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Research Article

Isolation of BAC Clones Containing Conserved Genes from Libraries of Three Distantly Related Moths: A Useful Resource for Comparative Genomics of Lepidoptera

Yuji Yasukochi,1 Makiko Tanaka-Okuyama,1 Manabu Kamimura,1 Ryo Nakano,2,3 Yota Naito,4 Yukio Ishikawa,2 and Ken Sahara4

1 Insect Genome Research Unit, National Institute of Agrobiological Sciences, Owashi 1-2, Tsukuba, Ibaraki 305-8634, Japan
2 Department of Agricultural and Environmental Biology, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Tokyo 113-8657, Japan
3 Entomology Research Team, National Institute of Fruit Tree Science, National Agriculture and Food Research Organization, Tsukuba, Ibaraki 305-8605, Japan
4 Laboratory of Applied Molecular Entomology, Research Institute of Agriculture, Hokkaido University, N9, W9, Kita-ku, Sapporo 060-8589, Japan

Correspondence should be addressed to Yuji Yasukochi, yaskoch@affrc.go.jp

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Lepidoptera, butterflies and moths, is the second largest animal order and includes numerous agricultural pests. To facilitate comparative genomics in Lepidoptera, we isolated BAC clones containing conserved and putative single-copy genes from libraries of three pests, Heliothis virescens, Ostrinia nubilalis, and Plutella xylostella, harboring the haploid chromosome number, \( n = 31 \), which are not closely related with each other or with the silkworm, Bombyx mori, \(( n = 28 )\), the sequenced model lepidopteran. A total of 108–184 clones representing 101–182 conserved genes were isolated for each species. For 79 genes, clones were isolated from more than two species, which will be useful as common markers for analysis using fluorescence in situ hybridization (FISH), as well as for comparison of genome sequence among multiple species. The PCR-based clone isolation method presented here is applicable to species which lack a sequenced genome but have a significant collection of cDNA or EST sequences.

1. Introduction

Bacterial artificial chromosome (BAC) libraries play a critical role in determination of genome organization and chromosome walking. In addition, we have utilized BAC libraries for linkage analysis and physical mapping of Lepidoptera, butterflies and moths. We reported construction of the first lepidopteran BAC library from the silkworm, Bombyx mori [1], which was used for characterization of the Hox gene cluster [2]. BAC clones isolated with monomorphic sequence tagged sites (STSs) were utilized for finding polymorphisms from flanking regions of the original STSs and construction of BAC contigs covering 22% of the B. mori genome, enabling us to localize genes which could not be mapped genetically [3]. We showed that BAC clones could be used effectively as probes for fluorescence in situ hybridization (FISH) in this species despite the limited cytological differentiation of individual chromosomes [2–4] and defined a karyotype for B. mori using this technique [4].

BAC libraries have since been constructed for several other lepidopteran species [5–9] and used to reveal longer range genome organization [8–11]. We previously showed that the gene order is well conserved between B. mori and the tobacco horn worm, Manduca sexta, by mapping M. sexta orthologs of 124 conserved and putative single-copy genes using BAC-FISH technology, which is suitable for genetically uncharacterized species [12]. However, B. mori and M. sexta belong to the same superfamily, Bombycoidea, and analysis
2. Materials and Methods

2.1. cDNA Sequencing of O. nubilalis. Total RNA was isolated from tissues and whole bodies of embryos, larvae, pharate pupae, pupae, and adults. cDNA was synthesized using a Super SMART PCR cDNA synthesis kit (Clontech) and cloned into a pGEM-T easy plasmid vector (Promega). A total of 12 cDNA libraries were constructed, and nucleotide sequences of randomly selected clones were determined using an ABI3730 DNA sequencer (Applied Biosystems) (Table S1). The DNA sequences were analyzed using a BLAST program (http://blast.ncbi.nlm.nih.gov/Blast.cgi) to identify genes associated with a database of the silkworm genome, Kaikobase.

2.2. Cloning of O. nubilalis Genes. Single-step or nested PCR amplifications were performed using degenerate primers designed from conserved genes previously mapped in B. mori. Single-step PCR amplification was performed using genomic DNA as template except for the small heat shock protein genes (Table S2), for which RT-PCR and 3’-RACE analyses were performed (Table S2). Other sequences were amplified from cDNA by nested PCR (Table S2). PCR products were then cloned into a pGEM-T easy plasmid vector (Promega) and sequenced with an ABI3730 DNA sequencer.

2.3. Selection of Genes for BAC Isolation. Sequences of H. virescens, O. nubilalis, and P. xylostella genes and ESTs were obtained from public databases or by EST sequencing as described above and used as queries for TBLASTN (sequences with CDS) or TBLASTX (sequences without CDS) searches against assembled genome sequences of B. mori [22] using the BLAST tool (http://kaikoblast.dna.affrc.go.jp/) associated with a database of the silkworm genome, Kaikobase.

Genes and ESTs showing significant similarity to putative single-copy B. mori genome sequences were selected and checked for localization of their B. mori orthologs in our previous studies by inheritance-based gene mapping and analysis of BAC contigs [2, 12, 23]. We performed PCR-based linkage analysis of unmapped orthologs with newly designed primers for sequence-tagged sites (STSs) (see in Supplementary Material available online at doi: 10.1155/2011/165894 Table S3) using 22–166 F2 individuals of B. mori from a single pair-mating of a strain C108 female by a strain p50 male, as reported previously [23], for the confirmation of chromosomal locations obtained from Kaikobase.

When PCR products amplified from B. mori orthologs were monomorphic in our mapping population, PCR-based screening of a B. mori p50 BAC library was performed in the same manner as described elsewhere [24] to confirm whether unmapped B. mori orthologs were localized on previously mapped BAC contigs.

