., 2011). Within subspecies, meioses were generally found to be regular with bivalents. In addition, genetic mapping studies involving *M. acuminata* hybrids revealed substantial segregation distortion involving a few linkage groups (Fauré et al., 1993; Hippolyte et al., 2010; Mbanjo et al., 2012; Noumbissié et al., 2016). The presence of large chromosomal structural variations between species and subspecies was suggested to be responsible for these irregularities. Based on the study of pairing configurations in a limited number of *M. acuminata* intersubspecific hybrids, Shepherd (1999) proposed that six translocation groups exist, differing from a ‘Standard’ (ST) group by 1–3 translocations. These groups are only partly concordant with subspecies delimitation, with the ‘Standard’ group being the largest one and comprised *banksii*, *microcarpa* and *malaccensis* ssp. accessions.

The availability of a *M. acuminata* reference genome sequence (D’Hont et al., 2012; Martin et al., 2016) allowed us to implement next-generation sequencing (NGS) technologies and comparative genomics to investigate large structural variations within *Musa*. A first large reciprocal translocation between chromosomes 1 and 4 was identified as compared with the *M. acuminata* reference genome sequence obtained from the ‘DH-Pahang’ *M. acuminata* ssp. *malaccensis* accession. Among wild accessions, this 1/4 translocation was found only in some of the ssp. *malaccensis* accessions, suggesting that it emerged within this subspecies (Martin et al., 2017). The 1/4 translocation was suggested to correspond to the ‘Northern Malayan’ karyotypic group proposed by Shepherd (1999), and the *M. acuminata* reference genome sequence was suggested to correspond to the ST group. Strong segregation distortion and reduced recombination were observed around translocation breakpoints in progeny from structurally heterozygous accessions. Interestingly, the ‘Northern Malayan’ structure was found to be preferentially transmitted to the progeny (Martin et al., 2017).

Another large reciprocal translocation between chromosomes 1 and 3 and a large inversion on chromosome 5 were characterized in *M. balbisiana* as compared with the *M. acuminata* reference genome sequence (Baurens et al., 2019). A high proportion of aneuploids was observed, involving chromosomes 1, 3 and 5, in the progeny of a tetraploid accession bearing this *M. balbisiana* chromosome structure in one copy and three copies of the standard *M. acuminata* structure. Moreover, high segregation distortion and reduced recombination were observed for these chromosomes (Baurens et al., 2019).

These studies showed that large structural variations cause segregation distortion and recombination reduction or suppression in *Musa* structural hybrids, as observed in several other plants such as *Lens*, *Helianthus* and peach (Tadmor et al., 1987; Quillet et al., 1995; Jürgens et al., 2001). Characterizing such rearrangements is thus important to facilitate the use of genetic resources in breeding programmes, in particular to improve disease resistance.

In this study, we analysed the segregation of a self-progeny of a wild *M. acuminata* ssp. *burmannicoides* accession and detected two large reciprocal translocations compared with the *M. acuminata* ssp. *malaccensis* reference sequence. We then accurately characterized breakpoints of these structural variations through discordant mate-pair read analysis. We developed an *in silico* approach based on signature segment junctions to detect translocation breakpoints in paired-end sequences from 123 accessions representative of *M. acuminata* germplasm.

**MATERIALS AND METHODS**

**Plant and sequencing material**

A self-progeny of 76 individuals from the ‘Calcutta 4’ accession (PT-BA-00051, CRB Plantes Tropicale, Guadeloupe) was produced at the CRIB research station in Guadeloupe. DNA was extracted, and sequencing libraries were constructed using a genotyping by sequencing (GBS) approach and sequenced on the GeT-PlaGe platform (https://get.genotoul.fr/) using the Illumina Hiseq3000 sequencer.

Another banana plant material was obtained either from CRB Plantes Tropicales (Guadeloupe, French West Indies, http://crb-tropicaux.com/Portail) or from the Bioversity International Musa Germplasm Transit Centre (Ruas et al., 2017) (Supplementary data Table S1).

A total of 123 accessions were sequenced to obtain standard Illumina 2 × 150 paired-end reads using the HiSeq4000 platform at Genoscope (http://www.genoscope.cns.fr).

