Double rolling circle replication (DRCR) is recombinogenic

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Homologous recombination plays a critical role in maintaining genetic diversity as well as genome stability. Interesting examples implying hyper-recombination are found in nature. In chloroplast DNA (cpDNA) and the herpes simplex virus 1 (HSV-1) genome, DNA sequences flanked by inverted repeats undergo inversion very frequently, suggesting hyper-recombinational events. However, mechanisms responsible for these events remain unknown. We previously observed very frequent inversion in a designed amplification system based on double rolling circle replication (DRCR). Here, utilizing the yeast 2-μm plasmid and an amplification system, we show that DRCR is closely related to hyper-recombinational events. Inverted repeats or direct repeats inserted into these systems frequently caused inversion or deletion/duplication, respectively, in a DRCR-dependent manner. Based on these observations, we suggest that DRCR might be also involved in naturally occurring chromosome rearrangement associated with gene amplification and the replication of cpDNA and HSV genomes. We propose a model in which DRCR markedly stimulates homologous recombination.

Introduction

Homologous recombination plays a central role in processes involved in genome instability, such as chromosomal rearrangements, gene diversification and molecular evolution, as well as in genome stability. In nature, interesting examples are found that suggest hyper-recombination phenomena involved in genome instability. The chloroplast genome (cpDNA) is circular, containing a pair of long inverted repeats [Fig. 1A, example of Arabidopsis thaliana; (Sato et al. 1999)]. Two structural isomers are present as an equimolar mixture (Palmer 1983), suggesting that frequent inversions occur during replication via hyper-recombination. Herpes simplex virus-1 (HSV-1) has a linear genome consisting of two unique sequences (U L and U S) flanked by inverted sequences ab-h’/a’ and a’–c’–ca, respectively (Fig. 1B). Four structural isomers are formed by inversions of the two unique sequences and are also detected at equimolar ratios (Bataille & Epstein 1995), suggesting that free inversion should occur between inverted repeats. However, the mechanism responsible for hyper-recombination phenomena resulting in frequent inversions remains unknown.

We previously observed very frequent inversion in designed amplification systems based on double rolling circle replication (DRCR) (Watanabe & Horiuchi 2005). Free inversions occurred in the inverted array of intrachromosomal amplification products. The DRCR process was first experimentally confirmed for amplification of the yeast 2-μm plasmid (Broach & Volkert 1991). This plasmid encodes a site-specific recombinase, Flp1p, and contains a pair of inverted repeats (599 bp) containing Flp1p recombinase target (FRT) sites. Flp1-FRT recombination produces equal amount of two structural isomers (Fig. 1C) and can initiate DRCR if Flp1-FRT recombination occurs just after either FRT site is replicated, as shown in
Fig. 1D. Interestingly, Jayaram & Broach (1983) found very frequent inversion of Tn5 inserted into 2-lm plasmids, and Jayaram (1986) later showed that whereas two-isomer formation is Flp1-FRT dependent, the Tn5 inversion is RAD52 dependent. The bacterial transposon Tn5 (Jorgensen et al. 1979) consists of a unique central region flanked by a pair of inverted IS50 components; inversion of this central region is an extremely rare event in Escherichia coli (Weber et al. 1988b). However, they found that inversion was extremely common, when Tn5 was inserted into the HSV-1 genome (Weber et al. 1988a).

To elucidate the relationship between DRCR and frequent homologous recombination, here we exploited 2-lm circular plasmid and yeast linear genomes under DRCR conditions to test whether the DRCR process activates not only inversion of Tn5 but also deletion/duplication of a direct repeat. We found that, regardless of DNA forms, DRCR strongly activates all three types of recombinational events.

