Anchoring Linkage Groups of the Rosa Genetic Map to Physical Chromosomes with Tyramide-FISH and EST-SNP Markers

Ilya Kirov1,2,3, Katrijn Van Laere3, Jan De Riek3, Ellen De Keyser3, Nadine Van Roy4, Ludmila Khrustaleva1,2

1 Center of Molecular Biotechnology, Russian State Agrarian University - Moscow Timiryazev Agricultural Academy, Moscow, Russia, 2 Department of Genetics and Biotechnology, Russian State Agrarian University - Moscow Timiryazev Agricultural Academy, Moscow, Russia, 3 Institute for Agricultural and Fisheries Research (ILVO), Plant Sciences Unit, Applied Genetics and Breeding, Melle, Belgium, 4 Center of Medical Genetics, Faculty of Medicine and Health Sciences, Ghent University, Ghent, Belgium

Abstract

In order to anchor Rosa linkage groups to physical chromosomes, a combination of the Tyramide-FISH technology and the modern molecular marker system based on High Resolution Melting (HRM) is an efficient approach. Although, Tyramide-FISH is a very promising technique for the visualization of short DNA probes, it is very challenging for plant species with small chromosomes such as Rosa. In this study, we successfully applied the Tyramide-FISH technique for Rosa and compared different detection systems. An indirect detection system exploiting biotinylated tyramides was shown to be the most suitable technique for reliable signal detection. Three gene fragments with a size of 1100 pb–1700 bp (Phenylalanine Ammonia Lyase, Pyrroline-5-Carboxylate Synthase and Orsinol O-Methyl Transferase) have been physically mapped on chromosomes 7, 4 and 1, respectively, of Rosa wichurana. The signal frequency was between 25% and 40%. HRM markers of these 3 gene fragments were used to include the gene fragments on the existing genetic linkage map of Rosa wichurana. As a result, three linkage groups could be anchored to their physical chromosomes. The information was used to check for synteny between the Rosa chromosomes and Fragaria.

Introduction

Genome structure and function may be studied when comparing the genetic positions of genes with their physical locations on chromosomes. In former times, to assign linkage groups to physical chromosomes it was needed to create monosomic addition lines, nullisomic lines, chromosome substitution lines or translocation lines [1–3]. This is a very time consuming task. Nowadays, a more efficient approach exists by direct visualization of genetically mapped markers on chromosomes using fluorescent in situ hybridization (FISH) to locate large genomic clones (BAC, YAC, cosmids etc.) containing the markers. However, FISH with large genomic DNA fragments often results in many non-specific hybridizations due to the presence of huge amounts of repetitive DNA in plant genomes [4,5]. To overcome this problem, FISH using direct labeled individual genes can be applied [6–8]. This approach however still is very challenging for most ornamental species and in particular for woody species, such as Rosa.

The genus Rosa, a member of the Rosaceae, consists of approximately 200 species and 20000 cultivars, most of complex hybrid origin. The genus has a wide phenotypic variability and a high level of genetic heterozygosity [9]. Despite the crop’s long domestication history, intensive breeding and economic importance, relatively little is known about the genetics and cytogenetics of roses [10,11]. Nevertheless, several characteristics of rose make it a worthy candidate for a model system for genomic research in woody species [11].