For 11 of these accessions, 5 kb insert mate-pair libraries were constructed and sequenced using the Illumina Hiseq2500 platform at Genoscope (http://www.genoscope.cns.fr). This data set was supplemented by Illumina 5 kb mate-pair sequencing data generated by Rouard et al. (2018) for three accessions (‘Banksi’, ‘Maia’Oa’ and ‘Calcutta 4’) and deposited in the National Center for Biotechnology Information (NCBI) Sequence Read Archive (SRA) under run IDs SRR7013759, SRR7013765 and SRR7013755. The assembly of the *M. acuminata* ssp. *banksii* accession ‘Banksi’ published by these authors, as well as PacBio reads related to this project (SRA ID SRR7013757), were also used.

Finally, ‘Calcutta 4’ and ‘Maia’Oa’ accessions were sequenced with a MiniION nanopore sequencer from Oxford Nanopore Technologies (Jain et al., 2016). As described by Belser et al. (2018), a 30× sub-set of the longest nanopore reads was extracted from the total read set. These reads were then assembled using the Smartdenovo assembler (Jue Ruan, https://github.com/ruanjue/smartdenovo, git-commit 3d9c22e) with –k 17, as advised by the developer for larger genomes, and –c 1 to generate a consensus sequence.

**SNP marker segregation analysis**

Raw GBS sequencing data from the self-progeny were demultiplexed using GBXS version 1.2 (Herten et al., 2015) and adaptors were removed with cutadapt (Martin, 2011). Variant calling was processed as described by Garsmeur et al. (2018), using the VcfHunter package (https://github.com/SouthGreenPlatform/VcfHunter). Mapping was performed on
the *M. acuminata* reference sequence version 2 (Martin et al., 2016). Sites with read depths of <10 and >1000 were excluded. Sites with a minor allele frequency of <5% were considered homozygous. Sites with an alternate allele frequency of >15% supported by at least three reads were considered heterozygous. Other sites were converted into missing data. Single nucleotide polymorphism (SNP) markers were then filtered out based on their segregation ratio in the mapping population: a P-value threshold of 4e-06 was applied with a χ² test to compare the observed marker segregation with the expected marker segregation (1:2:1 with a self-population). SNP markers with >2.5% missing data and individuals with >1% missing data were removed from the SNP data set. Finally, 67 individuals were kept and 5281 SNP markers were selected to build the genetic map.

**Five kilobase discordant mate-pair read analysis**

To refine the location of the rearrangement breakpoints and to characterize the chromosome structures of 14 accessions, large insert mate-pair reads from the 14 mate-pair sequenced accessions were aligned to the *M. acuminata* ‘DH-Pahang’ reference genome sequence (version 2) available on the Banana Genome Hub (Droc et al., 2013). They were analysed to identify discordant read clusters according to the methodology described in Martin et al. (2017), using Scaffremodler tools (Martin et al., 2016) available on the South Green platform (Southgreen Collaborators, 2016). Discordant read clusters were viewed using CIRCOS software (Krzywinski et al., 2009).

**Alignment of translocation breakpoints between ‘DH-Pahang’ and ‘Calcutta 4’**

To precisely compare the rearrangement breakpoints between ‘DH-Pahang’ and ‘Calcutta’, the four genomic regions of the ‘DH-Pahang’ reference genome (version 2) corresponding to translocation breakpoint regions (chromosome 1 between 8.23 and 8.27 Mb, chromosome 2 between 29.26 and 29.28 Mb, chromosome 8 between 37.715 and 37.735 Mb and chromosome 9 between 11.57 and 12.61 Mb) were aligned to the ‘Calcutta 4’ preliminary assembly using blastn (BLAST+ 2.6.0; Camacho et al., 2009) with an e-value threshold of 1e-20 and without masking low-complexity regions. Then comparisons between sequences were performed using Gepard (Krumsieck et al., 2007) (Supplementary data Table S2).

**Signature segment junction detection**

In order to characterize the chromosome structure of the 123 studied *Musa* accessions, paired reads from 123 accessions were aligned to the complete *M. acuminata* ‘DH-Pahang’ reference genome, the ‘Calcutta 4’ assembly, the ‘Maia’Oa’ assembly and the ‘Banksii’ corrected assembly using bowtie2 in very sensitive mode (see next section). Pairs properly mapped with reads on either side of a signature segment junction (SSJ; i.e. the junction between two genomic segments that is specific to one of the chromosome structures; Supplementary data Fig. S1) in a flanking window of 1000 bp around the SSJ were counted.