2.4. Isolation of BAC Clones. BAC libraries used in this study were an H. virescens library, HVB, (Average insert size 171 kb), obtained from the GENE finder Genomic Resources (Texas A&M University, College Station, TX, USA) [7], an O. nubilalis library, ON_Ba, (Average insert size 125 kb) and a P. xylostella library, PXCDBa, (Average insert size 125 kb).
Figure 2: Strategy for selection of genes and ESTs in this experiment. Known genes and ESTs [13, 16, 25] were used as queries against a B. mori genome database, Kaikobase [20]. ESTs published later [14, 15, 17] were searched when no candidates were found in the first selection.

3. Results

3.1. EST Analysis and Gene Cloning of O. nubilalis. When we started this experiment, there were no published O. nubilalis EST data. We constructed twelve cDNA libraries from various tissues and stages and determined the sequences of 625 clones randomly selected from them (Table S1). We also attempted to clone O. nubilalis orthologs of B. mori single-copy genes which we had previously mapped (Table S2) [2, 12, 23]. However, larger-scale EST analyses of O. nubilalis were published later [16, 17], which provided a sufficient number of candidate genes. Thus, we decided not to continue independent EST sequencing and gene cloning.

3.2. Mapping of Conserved Genes in Bombyx mori. The strategy we used for the selection of genes used for BAC isolation is summarized in Figure 2. DNA sequences of known genes and ESTs of H. virescens [13], O. nubilalis [16], and P. xylostella [25] were used to find orthologs in B. mori by TBLASTN/TBLASTX search against genome sequences in Kaikobase [22]. ESTs of H. virescens [14, 15] and O. nubilalis [17] were published after the first selection of candidate genes and yielded too many for a manual similarity search using Kaikobase. Instead, TBLASTX search against ESTs in the DNA Data Bank of Japan (http://www.ddbj.nig.ac.jp/search/top-e.html) was performed in H. virescens or O. nubilalis orthologs when no candidates were found in the first search or ESTs were too short to design PCR primers.

In the previous study, we found some incorrect mapping information in Kaikobase [12] and subsequently had to carry out experimental confirmation of the chromosomal location of B. mori orthologs to avoid being misled by false gene translocations. To minimize additional mapping efforts in B. mori, we gave priority to finding orthologs of B. mori genes which had been confirmed in the previous reports [2, 12, 23]. Putting this limitation on genes for this type of study also leads to the isolation of orthologous BACs from different species, which facilitates comparison among multiple genomes.

More than 800 candidates were identified, which showed significant similarity and seemed to be single-copy in the
genome of B. mori. Two hundred thirty-six of them had been mapped genetically onto a linkage map of B. mori or localized to the mapped BAC contigs in our previous reports [2, 12, 23] (Table S4). To improve the resolution for comparing genomes, we designed 246 additional pairs of new primers for B. mori orthologs to select and clone BAC probes where the interval between markers was relatively long. In all, we identified 482 putative single-copy conserved genes in B. mori which were orthologous to known genes and ESTs of the three species (Table S4).

3.3. Isolation of BAC Clones. To isolate BAC clones of H. virescens, O. nubilalis, and P. xylostella using PCR-based screening, we designed primer sets to avoid including putative exon–intron junctions predicted from the alignment of cDNA sequences with genome sequences of B. mori. Ultimately, 181, 150, and 101 primer pairs could be used to screen H. virescens, O. nubilalis, and P. xylostella BAC libraries (Tables S5–7) and yielded 188, 163, and 108 BACs for 332 orthologous genes, respectively (Table S8).

We found 24 pairs and two sets of three genes for which orthologs closely spaced in B. mori were positive for identical clones in the three screened species (Table S8). Similar colocalization on BAC clones was also observed between clones in the three screened species (Table S8). Similar colocalization on BAC clones was a major factor that improved efficiency in this study. In situ hybridization using high-density replica (HDR) filters is the most commonly used method to screen BAC libraries. However, HDR filters are usually designed with sufficient redundancy to avoid failures in screening and are too large for the isolation of a minimum number of clones used in studies like ours. PCR-based screening can be carried out using standard thermal cyclers without any special skills, and stepwise changes in the scale of screening using a pooling strategy reduce time and labor. In addition, PCR-based screening can be easily performed for gene sequences downloaded from public databases, whereas DNA probes for in situ hybridization either have to be obtained from the original investigators or prepared independently. Thus, we could carefully eliminate genes which were likely to be duplicated in the B. mori genome including putative pseudogenes from the candidates for BAC isolation.

On the other hand, preparation of DNA pools for PCR-based screening is laborious, and high efficiency is not accomplished in a small-scale analysis. Ideally, a catalogue linking BACs with located genes should be constructed and published, which will release inexperienced researchers of nonsequenced species from the technical labor of BAC isolation and let them concentrate on functional analysis. The present study is the first step to this final goal in the future.

The species used in this study, H. virescens, O. nubilalis, and P. xylostella, are not closely related to each other (Figure 1), but share a haploid karyotype of n = 31. This karyotype is considered the basal number in Lepidoptera since a survey of more than 1,000 species revealed that more than half from many independent lineages carry this chromosome number [26]. The four lepidopteran species for which their chromosome organization has been characterized in detail are either n = 28 (B. mori, M. sexta, Bicyclus anynana [27]) or n = 21 (Heliconius melpomene [28]), indicating that several chromosomal fusions occurred in their lineages. We are now analyzing the chromosomal organization of the tobacco bollworm, Helicoverpa armigera, a noctuid species closely related to H. virescens using BAC probes from H. virescens in parallel with the analysis of O. nubilalis. The identification of the karyotypes of the three species used in this experiment will reveal the
ancestral karyotype and chromosome rearrangements which have occurred in each of these representative lepidopteran lineages.

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