Performing cytogenetic analyses for roses is difficult because of their genome size (the diploid genome size is 0.83 to 1.30 pg/2C; [12]) and very small chromosomes. The mitotic index is generally low in shoot and root tips, root development is weak and roots are thin in mature individuals for several Rosa species [13]. The basic chromosome number of roses is 7 [14,15] and ploidy levels range from diploid (2n = 2x = 14) to octoploid (2n = 8x = 56) [16]. A number of basic cytogenetic studies, including chromosome counts and karyotyping, have been done on roses [14–31]. A karyotype with indication of 45 S and 5 S rDNA sites was constructed for some wild species [24–27]. Repetitive sequences, such as 45 S and 5 S rDNA, are rather easy to map, compared to low-copy genes. Reports of physical mapping of low copy genes are found in several genera, such as tomato [32], rice [33], barley [34], wheat [35], sugar beet [36], Sorghum [37], maize [7], Populus trichocarpa [38] and safflower [39], among others. However, physical mapping of low-copy genes remains a problem in lots of other species and genera and also in Rosa. Moreover, in most reports showing conventional FISH results, the target DNA sequences were over 10 kb. Since EST-markers are good candidates to anchor linkage groups to physical chromosomes, lowering the
probe-size detection limit should be obtained. Significant improvements in detection limits have been reported, such as the use of a cooled-charge-coupled device (CCD) camera and primed in situ DNA labeling (reviewed by Figueroa and Bass [40]). An alternative FISH method used to detect very small probes is tyramide signal amplification (TSA-FISH), or Tyramide-FISH, a multi-step procedure involving (1) in situ hybridization with a labeled probe, (2) signal amplification by streptavidin-horseradish peroxidase (SA-HRP) and tyramides and (3) detection and imaging of the amplified signal [41]. This method was originally introduced by Bobrow et al. [42] for microplate immunosassays. Raap et al. [43] introduced the use of fluorescent tyramide conjugates as substrates for Horse Radish Peroxidase (HRP) into FISH technology. With Tyramide-FISH, the detection sensitivity can be increased up to 100 times compared to the conventional FISH procedures [44]. Tyramide-FISH has been successfully used in human genetics for single-copy gene detection [41,45–52]. In plants, however, Tyramide-FISH has only been used in a few studies [53–56].

Molecular markers have been developed in roses to enhance breeding efficiency through the identification and characterization of genes controlling important traits [9,57,58]. Major efforts for the construction of genetic linkage maps in the Rosa genus have been concentrated at the diploid level [57,59–63]. Four mapping populations allowed the construction of an integrated consensus map consisting of about 600 markers distributed across 7 linkage groups, with an overall length of 530 cM [58]. Recently, interest in mapping at the tetraploid level has been renewed [64,65]. Some major rose traits have been located on the rose genetic maps, such as flower color and double corolla [59] and resistance to powdery mildew [61,62,63]. To date, no genome sequence is available for the Rosa genus that allows validation of the positions of markers located to linkage maps. But Rosa is well-supported by the closest sister taxon, which contains the genus Fragaria, and also shows sequence homology with Malus and Prunus [65–68]. Developing markers in EST fragments of genes can be based on this sequence homology with other Rosaceae. Although ESTs are widespread in the plant genome, the number of ESTs containing an SSR motif can be quite limited [69]. EST-SNPs have more potential as a functional marker. Due to the conserved nature of the coding sequence, these markers are also appropriate for the comparison of genetic maps between species [70,71]. High Resolution Melting (HRM) analysis is the method of choice for EST-SNP genotyping, because SNP sequence information is not a prerequisite [72]. HRM was originally introduced as a method for mutation scanning in human genetics [73] and has the ability to simultaneously detect and genotype DNA polymorphisms [74].

The use of HRM for EST-SNP marker development and consecutive mapping in plants has already been reported in several crops such as barley [72], alfalfa [75] and apple [76] but not yet in rose.

The combination of opportunities of Tyramide-FISH and the HRM molecular marker system may result in an effective integration of physical and genetic maps. The present study had two main aims: 1) to optimize the Tyramide-FISH technology for roses in order to cytogenetically map single-copy genes and 2) to connect their physical position with their genetic position on the linkage groups of Rosa wichurana (Moghaddam et al. 2012) using HRM technology.

**Materials and Methods**

**Plant Material**

The plant material used in this study was *Rosa wichurana*, Rosa ‘Yesterday’ and 90 F1 hybrids of Rosa ‘Yesterday’ x *Rosa wichurana*. Both parent plants and the hybrid progeny are diploid (2n = 2x = 14). The plants were own-rooted and grown in the field. For chromosome slide preparations, cuttings of *Rosa wichurana* were made. Rooted cuttings were transferred to terracotta stone pots and grown in the greenhouse without artificial light or temperature regulation. The conditions inside the greenhouse were thus dependent on the moderate climatic conditions typical for the East Flanders region of Belgium.