Local reassembly of the chromosome 8 translocation breakpoint in ‘Maia’Oa’ and ‘Banksii’ accessions

To precisely characterize the positions of the SSJs relative to the breakpoint region of chromosome 8 in two accessions representative of *zebrina* and *banksii* subspecies, long reads from ‘Maia’Oa’ and ‘Banksii’ were compared with the *M. acuminata* ‘DH-Pahang’ reference chromosome 8 breakpoint region. Raw long reads from ‘Maia’Oa’ and ‘Banksii’ accessions were corrected using the correct option of Canu 1.6 (Koren et al., 2017) with default parameters. Corrected reads were aligned to the *M. acuminata* ‘DH-Pahang’ reference genome version 2 using Graphmap (Sović et al., 2016) with default parameters. For each accession, the longest read overlapping the two SSJs of *M. acuminata* ‘DH-Pahang’ reference chromosome 8 was kept. Selected long reads were corrected by aligning Illumina short reads from their respective accessions with bwa mem (Li and Durbin, 2009) with default parameters. Consensus between short reads was calculated with bcftools (Li, 2011).

The resulting consensus sequences were compared with the 37.718–37.732 Mb region of *M. acuminata* ‘DH-Pahang’ reference chromosome 8 using Gepard. Then we compared the ‘Maia’Oa’ consensus sequences of the chromosome 8 breakpoint with the ‘Maia’Oa’ scaffolds and the ‘Banksii’ consensus sequences of the chromosome 8 breakpoint with the ‘Banksii’ scaffolds using blastn, with an e-value threshold of 1e-20, while not masking low-complexity regions to confirm that the region has been correctly assembled. An inconsistency between the ‘Banksii’ corrected long read and its assembly was noticed, probably due to a short read assembly error. The genomic region in the original assembly was thus replaced by the new consensus sequence. Finally, the corresponding regions of the ‘Banksii’ and ‘Maia’Oa’ assembly were aligned and compared with the 1000 bp flanking window around the two *M. acuminata* ‘DH-Pahang’ reference chromosome 8 SSJs.

**Factorial analysis using SNP data**

To investigate the distribution of the translocated chromosomes in *M. acuminata*, a factorial analysis was performed. Paired-end reads (2 × 150) Illumina sequencing data from the 83 *M. acuminata* diploid accession studied were used to produce a genotype call for each accession using vcfHunter tools (Garsmeur et al., 2018; https://github.com/SouthGreenPlatform/VcfHunter). The process_reseq_1.0.py and VcfPrefilter.1.0.py programs were used to (1) align Illumina reads along the *M. acuminata* ‘DH-Pahang’ reference genome sequence (version 2) (Martin et al., 2016) using Burrows–Wheeler Alignment version 0.7.15; (2) remove duplicates using the MarkDuplicates option of Picard Tools (version 2.7) (http://broadinstitute.github.io/picard/); (3) locally realign reads around indels using the IndelRealigner tool of the GATK software package (version 3.6) (McKenna et al., 2010); (4) count all mapping bases that had a mapping quality ≥10 with the bam-readcount program (https://github.com/genome/bam-readcount); and (5) call a genotype based on the maximum likelihood of the genotype according to a binomial distribution assuming a sequencing error rate of 0.005. The variant calling file was formatted in VCF format. The VCF file was then filtered using the vcfFilter.1.0.py program with the following options: a minimal coverage by
accession of 10 (–MinCov 10), a maximal coverage by accession of 119 (–MaxCov 119), a minimal relative allele frequency by accession of 0.1 (–MinFreq 0.1), a minimal absolute allele frequency by accession of 3 (–MinAl 3), no missing genotypes in a line allowed (–nMiss 0), filtering out indels (–RmType INDELS) and non-diallelic sites (–RmAlAlt 1:3:4:5). A sub-set of 3092 polymorphous SNPs dispersed along the 11 chromosomes of the reference sequence was used to calculate a dissimilarity matrix using vcf2dis.1.0.py script. The dissimilarity index between two accessions was calculated from the VCF file as the proportion of unmatching alleles between two accessions. The dissimilarity matrix was used to perform a factorial analysis using R version 3.2.4 software (http://www.r-project.org). Since the cultivated accessions originated from the wild banana gene pool, the factorial analysis was performed with the 32 wild accessions. The 51 cultivated accessions were then projected along the synthetic axes.

RESULTS

Genetic evidence of two large reciprocal translocations in the ‘Calcutta 4’ accession

A self-progeny from the ‘Calcutta 4’ accession was genotyped by sequencing. A total of 5281 markers segregating in 67 individuals with a 1:2:1 ratio were selected. Pairwise associations between ‘Calcutta 4’ markers projected on the 11 M. acuminata reference chromosome sequence showed, for most markers physically close on the reference sequence, strong genetic linkage, as expected (Supplementary data Fig. S2A, B). However, a complete break in genetic linkage was observed within a few chromosomes. Linkage breaks were observed on chromosome 2 at position 29.2 Mb and on chromosome 8 at position 37.7 Mb (Fig. 1A). In addition, a small cluster of markers (four markers) from the distal region of reference chromosome 2 was found in ‘Calcutta 4’ genetically linked with chromosome 8 markers, whereas a distal part of reference chromosome 8 was found to be linked with chromosome 2 in ‘Calcutta 4’.