**Results**

**DRCR-dependent activation of inversion of Tn5 inserted into 2-lm plasmids**

Plasmid pCV21 (Broach et al. 1982) is a 2-lm hybrid plasmid containing the bacterial pBR322 plasmid DNA and the LEU2 gene (Fig. 2A). To construct a 2-lm-based system with a pair of inverted repeats (IR), we transposed Tn5 into pCV21. One of the resultant plasmids was designated pCV21::Tn5(#1) (Fig. 2A). A derivative from this plasmid, which had its FRT sites disrupted (see Experimental Procedures; Construction of FRT site-disrupted plasmids), was generated and designated pCV21::Tn5(#1)(frt−) (Fig. 2A). This plasmid should undergo normal replication but not DRCR. These plasmids were first multiplied in E. coli, extracted and then transformed into a yeast strain without the 2-lm plasmid (MRG5; cir0). The plasmid DNA was extracted, digested with EcoRI and SalI, separated by agarose gel electrophoresis and analyzed by Southern hybridization using IS50 as a probe. The results are shown in...
The digestion patterns of both pretransformed \((\text{FRT}^+ \text{ and frt})\) plasmids appeared to be identical (3.1 and 6.8 kb; Fig. 2C and data not shown), indicating no detectable recombination in *E. coli* \((\text{recA}^-)\). In yeast, as shown in Fig. 2C, although the \(\text{frt}^-\) mutant plasmid showed the same digestion pattern of the pretransformed plasmid, the \(\text{pCV21::Tn}5^-\text{(1)}\) produces multiple DNA fragments, six of which correspond to those derived from four structural isomers (form I to IV in Fig. 2B) produced by Flp1p-FRT recombination and Tn5 inversion. The low-density 6.4- and 4.7-kb bands are consistent with previous data by Jayaram & Broach (1983). The Tn5 inversion was also blocked by \(\text{FLP1}\) disruption and restored by exogenous \(\text{FLP1}\) expression (Fig. 2D). However, blockade of Tn5 inversion by \(\text{FRT}\) disruption was not reversed by \(\text{FLP1}\) expression (Fig. 2E). Another, independent, Tn5-inserted plasmid, \(\text{pCV21::Tn}5^-\text{(2)}\) (the Tn5 orientation opposite to that of the \(\text{pCV21::Tn}5^-\text{(1)}\), Fig. 2A), also required intact \(\text{FRT}\) sites for Tn5 inversion (unpublished data). It is known that DRCR depends on both the \(\text{FRT}\) site and the \(\text{FLP1}\) gene (Jayaram & Broach 1983). The present results show that the \(\text{cis}\) (\(\text{FRT}\) site) and \(\text{trans}\) (\(\text{FLP1}\) gene) elements are also required for Tn5 inversion.

**Deletion and duplication are also activated by DRCR in 2-\(\mu\)m plasmids**

In addition to inversion, structural changes caused by homologous recombination also include deletion/duplication. To investigate whether DRCR activates deletion/duplication, we artificially inverted one of the two IS50 of the \(\text{pCV21::Tn}5^-\text{(2)}\) plasmid (Fig. 2A), constructing another 2-\(\mu\)m derivative plasmid.
with a pair of direct repeats (DR), designated pCV21 (DR) (Fig. 3A). We carried out similar experiments to those in the preceding section using KpnI/SwaI digestion and REP1, Kmr or IS50 probes. The plasmid DNA remains unchanged in *E. coli*, producing a single 11.7-kb band, but produced six bands in yeast, as shown in Fig. 3C. In addition to two main bands (11.7 and 10.4 kb) derived from two isoformers produced by Flp1-FRT recombination, two lower (7.7 and 6.3 kb) and two higher bands (15.9 and 14.5 kb) were detected. This result can be explained, as shown in Fig. 3B, by 4.1 kb loss and gain by deletion and duplication via recombination between the direct repeats, respectively. In fact, the two lower bands did not hybridize with the Km' gene (Fig. 3D), which is located between the direct repeats, indicating the presence of a deletion. The deletion/duplication was also detected using other restriction enzymes, including NdeI (data not shown). Furthermore, disruption of either the FRT site (Fig. 3C) or the FLP1 gene (Fig. 3E) inhibited the deletion/duplication as well as DRCR. Finally, whereas *flp1* defectiveness was complemented by the FLP1 gene (Fig. 3E), the *frt* mutant was not complemented by the FLP1 gene (Fig. 3F). These results strongly suggest that inversion and deletion/duplication depend on DRCR processes of the 2-μm plasmid.