**Chromosome preparation**

Somatic metaphase chromosome spreads were prepared from shoot meristems collected and pretreated according to [13]. Briefly, young shoot meristems (2–3 mm) from which upper green leaves were removed, were collected in ice-cold 1 mM 8-hydroxyquinoline and 0.1% choline solution and incubated for 3.5 hours at room temperature in the dark. Afterwards, meristems were fixated in 3:1 ethanol/glacial acetic acid for 45–60 minutes and stored in 70% ethanol at ~20°C. Chromosome slide preparation was carried out according to the spreading protocol of Pijnacker and Ferwerda [77] or to the “SteamDrop” method of Kirov et al. [78].

**Primer and probe design**

DNA of *Rosa wichurana*, Rosa ‘Yesterday’ and their hybrids was extracted from young leaves using the Qiagen DNeasy Plant Mini Kit (Chatworth, CA). The genes *PAL*, *P5CS* and *OOMT* were isolated according to Razavi et al. [79] starting from ESTs available in the Genome Database of Rosaceae [80]. These genes are known to be involved in abiotic stress response (*Phytoanenine Ammonia Lyase* (*PAL*) and *Pyrophosphate-Carboxylate Synthase* (*P5CS*), [81,82]) and rose scent production (*Orcinol O-Methyl Transferase* (*OOMT*), [83]), which are important traits for roses.

To have good probes to use in Tyramide-FISH, we designed primers in order to obtain PCR fragments of about 1500 bp (see Table 1). Plasmid DNA of the cloned gene fragments was labeled using the Biotin Nick Translation Mix (Roche) according to the manufacturer’s instructions. As a control, the pTA71 plasmid (containing a 9 kb fragment of 45 S rDNA, [84]) was labeled with biotin.

To generate EST-SNPs for HRM, we searched for SNPs between *Rosa wichurana* and Rosa ‘Yesterday’ in the sequences of the cloned genes *PAL*, *P5CS* and *OOMT*. Primers flanking a single SNP were developed for amplification of the EST-SNPs (Table 2). Primers were tested on the parents and 5 siblings of the mapping population *Rosa ‘Yesterday’* x *Rosa wichurana*. Good primers were then applied to the entire mapping population.

**Tyramide-FISH optimization**

Probe hybridization was performed according to Khurstaleva and Kik [53] with minor modifications. Slides were fixed in 4% buffered paraformaldehyde in 1xPBS (10xPBS: 1.3 M NaCl, 70 mM Na2HPO4, 30 mM NaH2PO4, pH 7.5) for 8 min before the RNase treatment and 10 min before denaturation. Inactivation of endogenous peroxidases was done by incubating the slides in 0.01 M HCl for 8 min. Pepsin treatment was performed during 30 sec at room temperature. The hybridization mixture contained 50% (v/v) deionized formamide, 10% (v/v) dextran sulphate, 2xSSC, 0.25% sodium dodecyl sulphate and 2.00 ng/μl probe DNA. The hybridization mix was denatured at 80°C for 5 min, subsequently placed on ice for 5 min, and added to the chromosome slides. Slides were then denatured for 5 min at 80°C and hybridization was carried out at 37°C overnight. A 82% stringency washing was attained by washing the slides twice in 2xSSC for 5 min at 37°C, twice in 25% (v/v) formamide in
Table 1. Overview of the primers used to isolate the genes PAL (Phenylalanine Ammonia Lyase), OOMT (Orcinol O-Methyl Transferase) and P5CS (Pyrroline-5-Carboxylate Synthase).