A similar situation was observed for chromosomes 1 and 9. Linkage breaks were observed on chromosomes 1 and 9 at 8.2 and 11.4 Mb, respectively (Fig. 1B). Markers surrounding these breaks linked, in ‘Calcutta 4’, a distal region of reference chromosome 1 to reference chromosome 9 and the rest of chromosome 1 to a distal part of reference chromosome 9.

These observations suggested the presence of distinct chromosome structures in ‘Calcutta 4’ as compared with the M. acuminata reference sequence. These structures resulted from two reciprocal translocations, one involving chromosomes 1 and 9 and the other involving chromosomes 2 and 8. The observed linkage breaks were complete, indicating that ‘Calcutta 4’ is structurally homozygous for these translocations.

Characterization of the translocation breakpoints

Translocation breakpoints were further characterized using 5 kb mate-pair reads from ‘Calcutta 4’ aligned to the ‘DH-Pahang’ reference sequence to search for discordant read alignments.

For chromosomes 2 and 8, two clusters of discordant reads were detected in the region of chromosomes 2 and 8 and found to be genetically linked in the self-progeny of ‘Calcutta 4’ (Fig. 2A). Using Scaffremodler, these discordant read clusters were identified as resulting from the presence of a reciprocal translocation in ‘Calcutta 4’ as compared with the reference sequence (Fig. 2B). Cluster 2 linked a distal region of 240 kb (c) of chromosome 2 to 45 Mb of chromosome 8 (d), resulting in a distinct chromosome structure hereafter referred to as 8T2 (Fig. 2B). Cluster 1 linked a distal region of 7.2 Mb from chromosome 8 (f) to 29.3 Mb of chromosome 2 (a), resulting in a distinct chromosome structure hereafter referred to as 2T8 (Fig. 2B). On reference chromosomes 2 and 8, the two discordant read clusters are separated by small chromosome segments of 3 kb (e) and 1.2 kb (b), respectively, that were not covered by any read sequences in ‘Calcutta 4’, thus suggesting their absence in this accession (Fig. 2A). No discordant reads overlapped the breakpoint regions, thus indicating that ‘Calcutta 4’ is homozygous for this translocation.

For chromosomes 1 and 9, the Scaffremodler program could not automatically interpret the discordant read cluster pattern. Therefore, we manually explored discordant read clusters linking those chromosomes and found a complex pattern of interchromosomal and intrachromosomal discordant read clusters (Fig. 2C). Discordant read cluster 3 and discordant reads along the k2 segment indicated the deletion of this segment in one chromosome. Discordant read cluster 1 linked the k1–k2 segment to the h segment, resulting in k1–k2–h and k1–k2–k2–l chromosome fragments. Finally, cluster 2 linking the h fragment to the k2 fragment reduced possible combinations to reconstruct the chromosome regions, without missing any segment, to a g–h–k1–k2–l structure for one chromosome and a j–k2–h–k1–i structure for the other. These chromosome structures corresponded to a reciprocal translocation that occurred in two distinct chromosomes. The first one, hereafter referred to as 1T9, linked a 8.24 Mb distal region of chromosome 1 (g) with 29.7 Mb of chromosome 9 (l). The second one, hereafter referred to as 9T1, linked an 11.6 Mb distal region of chromosome 9 (j), with 20.8 Mb of chromosome 1 (i) (Fig. 2D).

Fig. 1. Genetic linkage between SNP markers in the ‘Calcutta 4’ self-progeny projected on M. acuminata reference chromosomes 2 and 8 (A) and 1 and 9 (B). Each dot represents linkage between two markers. Linkage intensity is represented by a warm–cool colour gradient from dark red (strong) to blue (weak).
Refining the translocation breakpoints in ‘Calcutta 4’

A ‘Calcutta 4’ preliminary assembly was compared with the ‘DH-Pahang’ M. acuminata reference sequence to identify ‘Calcutta 4’ scaffolds overlapping the translocation breakpoints. Two large scaffolds were identified for the 2/8 translocation. One scaffold (2.54 Mb long) contained the 2T8 breakpoint with a segment that aligned to reference chromosome 2 (a) and a segment that aligned to reference chromosome 8 (f) separated by a 600 bp segment (x) with no similarity to the corresponding region in reference chromosomes 2 (b) or 8 (e) (Fig. 3A). The second scaffold (3.15 Mb long) contained the 8T2 breakpoint, with a segment that aligned to reference chromosome 8 (d) and another that aligned to reference chromosome 2 (c) separated by a 1.2 kb segment (y), with no similarity to the corresponding region in reference chromosomes 2 (b) or 8 (e) (Fig. 3A).