**Figure 3** High frequency of deletion/duplication between direct repeats in the 2-μm plasmid. (A) Structures of plasmid pCV21::Tn5 (#2) and pCV21(DR). For markers of the different structures, see Fig. 2. The methods of the construction of pCV21(DR) were carried out as described in Experimental Procedures. (B) Structures of six isomers are shown. They were derived from Flp1p-FTR recombination and deletion/duplication of direct repeats. The restriction sites (gray heavy lines; K: KpnI, S: SwaI) and the sizes (kb) of fragments that hybridize with the REP1 or IS50 probe are shown. (C) Southern analysis of KpnI/SwaI-digested DNA of pCV21(DR) in *E. coli*. (left, pretransformed) and a pCV21(DR) (FRT) and its *frt* mutant (Δfrt) in yeast strain MRG5 (right) with the REP1 probe. Agarose gel electrophoresis and Southern analysis were carried out as described in Experimental Procedures. (D) The same experiment as in (C), except the Km' gene was used as the probe. (E) The same experiment as in C, except pCV21(DR)Δflp1 plasmid in yeast strains in the absence or presence of pFLP1. (F) The same experiment as in C, except MRG1 (cir+: 2-μm plasmid-containing yeast strain) was used as the host.
DRCR induced in yeast linear chromosomes also activates deletion and duplication

Finally, to examine whether DRCR on the yeast linear chromosome can activate deletion/duplication, we constructed a DR structure (Fig. 4A and Fig. S1 in Supporting Information) within the amplification cassette described previously (Watanabe & Horiuchi 2005). This system contains two inverted pairs of genomic sequence, termed YF2 (gray arrow in Fig. 4A) and YF4 (white arrow). Following HO cutting, the cassette generates two chromosomal fragments, whose ends are designed to invade each other via the YF2 and YF4 sequences. This recombination-dependent replication process is known as break-induced replication (BIR). The double BIR is expected to induce DRCR (Fig. 4A). This system produces intra- and extrachromosomal products resembling products seen in higher eukaryotes, namely homogeneous staining regions (HSR) and DM-type products.

![Diagram](https://example.com/diagram.png)