<table>
<thead>
<tr>
<th>Gene</th>
<th>Primers (5'-3')</th>
<th>Tm (°C)</th>
<th>Source sequence</th>
<th>Amplicon (bp)</th>
</tr>
</thead>
<tbody>
<tr>
<td>PAL</td>
<td>ACCACTGGTATGGTGACCCGATCCCTAAAATCCCAA</td>
<td>59.9</td>
<td>Prunus persica</td>
<td>1700</td>
</tr>
<tr>
<td>OOMT</td>
<td>TGCACTACCAACTCTACGCCAATGCGAACATTTGGCCTT</td>
<td>59.9</td>
<td>Rosa chinensis 'Old Blush'</td>
<td>1100</td>
</tr>
<tr>
<td>P5CS</td>
<td>GCTGGCATCCCTGTTGATATCTTCGGATCGCTAATGAAGC</td>
<td>59.9</td>
<td>Prunus persica</td>
<td>1700</td>
</tr>
</tbody>
</table>

The length of the obtained amplicons is indicated as well as the Tm and source sequence.

doi:10.1371/journal.pone.0095793.t001

Results

Tyramide-FISH optimization

Using the direct detection system to detect the single-copy gene PAL, many nonspecific signals were observed, although for the control probe pTa71, 45 S rDNA sites could be detected (Fig. 1D). Therefore, the indirect detection and indirect detection with two rounds of amplification systems were optimized for single-copy gene detection. In the indirect detection system, PAL signals became visible in 30–40% of the observed metaphases. Because indirect detection is more time consuming than indirect detection, we used indirect detection for the subsequent physical mapping of the genes.

Anchoring Rosa Linkage Groups to Chromosomes

Karyotype Analysis

A karyotype was constructed after measurement of five well-mapped chromosomes using Micromeasure version 3.3.

Genotyping and linkage mapping of EST-SNP markers

HRM was performed as described in [87] but using only the 0.8x LightCycler 480 High Resolution Melting Master Mix (Roche). LightCycler 480 Gene Scanning software was used for genotyping. Three EST-SNPs for the candidate genes PAL, OOMT and P5CS were amplified in the mapping population. A scoring matrix was calculated in Microsoft Excel. Segregation patterns of the new marker sets based on the HRM profiles for the offspring plants of the mapping population were added to the already existing mapping data described in Moghaddam et al. [63]. Estimation of the linkage groups and regression mapping was performed as described in [88] using JoinMap 4.0.

For probe detection, three tyramide amplification systems were used: direct detection (modified from Schriml et al. [47] and Khrustaleva and Kik [53]), indirect detection (modified from Schriml et al. [47] and Perez et al. [32]) and indirect detection with two rounds of amplification. The incubation time with the tyramide solution vary from 5 to 10 min. In the direct detection system, tyramide-FTIC (Tyr-FTIC) or tyramide-Cy3 (Tyr-Cy3) was used in dilutions 1:50. In the indirect detection system, biotinylated tyramides (Tyr-Bio, PerkinElmer, Belgium) were used in the dilutions 1:25 and 1:50 and the antibodies (Streptavidin-Cy3, or Streptavidin-Cy5) were 1:100 and 1:300 diluted. The concentration of Tyr-Bio and Streptavidin-HRP (SA-HRP) antibodies used in the first round of the indirect detection with two rounds of amplification systems were the same as in the indirect detection system. In the second round of amplification SA-HRP was diluted 1:300 or 1:200 and Tyr-Cy3 was used in dilutions 1:100, 1:300, 1:500 or 1:1000.

Images were taken using a fluorescence microscope Zeiss AxioImager M2 (400x and 1000x magnification) equipped with an AxioCam MRm camera and using Zen software (Zeiss, Zaventem, Belgium). Calculation of chromosome size, centromere index and signal positions was performed using the freeware computer application Micromeasure software, version 3.3.

Tyramide-FISH experiments, a BLASTN search against distinct sequences of the strawberry genes was performed. As a query, the parts of the Rosa wichuraiana sequences of the OOMT, PAL and P5CS genes corresponding to the gene fragments used in the Tyramide-FISH were used.