For the 1/9 translocation, two scaffolds were also identified. One scaffold (6.9 Mb long) contained the 1T9 breakpoint, with segments that aligned to reference chromosome 1 (g and h) and segments that aligned to reference chromosome 9 (k₁, k₂, k₃, and l) (Fig. 3B). The second scaffold (5.7 Mb long) contained the 9T1 breakpoint, with segments that aligned to reference chromosome 9 (j, k₁, and k₃) and segments that aligned to chromosome 1 (h and i).

These data validated the proposed chromosome structures based on discordant read analysis and revealed the presence, at the breakpoints, of chromosomes 2T8 and 8T2 of segments (x and y) not present in the reference sequence.

Distribution of the two translocations in Musa germplasm

Five kilobase mate-pair discordant read analysis. To analyse the distribution of the two translocations in Musa germplasm, we first used 5 kb mate-pair reads available from 13 M. acuminata accessions (five wild seedy accessions and eight hybrid cultivated accessions; Supplementary data Table S1). Paired reads
were aligned to the ‘DH-Pahang’ reference sequence, and discordant clusters identified in ‘Calcutta 4’ as corresponding to the 2T8, 8T2, 1T9 and 9T1 chromosome structures were searched (Supplementary data Fig. S3A, B).

Among the 13 M. acuminata accessions, 2T8 and 8T2 chromosome structures were detected in one accession, i.e. the ‘Manang’ diploid cultivar. In this accession, concordant mate-pair reads spanning the breakpoints were also observed, revealing that this accession is structurally heterozygous, with one set of reference chromosomes 2 and 8 and one set of chromosome structures 2T8 and 8T2. All other accessions were found to be homozygous with two sets of reference chromosomes 2 and 8 (Supplementary data Fig. S3A).

No discordant clusters corresponding to chromosomes 1T9 and 9T1 were observed in the 13 accessions surveyed, and all accessions showed concordant mate-pair reads corresponding to reference chromosomes 1 and 9. These accessions were thus homozygous for reference chromosomes 1 and 9 (Supplementary data Fig. S3B).

Signature segment junctions searched in whole-genome sequencing (WGS) data. To further characterize the distribution of 2T8, 8T2, 1T9 and 9T1 chromosome structures in Musa diversity, we used the Illumina paired-end sequence generated on 123 accessions. These accessions included 97 M. acuminata accessions with 32 diploid wild seedy accessions and 65 cultivated intersubspecific hybrids (51 diploids and 14 triploids), four diploid accessions from other species (two M. balbisiana and two M. schizocarpa) and 22 interspecific cultivated hybrids involving M. acuminata (four diploids and 18 triploids) (Supplementary data Table S1).

In the distinct chromosomal structures, distinct chromosomal segments were juxtaposed, so a junction between chromosome segments could be specific to one chromosomal structure and constitute a signature of this structure (hereafter referred to as an SSJ). Such SSJs were searched at the 2/8 and 1/9 translocation breakpoints in ‘Calcutta 4’ and in the corresponding region of the ‘DH-Pahang’ reference genome sequence.

Eight SSJs could be identified for translocation 2/8, with two per chromosome structure: a–b and b–c segment junctions for chromosome 2, d–e and e–f segment junctions for chromosome 8, a–x and x–f segment junctions for chromosome 2T8, and d–y and y–c segment junctions for chromosome 8T2 (Fig. 2; Supplementary data Table S3).

In a first round of analysis, for many accessions we detected SSJs of reference chromosome 2 but did not detect the signatures of reference chromosome 8. We thus compared the d–e–f breakpoint region of ‘DH-Pahang’ with the corresponding region of two additional accessions, for which long read sequences and sequence scaffolds were available (accession ‘Banksi’ from ssp. banksii and accession ‘Maia’Oa’ from ssp. zebrina). The comparison revealed small structural variations in ‘Maia’Oa’ and ‘Banksi’ compared with ‘DH-Pahang’ (Fig. 4). These structural variations, when present in the tested accession, resulted in paired-end reads that could not map on the sequence used as reference for the alignment (here ‘DH-Pahang’), which may explain why SSJs of reference chromosome 8 could not be detected in some accessions. To increase the chance of detecting SSJs corresponding to chromosome 8, we accurately identified their positions on the ‘Maia’Oa’ preliminary assembly and the ‘Banksi’ corrected assembly, and aligned paired-end data from the 123 accessions using these assemblies.