**Figure 4** Double rolling circle replication (DRCR) induced on the yeast chromosome activates deletion/duplication between direct repeats. (A) DNA structure of pre-amplification clone and DRCR induction through DSBs (shown by red arrows) by HO endonuclease induction. This amplification cassette contains a pair of direct repeat of YF6 (blue arrow) and can be amplified via DRCR induced by BIR (break-induced replication) described previously (Watanabe & Horiuchi 2005). (B) DNA structure of DM-type product. (C) Three types of DNA structure, the expected, deletion and duplication, of homogeneous staining regions (HSR)-type product. (D) Pulsed-field gel electrophoresis (PFGE) and Southern analysis of a pre-amplification, one DM-type and two independent HSR-type samples. The leu2d gene was used as the probe. (E) Agarose gel electrophoresis and Southern analysis of SalI-digested DNA of the samples from D with the leu2d probe.
double minutes (DMs), respectively. The resulting amplification cassette contains the Km\(^r\) gene (2.2 kb) flanked by a direct repeat of genomic nonspecific sequences termed YF6 (1.55 kb: blue arrow in Fig. 4A) and is located at the right terminus region of chromosome VI. The amplification marker \textit{leu2d} (black arrow in Fig. 4A) has slight transcriptional activity and can complement leucine auxotrophy only if amplified. This strain lacks the native HO site and has a chromosomal HO endonuclease gene under the control of the GAL10 promoter (Butler \textit{et al.} 1996). We plated approximately \(1 \times 10^5\) cells, a yeast strain with the amplification cassette unit containing DR structure (see Fig. 4A), on galactose plates lacking leucine to induce DRCR, as shown in Fig. 4A, and obtained \(357\) \textit{Leu}\(^+\) colonies. Randomly selected \(161\) \textit{Leu}\(^+\) clones were analyzed their genome structure using pulsed-field gel electrophoresis (PFGE). From these PFGE gel patterns, four HSR-type and \(86\) DMs-type clones were found. In addition, \(60\) colonies had chromosomal amplification products with lower copy number, and \(11\) colonies underwent \textit{Leu}\(^+\) recombination between the \textit{leu2d} gene and the original \textit{leu2} fragment on chromosome III. The latter two types of \textit{Leu}\(^+\) clones were described previously (Watanabe & Horiuchi 2005). Pulsed-field gel patterns of one DMs- and two independent HSR-type amplified clones (Fig. 4B,C) together with the pre-amplification control clone (the top structure in Fig. 4A) are shown in Fig. 4D. Next, \textit{SalI}-digested DNA from these samples was separated by agarose gel electrophoresis and hybridized with the \textit{leu2d} gene as the probe (Fig. 4E). The control \textit{SalI}-digested sample produced \(5.2\)- and \(12.6\)-kb bands from the cassette on chromosome VI (Fig. 4A) and approximately \(15\)-kb band from the \textit{leu2} fragment previously used to disrupt an native HO site (Sandell & Zakian 1993). Neither DNA band appeared in the amplified samples, because the signal intensities of these single-copy DNA (at 5.2, 12.6 and approximately 15 kb) are much lower than those of the amplified \textit{leu2d}. The \textit{SalI} digestion pattern of extrachromosomal products, which are formed not by DRCR, but by single BIR (Watanabe & Horiuchi 2005), showed a single 12.6-kb band. In contrast, the corresponding intrachromosomal products showed lower (9.0 kb) and higher (16.6 kb) DNA bands in addition to the 12.8-kb main band. This result can be explained by 3.8 kb loss and gain by deletion and duplication through the YF6 direct repeats, respectively, as shown in Fig. 4C. The lower band did not hybridize with the Km\(^r\) gene (data not shown), which is located between the direct repeats, indicating a deletion. These results strongly suggest that DRCR activates all three kinds of recombinational events, inversion, deletion and duplication, regardless of whether DRCR is induced on circular or linear DNA.

**Discussion**

**DRCR is a recombinogenic process**

Previously, we constructed a gene amplification system in yeast, in which DRCR induced by BIR produced two types of gene amplification product; both were analogous to two types of gene amplification products in tissue cultured cells, HSR and DMs. Moreover, we found that sequences flanked by inverted repeats in the HSR-type products randomly oriented. This means that recombination between the inverted repeats occurred freely (Watanabe & Horiuchi 2005).

Here, we investigated the relationship between the frequent recombination and DRCR. We constructed IR and DR structures in 2-μm plasmid DNA or yeast chromsome and examined whether inversion, deletion and duplication occurred under DRCR or normal replication. The results were clear-cut; all three types of recombination were extremely activated under DRCR, but not under normal replication. Thus, we conclude that DRCR itself is recombinogenic.

**What is the physiological function(s) of DRCR-dependent hyper-recombination?**

When \textit{leu2d} is used as an amplification selective marker, \(10–20\) copies of \textit{leu2d} are enough to complement \textit{Leu} auxotrophy (Watanabe & Horiuchi 2005). However, the actual copy numbers of \textit{leu2d} in HSR-type products increase markedly to more than 100 copies, suggesting the existence of some mechanism stabilizing high \textit{leu2d} copy number. One such possible mechanism is DRCR-dependent frequent inversion, because active inversions should destroy any very large palindromic structure that would be expected from deduced DRCR modeling, presumably resulting in stabilization of the amplified product. On the other hand, it has been generally observed that in cultured mammalian cells, the initial amplification unit (amplicon) is very long, but shortens, and the copy number increases drastically as selective pressure increases (Smith \textit{et al.} 1992; Toledo \textit{et al.} 1992; Ma \textit{et al.} 1993). Indeed, in \textit{CHO} cells, we observed that
HSR-type products obtained through DRCR induced via the Cre-lox system were also extensively rearranged (Watanabe and Horiuchi, unpubl. data, 2010). However, the cause of such a drastic genomic rearrangement remains to be determined. It is well known that there is a large amount of repetitive sequences present in the higher eukaryotic genome, such as LINEs (17%) and retro-transposons (8%) in the total human genome (Krebs et al. 2009). Therefore, DRCR-dependent recombinogenic replication should contribute to the deletion of large unnecessary regions and leave only essential genes, resulting in shortened amplicons, increase in the copy number and stabilization of highly repetitive structures. Interestingly, in yeast, we have not found any intensive rearrangements in either HSR- or DMs-type amplification products. This can be explained at least in part by the fact that there are not so many repeated sequences, such as Ty elements (1.8%), in the total yeast chromosome as in the mammalian genome (Krebs et al. 2009).