Determination of the position of OOMT, PAL and P5CS genes on Fragaria vesca pseudo-chromosomes

Positions of the PAL and P5CS genes on the pseudochromosomes of Fragaria vesca (FrasVHSaHawaii_1.0) were determined in the gene database at NCBI. Localization of the OOMT gene was identified by an alignment of a Rosa chinensis OOMT1 partial gene sequence (AJ786302) with each of the F. vesca pseudochromosome (CM001053.1-CM001059.1) using the BLASTN tool. The E-value threshold was fixed at e-15. To identify the closest strawberry orthologous to the Rosa wichuraiana genes used in our Tyramide-FISH experiments, a BLASTN search against distinct copies of the strawberry genes was performed. As a query, the parts of the Rosa wichuraiana sequences of the OOMT, PAL and P5CS genes were used in the Tyramide-FISH were used.

For probe detection, three tyramide amplification systems were used: direct detection (modified from Schriml et al. [47] and Khrustaleva and Kik [53]), indirect detection (modified from Schriml et al. [47] and Perez et al. [32]) and indirect detection with two rounds of amplification. The incubation time with the tyramide solution vary from 5 to 10 min. In the direct detection system, tyramide-FTIC (Tyr-FTIC) or tyramide-Cy3 (Tyr-Cy3) was used in dilutions 1:50. In the indirect detection system, biotinylated tyramides (Tyr-Bio, PerkinElmer, Belgium) were used in the dilutions 1:25 and 1:50 and the antibodies (Streptavidin-Cy3, or Streptavidin-Cy5) were 1:100 and 1:300 diluted. The concentration of Tyr-Bio and Streptavidin-HRP (SA-HRP) antibodies used in the first round of the indirect detection with two rounds of amplification systems were the same as in the indirect detection system. In the second round of amplification SA-HRP was diluted 1:300 or 1:200 and Tyr-Cy3 was used in dilutions 1:100, 1:300, 1:500 or 1:1000.

Images were taken using a fluorescence microscope Zeiss AxioImager M2 (400x and 1000x magnification) equipped with an AxioCam MRm camera and using Zen software (Zeiss, Zaventem, Belgium). Calculation of chromosome size, centromere index and signal positions was performed using the freeware computer application Micromeasure software, version 3.3.
Physical mapping of genes using ID

To be able to link the Tyramide-FISH signals to a certain chromosome and to identify the NOR-bearing chromosome, the karyotype of *Rosa wichurana* was constructed for the first time (Table 3; Fig. 2). The karyotype contains 7 pairs of chromosomes with the chromosome formula 5M+1SM+1ST. The length of the chromosomes ranges between 2.2 μm and 3.7 μm (Table 3). The smallest chromosome bears a NOR-satellite, as confirmed by Tyramide-FISH with 45 S rDNA (Fig. 1D). Chromosomes 1 and 7 can be easily distinguished based on their size and centromeric indexes. In addition, it is also possible to discern the only submetacentric chromosome 4. The condensation index of indexes. In addition, it is also possible to discern the only submetacentric chromosome 4. The condensation index of

Table 2. Overview of HRM primers for PAL (Phenylalanine Ammonia Lyase), OOMT (Orcinol O-Methyl Transferase) and P5CS (Pyrroline-5-Carboxylate Synthase).

<table>
<thead>
<tr>
<th>Gene</th>
<th>Primers (5'-3')</th>
<th>Amplicon (bp)</th>
<th>N° of introns</th>
<th>N° of SNP's</th>
</tr>
</thead>
<tbody>
<tr>
<td>PAL</td>
<td>TTTGAGGTTCAAGAGTTACC CCAAGAGCAGAAAAGCTCA</td>
<td>227</td>
<td>1</td>
<td>/</td>
</tr>
<tr>
<td>OOMT</td>
<td>GTTGAGGCGAGCTCTTCGT GGTCTTTGTCAGTGGAG</td>
<td>223</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>P5CS</td>
<td>GTGCTTGAACATCGGAATA GGTGCTCTAGTTGGCAAAA</td>
<td>204</td>
<td>1</td>
<td>1</td>
</tr>
</tbody>
</table>

AmpliSeq length, amount of introns present in the amplicon and the number of SNP's in the amplicon are indicated.