Fig. 3. Dot-plot representation of alignments between ‘Calcutta 4’ scaffolds and the M. acuminata reference chromosome sequence at translocation breakpoints. (A) Translocation 2/8: ‘Calcutta 4’ for breakpoint regions of chromosomes 2T8 (scaffold utg154) and 8T2 (scaffold utg170) are represented on the horizontal axis. The corresponding regions in the M. acuminata reference genome are represented on the vertical axis. Each compared region is 6 kb long. A small deletion in segment c of chromosome 2 can be noticed, which corresponds to part of the 5 kb deletion observed in Fig. 2A. (B) Translocation 1/9: ‘Calcutta 4’ for breakpoint regions of chromosomes 1T9 (scaffold utg195) and 9T1 (scaffold utg94) are represented on the horizontal axis. The corresponding regions in the M. acuminata reference genome are represented on the vertical axis. Each compared region is 70 kb long. The colour coding is the same as in Fig. 2.
as additional references (Supplementary data Table S1) (see the Materials and Method for ‘Banksii’ assembly correction).

The expected SSJs were detected for the four accessions used as sequence template to align the paired reads (‘DH-Pahang’, ‘Maia’Oa’, ‘Banksii’ and ‘Calcutta 4’). SSJs of chromosome 2T8 and of chromosome 8T2 were detected as expected in ‘Calcutta 4’. SSJs of chromosome 2 were detected in ‘Pahang’, ‘Maia’Oa’ and ‘Banksii’. However, SSJs of reference chromosome 8 were detected in paired-end reads from ‘Pahang’, ‘Maia’Oa’ or ‘Banksii’ only when alignment was performed on scaffolds from the same accession. This confirmed that small structural variations within accessions can hamper proper detection of SSJs and thus that only a positive result for the presence of an SSJ can be directly interpreted with confidence. However, since ‘DH-Pahang’, ‘Banksii’ and ‘Maia’Oa’ share the same macrostructure for chromosome 8 (Fig. 4A), the detection of SSJs in any of these three accessions was hereafter interpreted as indicating the presence of the chromosome 8 structure.

Among the 123 accessions tested, only seven displayed signatures of chromosome 2T8 and chromosome 8T2. Five wild M. accesses (‘Long Tavoy’, ‘Pisang Prentel’, ‘Calcutta 4’, ‘Khue Phrae’ and ‘Pa Rayong’) displayed the four signatures of chromosome 2T8 and chromosome 8T2, but no SSJs of reference chromosomes 2 and 8. Moreover, two M. acuminata cultivated accessions displayed some signatures of chromosomes 2T8 and 8T2. Accession ‘Hom’ had four SSJs of reference
chromosomes 2 and 8 and three signatures of chromosomes 2T8 and 8T2, and was thus classified as structurally heterozygous with chromosomes 2, 8, 2T8 and 8T2 structures. The ‘Manang’ accession had three SSJs for reference chromosomes 2 and 8 and two SSJs for chromosome 2T8, thus supporting its structurally heterozygous classification based on the 5 kb mate-pair discordant read analysis.

Among the remaining 90 *M. acuminata* accessions, 82 displayed the four SSJs for reference chromosomes 2 and 8 and eight accessions had at least one signature for reference chromosome 2 and one SSJ for reference chromosome 8 (Supplementary data Table S1). Two other *M. acuminata* accessions (‘Pa Patthalong’ and ‘Pisang Serun 400’) had SSJs only for reference chromosome 2.

Among the four accessions representative of other *Musa* species, one *M. schizocarpa* accession (ITC0926) had the four signatures of chromosomes 2 and 8. The other *M. schizocarpa* accession (ITC0599) and both *M. balbisiana* accessions only displayed the two SSJs of reference chromosome 2.

Finally, the 22 interspecific hybrid accessions showed 3–4 SSJs of chromosomes 2 and 8, and were thus identified as having at least one copy of reference chromosomes 2 and 8.