**Recombinogenic DRCR model**

How does DRCR-dependent recombination become so activated? One possibility is that highly repeated structures produced by DRCR may be recombinogenic themselves. In fact, HSR products, for example, are highly repeated structures compared to unique sequence chromosomes, so that it should come as no surprise that the structure itself is recombinogenic. However, it is known that a single Tn5 transposed into HSV-1 virus DNA inverts frequently (Weber et al. 1988a). It is hard to explain why a pair of inverted IS50 (1.5 kb each) in Tn5 transposed into the HSV-1 (150 kb) genome become so activated.

Our model is shown in Fig. 5. In eukaryotes, it is well known that as replication proceeds, a protein complex, cohesin, bundles pairs of newly duplicated sister chromatids together until anaphase of the M period when the sister chromatids are separated from one another by proteolysis of the cohesin. Thus, one of the physiological functions of cohesin is to prevent two sister chromatids from separation (Nasmyth 1999). In addition, cohesin has a function in repair of DNA damage and transcription (Losada & Hirano 2005).

When DRCR initiates and proceeds in circular plasmids or chromosomes, two sister chromatids are produced and cohesin bundles them together, this being associated with replication in its initial stage. However, in the following stage, a pair of DCR forks proceeds on the circular genome, as shown in Fig. 5A, because two replication forks chase each other. This results in one of the sister chromatids, the red strand in Fig. 5A, being forcibly separated from the other. Probably because cohesin unlinks physically, a resulting single chromatid, named only-daughter chromatid, which breaks loose from cohesin, emerges. The only-daughter chromatid produced by DRCR on a circular genome should be able to recombine freely, as shown in the above results, between repeated sequences on the only-daughter chromatid. DRCR induced on a linear chromosome, as shown in Fig. 5B, behaves similarly as in the case of the circular genome. In either case, until DRCR terminates, highly recombinogenic conditions would prevail. There are several lines of evidence supporting this model. One is a mutant of rad21 (a component of cohesin in Shizosacharomyces pombe) in which homologous recombination is stimulated approximately 10-fold (Grossenbacher-Grunder & Thuriaux

**Figure 5** Double rolling circle replication (DRCR)-dependent recombinogenic model. (A) 2-μm plasmid-type DRCR. (B) linear chromosome-type DRCR. Arrow indicates replication fork, and blue oval structure indicates cohesin that bundles sister chromatids soon after replication. Red line indicates cohesin-free sister chromatid, which we designate the ‘only-daughter’ chromatid. See text in Discussion for more detail.
1981). Another is our own work (Kobayashi et al. 2004), in which we provided evidence that in yeast rDNA repeated clusters, both accumulation of extra-chromosomal rDNA circles and loss of the \( URA^+ \) marker inserted into rDNA significantly increased, approximately 9- and 4.2-fold, respectively, under cohesin-defective conditions. However, until now, because cohesin is essential for cell survival, it had not been possible to observe how cohesin-free sister chromatids behave in this context. If the model proposed here is correct, DRCR provides the first example of cohesin-free chromatids and cohesin should have an anti-recombinogenic function. We now investigate the relationship between DRCR and recombination proteins, such as Rad52.