Anchoring of linkage groups to *Rosa wichurana* chromosomes and *Fragaria vesca* pseudochromosomes

Searching for orthologous genes for OOMT, P5CS and PAL genes in strawberry genome revealed that they are represented in 3, 4 and 2 genes paralogous, respectively (Table 4). Sequence alignment showed that sequence diversity between the paralogous ranges from 66% (for OOMT) to 91% (for P5CS) (Table 4). Two paralogous OOMT genes are located on strawberry pseudochromosome 6 (FvChr6) and one on FvChr3. Two paralogous P5CS genes are located close to each other on FvChr2 and two on FvChr6. Paralogous for the PAL genes were found on FvChr6 and FvChr7. BLASTN comparison between the sequences of OOMT, P5CS and PAL from *Rosa wichurana* and all found paralogous in strawberry, revealed that three strawberry paralogues (highlighted in Table 4) show a high similarity and/or sequence coverage to the rose genes. These paralogues are used for making a comparison between the physical locations of OOMT, P5CS and PAL genes on the strawberry pseudochromosomes and the *Rosa wichurana* chromosomes (Fig. 4). OOMT is located in the centre of FvChr6 (Fig 4) and, as revealed in our Tyramide-FISH, in the centromeric region on chromosome 1 of *Rosa wichurana* (RwChr1; Fig 4). PAL is located distally on FvChr6 (Fig 4) and distally on chromosome 7 of *Rosa wichurana* (RwChr7; Fig 4). P5CS is located distally on pseudochromosome FvChr7 (Fig 4) and on the distal part of *Rosa wichurana* chromosome 4 (RwChr4; Fig 4).

Discussion

Short DNA fragments could be visualized on physical chromosomes using Tyramide-FISH

To the best of our knowledge this study reports the first successful use of Tyramide-FISH in a plant genus with small chromosomes. Previously, Tyramide-FISH has been applied to
visualize short DNA fragments for large chromosomes of several monocots including onion [53,92], barley [54], wheat [55] and oat [56]. Despite the difficulty of using rose as a cytogenetic object, we successfully visualized short DNA fragments (1.1–1.7 Kb) of genes using Tyramide-FISH. Although rose chromosomes are very small, the degree of chromosome condensation is rather low (28.1±2 Mbp μm⁻¹). This value is comparable with tomato (40.6 Mbp μm⁻¹, [93]) and humans (26.6 Mbp μm⁻¹, [94]), but is more than seven times lower than in onion (249.6 Mbp μm⁻¹, [95]).

The nature of chromosome structure and chromatin compaction influences the accessibility of target DNA. Low chromatin compaction may positively influence the Tyramide-FISH sensitivity by improving the probe penetration into the chromosomes. On the other hand, less compact chromatin theoretically can have a negative impact on Tyramide-FISH because it contains smaller amounts of proteins (e.g., histones) and electron rich amino acids (e.g., tyrosine, tryptophan) around the site of hybridization. Tyramides, used for signal amplification, are phenolic compounds that react and bind with these electron rich moieties in the presence of HRP and hydrogen peroxide. Therefore, a smaller amount of electron rich amino acids can hamper a successful tyramide-conjugate coupling reaction after oxidation by HRP [42].