Regarding the 1/9 translocation, the intricate duplications at translocation breakpoints complicated the identification of SSJs specific to the four chromosome structures. We identified two SSJs for chromosome 1T9 that corresponded to k₁–k₃ and k₄–h segment junctions, and one signature position for chromosome 9T1 that corresponded to the h–k₄ segment junction (Supplementary data Table S4). No segment junctions were specific to reference chromosomes 1 and 9, so no SSJs could be used to reveal these chromosome structures.

Within the 123 accessions tested, five accessions displayed one SSJ for chromosome 1T9 (SSJ k₃–k₄) (‘Calcutta 4’, ‘Pisang Prentel’, ‘Long Tavoy’, ‘Khae Phrae’ and ‘Pa Rayong’). In addition, ‘Calcutta 4’ showed the SSJ of chromosome 9T1 (Supplementary data Table S1). Among them, ‘Calcutta 4’ proved to be homozygous for chromosome structures 1T9 and 9T1 based on the segregation analysis findings.

**Factorial analysis with *Musa acuminata* diploid accessions.**

A factorial analysis was performed on 3092 SNPs identified from Illumina sequences of the 83 diploid wild and cultivated *M. acuminata* accessions (Fig. 5). The first axis separated ssp. *burmannica*, *burmannicoides* and *siamea* accessions from the others, and explained 27% of the SNP variance. The second axis separated ssp. *zebrina* and *banksii*, and explained 21% of the data variance. The third axis explained an additional 16% of the data variance and separated ssp. *malaccensis* from the other accessions (Supplementary data Fig S4).

The five wild accessions displaying only chromosomes 2T8 and 8T2 were confined in one genetic group, i.e. the *burmannica* group, which includes accessions for ssp. *burmannica*, *burmannicoides* and *siamea*. Those accessions were also those in which the translocation between chromosomes 1 and 9 was detected. Heterozygous accessions for chromosomes 2, 8, 2T8 and 8T2 (‘Hom’ and ‘Manang’) corresponded to cultivars and were located between the *burmannica* group and the rest of the accessions. ‘Hom’ was equidistant and isolated between both groups, while ‘Manang’ was closer to the non-*burmannica* group.

**DISCUSSION**

We identified two reciprocal translocations in the *Musa acuminata* ssp. *burmannicoides* accession ‘Calcutta 4’ compared with the reference genome sequence, i.e. *M. acuminata* ssp. *malaccensis* ‘DH-Pahang’. One reciprocal translocation involved chromosomes 2 and 8, resulting in chromosomes 2T8 and 8T2. The other one involved chromosomes 1 and 9, resulting in chromosomes 1T9 and 9T1. ‘Calcutta 4’ was found to be homozygous for both translocations.

These translocated chromosome structures were first searched in 13 accessions using 5 kb mate-pair discordant read analysis. In addition, SSJs specific to the distinct chromosome structures were searched in 123 accessions representative of *Musa* diversity involved in cultivated banana for which paired-end sequence data were available.

We found that these methods, particularly SSJ detection, were sensitive to the presence of polymorphism (SNPs and INDELs) and repeated sequences. Thus, only a positive result for the presence of an SSJ could be directly interpreted with confidence. However, in diploid accessions, we expected that an accession in which we detected chromosomes 1T9, 2T8, 2 or 1 also had the complementary chromosome structures 9T1, 8T2, 8 or 9, respectively. Otherwise, this accession would miss a chromosome segment, i.e. a configuration that would most probably be lethal (particularly during the haploid gametic stage). This assumption was confirmed in all cases where it could be verified. This was the case for ‘Pisang Madu’, ‘Manang’ and ‘Malaccensis Nain’ accessions for which chromosome 8 was detected by discordant 5 kb mate-pair read analysis, while not or partially being detected with SSJs.

Among the 36 wild accessions analysed, only five accessions were identified as having the 2T8 and 8T2 structure, most probably in the homozygous state. The same five accessions were the only ones identified as having at least one copy of the 1T9 and 9T1 chromosome structure. Chromosome 9T1 could not be detected in four of them. However, considering that the absence of the complementary structure would probably be lethal, these accessions were assumed to bear the 9T1 chromosomal structure. One of these accessions, ‘Calcutta 4’, proved to be homozygous for both translocations based on segregation analysis and on 5 kb mate-pair discordant read analysis. These five accessions corresponded to all wild accessions tested from ssp. *burmannicoides* (‘Calcutta 4’), *siamea* (‘Pa Rayong’ and ‘Khae Phrae’) and *burmannica* (‘Long Tavoy’ and ‘Pisang Prentel’). Twenty-six wild *M. acuminata* accessions were identified as having the 2 and 8 chromosomal structures, most probably in the homozygous state. Among them, four accessions (‘Malaccensis Nain’, ‘Pahang’, ‘Borneo’ and ‘Maia’Oa’) were shown to be homozygous for these structures based on 5 kb mate-pair discordant read analysis. One last wild *M. acuminata* accession (‘Pisang Serun 400’) could not be structurally characterized in our study.