**Other recombinogenic processes**

Are there any other events in which DRCR is involved? Although not yet confirmed, DRCR may be involved in replication of cpDNA and HSV-1 DNA. The cpDNA has a DM-type structure and two isomers present in equimolar amounts, as shown in Fig. 1A (Palmer 1983). On the other hand, HSV-1 has a highly characteristic structure, as shown in Fig. 1B. The genome is linear, consisting of two unique fragments, \( U_1 \) and \( U_2 \), each of which is flanked by \( ab \) and \( b'a' \), and \( a'c' \) and \( ca \) sequences, respectively. Interestingly, virus DNA in virus particles is mixture of four kinds of structural isomers (Bataille & Epstein 1995). These structures can induce DRCR, as shown in Fig. S2 in Supporting Information. DRCR can reasonably explain recombinogenic replication and finally produces four kinds of equimolar isofrom. Interestingly, there are common properties in replication intermediate structures in cpDNA and HSV-1; in both cases, replication is associated with recombination. Replication intermediates are such complex structures that the majority immobilizes and stays in its original starting position during PFGE analysis, although replication intermediates are treated with a single-cut enzyme. The structure is reported to have a many-branched and entangled form (Bataille & Epstein 1995; Bendich 2004). These characteristics would be explained by DRCR-dependent recombinogenic properties (Fig. S2 in Supporting Information). Although a minority of cpDNA has a single copy of rDNA, replication intermediates are similarly complex to major cpDNA with inverted rDNA (Shaver et al. 2008), suggesting that the former may replicate in another mode, such as rolling circle replication (RCR) as discussed next.

Rolling circle replication (RCR) is another mode of replication analogous to DRCR. If our model is correct, RCR should also be recombinogenic, because it is similar to DRCR, which is expected to produce only-daughter chromatids. Yeast mtDNA may be a possible example of duplication through RCR, and there is a report that it is genetically recombinogenic (Dujon 1981). There are many other examples seeming to document replication via RCR, such as in Baculovirus (Martin & Weber 1997; Oppenheimier & Volkman 1997), telomeres of linear mtDNA producing t-circles (Tomaska et al. 2009) and recombinational hot spots (Hot) DNA in \( E. coli \) (Kodama et al. 2002). They raise interesting questions to be answered in the future.

In conclusion, we believe that there is little doubt that DRCR provides the genome with a previously unknown ability, namely a recombinogenic property.

**Experimental procedures**

**Strains, plasmids, growth medium and cultivation**

Yeast strains MRG1 (Ansari & Gartenberg 1997) and MRG5 (Tsilk & Gartenberg 1998) were provided by Dr. M. Gartenberg and used as the parental host strains. The genotype of MRG1 is \( M_A f a, m a 3–52, k n a 2–A1, t r p 1–A63, h i s 3–A200, D a d e 2, c i r ^+ \). The genotype of MRG5 is the same as MRG1 except for \( c i r ^+ \) (Tsilk & Gartenberg 1998). Yeast strain LS20 was used for a host strain, into whose chromosome the amplification cassette was integrated (Butler et al. 1996). The following \( E. coli \) strains were used: MC1061 (hisD, merB, araD139, \( A(araABC-leu)7679, D a l a X 7 4, g a l U, g a l K, r p s L, t h i ) (\( C a s a d a b a n \& \) Cohen 1980), DH5\( \alpha \) (\( F^+ \), \( \Phi 80 d l a z A M 1 5, \Delta (l a z Z Y A a n g F) U 1 6 9, d e r, r e c A 1, e n d A 1, h i s D R 1 7 (K^c, M K^c), p h o A, s u p E 4 4, \lambda ^+ \), \( t h i - 1, g y r A 9 6, r e l A 4 1 \) (Hanahan 1983) and XL10-Gold Ultracompetent Cells (STRATAGENe) (\( T e c^+ \) \( D (m e c A) 1 8 3 \Delta (m e c C B h s d S M R-m n ) 1 7 3 e n d A 1 s u p E 4 4 t h i - 1 r e c A 1 g y r A 9 6 r e l A 1 l a c H z [ F' p r o A B l a d q Z A M 1 5 T n 1 0 (T e c^+) A m y C a n^-] \)). The latter two strains were used as competent cells. Yeast 2-\( \mu \)m hybrid plasmid pCV21 was provided by Dr. J.R. Broach (Broach et al. 1982). To transpose Tn5 into \( E. coli \) strain MC1061 carrying a pCHR381(Km\(^R\)) (Sasakawa & Yoshikawa 1984), the plasmid was transformed into E. coli strain MC1061 carrying a pCHR381 plasmid and Ap\(^R\) Kmr selected at 42 \( ^\circ \)C. Several hundred Ap\(^R\) Kmr colonies were selected, DNA was extracted, DNA samples were transfomed into DH5\( \alpha \). Ap\(^R\) Kmr clones were selected at 42 \( ^\circ \)C, and two independent transposed clones were obtained. These were designated pCV21::Tn5 (#1) and pCV21::Tn5 (#2). Tn5 was inserted into the long unique segment in both of these, as shown in Fig. 2A. Growth medium
and culture conditions were described previously (Watanabe & Horiuchi 2005).