We found that the commonly-used direct detection system with fluorescent labeled tyramides (Tyr-FITC, Tyr-Cy3) was not suitable for rose chromosomes. In that system, many nonspecific signals hampered the identification of signals from the PAL gene. Optimization using the indirect detection and indirect detection with two rounds of amplification overcame this problem. The indirect detection system has previously been applied to detect the Rod51 gene on wheat chromosomes [55] and several EST clones on human chromosomes [47]. In the study of Schriml et al. [47], the indirect detection system using avidin-FITC provided the best results, i.e., clear, distinct signals on one or both of the homologues; whereas both the Tyr-Cy3 and Tyr-FITC (direct detection) resulted in high background [47]. The frequency of signal detections was about 30–40% in our study. This is comparable with previous studies. In the study of Perez et al. [55], the Tyramide-FISH procedure using Tyr-Bio was able to detect target DNA sequences as small as 2 kb with a frequency of 37.5%. These frequencies are high enough to unequivocally locate small sequences (<2 kb) using a few metaphase cells and shows the effectiveness of our Tyramide-FISH detection system. In most cases, we observed the Tyramide-FISH signals only on one homologous. The same results were obtained on wheat [55] and Allium (Kirov et al. unpublished data) where short DNA probes were used. Since chromatin structure significantly influences FISH results, the unequal distribution of the signals among the homologous and the low frequency of the signals may be the results of variation in chromatin accessibility and/or chromatin disorder between chromosomes and metaphase plates, caused by chromosome preparation procedure.

The HRM technology for EST-SNP marker generation has several advantages

We successfully visualized the position of the OOMT, P5CS and PAL genes on the Rosa wichurana chromosomes 1, 4 and 7, respectively. Using EST-SNP markers for these genes, we could anchor three linkage groups of Rosa wichurana to their physical chromosomes for the first time. EST-SNP markers made it possible to connect the physical position of the OOMT, P5CS and PAL genes with their position on the genetic map. The HRM technology allowed detecting SNPs in a fast and efficient way. Unlike other technologies for gene mapping, HRM can be applied immediately after PCR without further handling [73]. During a single two-hour assay we amplified all 3 genes in a single-step procedure on a 384-well plate. This dramatically increases the genotyping throughput in a mapping population. Curve shapes cannot always be assigned to specific alleles [96], but this was not the case here. EST-SNP markers are situated in functional genes, therefore these markers are a valuable tool for the integration of the physical and genetic position of genes.
Tyramide-FISH showed single loci for members of multigene families

Surprisingly, by using Tyramide-FISH we only observed single loci for each gene even though they were described as members of multigene families [97,98]. To estimate the copy number of genes in a plant genome, a collection of EST sequences can be used [99]. For roses, more than 20000 rose EST sequences were uploaded in NCBI [83,100–102] of which only 1936 EST sequences [101] belong to Rosa wichurana. This number of EST sequences is not enough for the estimation of the copy number of the three genes that we studied in Rosa wichurana even not if EST sequences from another Rosa species would be used in our analysis. Variations in EST sequences can be explained by the copy numbers of a gene but also by allelic variations. Some Rosa species may have up to 16 allelic variants (for ploidy level 2n = 8x) per gene. Therefore, for a correct estimation of the copy number of the genes in Rosa wichurana using a database of EST sequences, it should contain more sequences (e.g. 120892 ESTs were used for tomato [99]) of cDNA clones isolated from different tissues. Moreover, an EST library represents only expressed genes and does not include pseudogenes that can be visualized by Tyramide-FISH.

To clarify our result we performed BLASTN searches of all PAL, OOMT and P5CS genes known in Fragaria, the closest relative of Rosa [65,103]. It has a completely sequenced genome [104]. We found 2, 4 and 3 hits for the PAL, P5CS and OOMT genes, respectively, distributed along 3 Fragaria pseudochromosomes 3, 6 and 7. However, the similarity between the Fragaria orthologous genes (66–76%) for OOMT and PAL genes is low. The 4 Fragaria orthologous genes for P5CS genes showed a higher level of intragenic similarity, but a pairwise alignment with the rose gene fragment for P5CS used in our Tyramide-FISH indicated only one strawberry orthologous gene with a high similarity (82%) and query coverage (99%). Therefore, if the rose genome contains a similar copy number of PAL, OOMT and P5CS and with similar intragenic differences as in the Fragaria vesca genome, with the hybridization and washing stringency we used in our study, we can specifically detect the particular orthologues PAL, OOMT and P5CS genes with high homology to the probe DNA sequence. Thus, for each orthologue we can get a clear locus on the chromosomes, which is a very important feature for anchoring linkage groups to physical chromosomes.