*Musa balbisiana* and *M. schizocarpa* were only partially characterized using SSJ analysis, but they were previously...
reported as being homozygous for reference chromosomes 2 and 8 at the 2/8 breakpoint and for chromosomes 1 and 9 at the 1/9 breakpoint (Belsel et al., 2018; Baurens et al., 2019).

Among the 87 cultivated accessions tested, only two accessions (‘Manang’ and ‘Hom’) were identified as having the 2/8 translocated structure, both in the heterozygous state. A total of 84 cultivated accessions were identified as having the 2 and 8 chromosome structure, most probably in the homozygous state. Among them, seven accessions (‘Akondro Main’, ‘Pisang Madu’, ‘Galeo’, ‘Pisang Lilin’, ‘Paka’, ‘Grande Naine’ and ‘IDN 110’) proved to be homozygous for these structures based on 5 kb mate-pair discordant read analysis. No structural characterization could be obtained for the diploid cultivated accession (‘Sinwobogi’).

Based on chromosomal pairing irregularities at meiosis in intersubspecific hybrids, Shepherd (1999) suggested the existence of seven M. acuminata translocation groups in which accessions were structurally homogeneous. The ‘Standard’ (ST) group is the largest one, consisting of ssp. banksii, microcarpa and malaccensis accessions. The other groups were named according to the geographic origins of their representatives. The ‘Northern Malayan’ (NM) group includes some malaccensis accessions, the ‘Northern 1’ group includes some burmannicoides and siamea accessions, the ‘Northern 2’ group includes other burmannica and siamea accessions, the ‘Malayan Highland’ group is based on one truncata accession and the Javanese group is based on two zebrina accessions, whereas the ‘East African’ group is based on one unclassified accession. Martin et al. (2017) identified a reciprocal translocation involving chromosomes 1 and 4, compared with the reference genome sequence, in several malaccensis accessions, and suggested that it corresponds to the NM group, while the reference genome sequence corresponds to the ST group. The Calcutta 4 accession considered in this study was used by Shepherd (1999) as a representative of the ‘Northern 1’ group. The ‘Northern 1’ group was suggested to differ from the ST group by two translocations. Our results showed that the two reciprocal translocations between chromosomes 2 and 8 and between chromosomes 1 and 9 corresponded to this ‘Northern 1’ group defined by Shepherd (1999).

Burmannica, siamea and burmannicoides subspecies were originally distinguished based on morphological characters and the geographical distribution (Simmonds, 1962; Perrier et al., 2009). Recent diversity studies based on diversity array technology (DArT) and simple sequence repeat (SSR)
The burmannica genetic group has been shown to constitute an interesting genetic reservoir of disease resistance: ‘Calcutta 4’ shows resistance to various pests and diseases such as nematodes or black leaf streak disease, while ‘Long Tavoy’ and ‘Khao Phrae’ show resistance to Fusarium oxysporum f.sp. cubense race 4 and nematodes, respectively (Vuylsteke et al., 1992; Jones, 2000; Quénéhervé et al., 2009).

Our study detected only two cultivated accessions (‘Manang’ and ‘Hom’) among the 87 tested as being heterozygous for the 2/8 translocated structure, while none was detected for the 1/9 translocated structure. This supports the hypothesis that the burmannica group and supported the hypothesis that the Musa reference genome obtained with the malacensis accession ‘DH-Pahang’ represented the ST group of Shepherd (1999) and the ancestral structure.

Supplementary data are available online at https://academic.oup.com/aob and consist of the following. Figure S1: principle of signature segment junction detection. Figure S2: genetic marker statistics along the 11 Musa acuminata chromosomes. Figure S3: paired read mapping of 14 Musa accessions focused on the two reciprocal translocations detected in ‘Calcutta 4’. Figure S4: factorial analysis performed on 32 wild M. acuminata accessions with projection of 51 cultivated accessions. Table S1: accessions tested for their structure on chromosomes 2, 8, 1 and 9. Table S2: genomic co-ordinates of compared sequences. Table S3: genomic position of the SSJs for the translocation 2/8. Table S4: genomic position of the SSJs for the translocation 1/9.

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