Construction of FRT site-disrupted plasmids

pCV21::Tn5 (#1) and (#2) DNA were partially digested with XbaI, and the single-cut product was separated from non- or double-digested product by agarose gel electrophoresis, extracted and purified using MonoFas DNA Purification Kit I (GL Science); the gap of the 5′-end was filled with KOD polymerase (TOYOBO), ligation was carried out with Ligation high Ver.2 (TOYOBO). DNA was transformed into E. coli using XL-10 Gold Ultracompetent Cells (STRATAGENE), and either XbaI site-disrupted plasmids were constructed. To disrupt another intact FRT site, the remaining XbaI site was completely digested, and similar procedures followed; two independent FRT site-disrupted plasmids, pVC21::Tn5 frt− (#1) and (#2), were generated.

DRCR-dependent inversion assay for 2-μm plasmid with Tn5 IR structure

Plasmid DNA to be assayed was transformed into yeast strain MRG5 [cir] using Frozen-EZ Yeast Transformation Kit II™ (ZYM0 RESEARCH), plated on SC, -Leu, 2% glucose plates and incubated at 30 °C. Colonies grown were cultured in 5 mL SC, -Leu, 2% glucose liquid medium for 48 h, and total DNA was extracted by the yeast DNA mini-prep method (Burke et al. 2000). Total DNA (approximately 25 μg) was digested with EcoRI and SacI and was used in Southern hybridization.

Construction of FLP1 gene-disrupted plasmids

There is a unique Ssul site within the FLP1 gene of the 2-μm plasmid. Thus, to disrupt the FLP1 gene, pCV21::Tn5 (#1) DNA was digested with Ssul and linker ligation was carried out. The following linkers were used: 5′-CTTACCCGGTAAACGATACAGTTGATCCCTACCAGGACTT-3′; 5′-AAGTCGGGTAAGGTACCACTGTATCGTTACCCGGGTAAG-3′. The two linkers were annealed, digested with Ssul and ligated with Ssul-linearized 2-μm plasmid DNA (pCV21::Tn5), and an FLP1-disrupted plasmid was constructed, designated pCV21::Tn5 Δflp1. Using the same procedures, the pCV21(DR)Δflp1 plasmid was also constructed.

Construction of pCV21(DR) in which a pair of IS50 of Tn5 is directly repeated

pCV21::Tn5 (#2) has two BamHI sites in pBR322 and the unique central region of Tn5 (Fig. 3A). This plasmid was digested by BamHI, and the two fragments were purified. The shorter fragment containing IS50 was re-inserted into the larger fragment in the opposite orientation, generating pCV21(DR) (Fig. 3A). The same construction procedures were used to create the pCV21(DR) frt−.