Comparative analysis of physical gene positions between Rosa wichurana and Fragaria vesca

A comparison of the physical position of the three genes between the Rosa wichurana chromosomes and the Fragaria vesca pseudochromosomes revealed that FwChr6 contains both orthologous PAL and OOMT genes, although they are located on different chromosomes of Rosa wichurana. Previously, Gar et al. [65] genetically mapped a set of orthologous EST markers on Rosa and compared this with their position on the Fragaria vesca chromosomes. They showed 10 rearrangements including 4 translocations and 6 inversions changing the gene order between Rosa and Fragaria vesca chromosomes. One of these rearrangements involved FwChr6, which was shared by markers from 2 Rosa linkage groups. Our results are thus in accordance with Gar et al. [65]. Physical mapping on the rose chromosomes of additional genes present on FwChr6 will shed light on the nature and the scale of this rearrangement.

In conclusion, our results demonstrate that Tyramide-FISH is a useful tool for physical mapping of short DNA fragments of genes on Rosa chromosomes. We could physically map 3 genes on the
chromosomes of *Rosa wichurana*. Using the opportunities of the Tyramide-FISH and the HRM technology, 3 linkage groups could be anchored to 3 physical chromosomes of *Rosa wichurana*. An integration of a cytogenetic and genetic map of rose is an indispensable tool for assistance in map based cloning. Moreover, the information obtained from the physical mapping of individual rose genes can be applied for contig and pseudochromosome

---

**Table 4.** Divergence among members of PAL, P5CS, OOMT orthologous genes of *Fragaria* and their similarity to *Rosa wichurana* gene fragments used in this study.

<table>
<thead>
<tr>
<th>Gene</th>
<th>Number of orthologous genes found in <em>Fragaria</em></th>
<th><em>Fragaria</em> orthologous gene localizations</th>
<th>Similarity between <em>Fragaria</em> orthologous genes</th>
<th>% similarity to <em>Rosa wichurana</em> gene fragments (E-value; % coverage)</th>
</tr>
</thead>
<tbody>
<tr>
<td>PAL</td>
<td>2</td>
<td>FvChr7:15014006–15017322 FvChr6:34874086–34877587</td>
<td>76%</td>
<td>75% (3e-35; 20%) 83% (0.0; 65%)</td>
</tr>
<tr>
<td>P5CS</td>
<td>4</td>
<td>FvChr7: 17624431–17630820 16924786–16929803 FvChr6: 8598452–8605103 33424492–33427031</td>
<td>78%–91%</td>
<td>82% (0.099%) 88% (2e-32;37%) 79% (2e-15; 21%) Not significant&lt;sup&gt;z&lt;/sup&gt;</td>
</tr>
<tr>
<td>OOMT</td>
<td>3</td>
<td>FvChr3: 7085125–7086298 FvChr6: 15275992–15277245 15267146–15267850</td>
<td>66–67%</td>
<td>70% (8e-37; 87%) 91% (0.0; 88%) 44% (8e-47; 62%)</td>
</tr>
</tbody>
</table>

<sup>z</sup>: Not significant: according to BLAST search.

doi:10.1371/journal.pone.0095793.t004
anchoring to physical chromosomes which will assist future genome sequencing in *Rosa*.

References


Author Contributions

Conceived and designed the experiments: IK KVL. EDK. JDR. LK. Analyzed the data: IK KVL. JDR. NVR. Contributed reagents/materials/analysis tools: IK KVL. JDR. NVR. Wrote the paper: IK KVL. JDR. LK.