Construction of FLP1 gene expression vectors and expression of the FLP1 gene

The FLP1 gene encoded in pCV21 was amplified by PCR using 20-bp homologous sequences as primers. To clone the FLP1 gene, the pSH47 plasmid (Guldener et al. 1996) was used. First, the Cre gene was removed by EcoRI and Xhol digestion of the pSH47 DNA, and then, the PCR products of the FLP1 gene were cloned into pSH47 using the In-Fusion PCR Cloning System (Clontech). The resulting plasmid, termed pFLP1, was transformed into MRG5 containing the following plasmids: pCV21::Tn5 (#1), pCV21::Tn5 frt− (#1), pCV21::Tn5Δflp1 or pCV21::Tn5 (DR)Δflp1 plated on SG-Ura-Leu plates. Colonies grown under selective conditions were purified, washed with distilled water, suspended in 3 mL of SC, -Ura, -Leu, 2% galactose liquid medium and cultured for 33–43 h to induce FLP1 gene expression.

Construction of a new amplification cassette with the DR structure

Plasmid pRR-HO, described previously (Watanabe & Horiuchi 2005), was used for making a new amplification cassette with a directly repeated (DR) structure, as shown in Fig. S1 in Supporting Information. To construct DR (YF6-Km†-YF6), the Km†-YF6 fragment was inserted into the 3′-side of the cassette plasmid (pRR-HO; Watanabe & Horiuchi 2005), as shown in Fig. S1A in Supporting Information. A pair of YF6 fragments (1.55 kb) has a DR structure, between which a Km fragment (2.2 kb) locates. The Km fragment, a derivative of transposon Tn5, consists of the Km gene and part of an IS50, as shown in Fig. S1A in Supporting Information.

First, the plasmid (pCV21::Tn5(#1)) was digested by Xhol and SacI, and the Km gene fragment derived from Tn5 was cloned into a SacI site of the plasmid vector Bluescript SK+ (STRATAGENE) generating pBS-Km (Fig. S1A in Supporting Information). The single BglII site of pBS-Km was digested by BglII and disrupted with Blunting High (TOYOBO). On the other hand, the YF6 fragment (1.55 kb) has a DR structure, between which a Km fragment (2.2 kb) locates. The Km fragment, a derivative of transposon Tn5, consists of the Km gene and part of an IS50, as shown in Fig. S1A in Supporting Information.

This vector was used as a template, and PCR was carried out using Fw-primer containing an artificially produced BamHI site sequence and Rev-primer containing a natural BglII sequence. The resulting PCR product was digested with BamHI and BglII and purified using MonoFas DNA Purification kit I (GL Science) (Fig. S1A in Supporting Information). This fragment was ligated with BglII-digested and dephosphorylated pRR-HO DNA, and pRR-HO DNA (DR) was obtained (Fig. S1A in Supporting Information). This plasmid was digested with BamHI and BglII, and the linear DNA fragment with BamHI and BglII ends (Fig. S1A in Supporting Information) was transformed into yeast using a Frozen-EZ Yeast
Transformation kit II (ZYMO Research). Recipient strain was the LS20 strain, in which YF5-lue2d-YF4-URA3-YF2-lou2d-YF6-Km’-YF6 (YF2 sequence position 257394-258454, of Saccharomyces cerevisiae chromosome VI, GenBank Accession ID, NC_-001138), YF4 (267165-268121), YF5 (262318-263257) and YF6 (263266-264862) are nonspecific sequences at the terminus region of chromosome VI) was integrated between the YF5 and YF6 fragments on the right terminus site of chromosome VI, generated and designated LS20RR-HO(DR). They were obtained under URA³ selective conditions, as shown in Fig. S1B in Supporting Information. The structure was confirmed by colony PCR [KOD FX (TOYOBO)] and Southern hybridization.

**PFGF and Southern analysis**

All procedures were carried out essentially according to the methods described previously (Watanabe & Horiuchi 2005). DIG-labeled IS50, REP1 or Km’ probes were prepared using the DIG labeling module (Roche).

**GalHO induction**

Induction of the HO endonuclease gene was as described previously (Watanabe & Horiuchi 2005).

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**References**


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Supporting Information/Supplementary material

The following Supporting Information can be found in the online version of the article:

Figure S1 Construction of the chromosome VI with new amplification cassette.

Figure S2 DRCR mode of HSV-1 genome.

Additional Supporting Information may be found in the online version of this article.

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