Chromosomal targeting of replicating plasmids in the yeast *Hansenula polymorpha*

KLAAS NICO FABER, GERT JAN SWAVING, FOLKERT FABER, GEERT AB, WIM HARDER, MARTEN VEENHUIS* and PETER HAIMA†

1Department of Microbiology, Biological Centre, University of Groningen, Kerklaan 30, 9751 NN Haren (Groningen), The Netherlands
2Department of Biochemistry, University of Groningen, Nijenborgh 4, 9747 AG Groningen, The Netherlands

(Received 31 March 1992; revised 7 July 1992; accepted 15 July 1992)

Using an optimized transformation protocol we have studied the possible interactions between transforming plasmid DNA and the *Hansenula polymorpha* genome. Plasmids consisting only of a pBR322 replicon, an antibiotic resistance marker for *Escherichia coli* and the *Saccharomyces cerevisiae* LEU2 gene were shown to replicate autonomously in the yeast at an approximate copy number of 6 (copies per genome equivalent). This autonomous behaviour is probably due to an *H. polymorpha* replicon-like sequence present on the *S. cerevisiae* LEU2 gene fragment. Plasmids replicated as multimers consisting of monomers connected in a head-to-tail configuration. Two out of nine transformants analysed appeared to contain plasmid multimers in which one of the monomers contained a deletion. Plasmids containing internal or flanking regions of the genomic alcohol oxidase gene were shown to integrate by homologous single or double cross-over recombination. Both single- and multi-copy (two or three) tandem integrations were observed. Targeted integration occurred in 1–22% of the cases and was only observed with plasmids linearized within the genomic sequences, indicating that homologous linear ends are recombinogenic in *H. polymorpha*. In the cases in which no targeted integration occurred, double-strand breaks were efficiently repaired in a homology-independent way. Repair of double-strand breaks was precise in 50–68% of the cases. Linearization within homologous as well as nonhomologous plasmid regions stimulated transformation frequencies up to 15-fold.

Introduction

The ability of the yeast *Hansenula polymorpha* to utilize methanol as a sole carbon and energy source renders this organism of considerable scientific and commercial interest. The biochemistry and physiology of methanol utilization has been studied extensively (for a recent review, see Van der Klei et al., 1991a). Part of the methanol metabolism is compartmentalized in peroxisomes which contain the enzyme alcohol oxidase (AO), catalysing the initial oxidation of methanol to formaldehyde. Under optimal expression conditions established in methanol-limited continuous culture, the AO protein constitutes up to 30–40% of cellular protein and is exclusively located in peroxisomes, which occupy over 80% of the total cell volume (Veenhuis et al., 1983). The ability of *H. polymorpha* to express the AO gene at such high levels renders this organism a very attractive host for expressing heterologous genes under control of the strong AO promoter. Expression of heterologous genes this way has been reported for e.g. the plant gene α-galactosidase (Fellinger et al., 1991; Sierkstra et al., 1991), the *Escherichia coli* β-lactamase (Eckart, 1988), L and S hepatitis B antigens (Shen et al., 1989; Janowicz et al., 1991) and human serum albumin (Hodgkins et al., 1990).

The induction, biogenesis and metabolic function of peroxisomes have been extensively studied in *H. polymorpha*. Proliferation and enzyme composition of the organelles can be precisely prescribed by manipulating growth conditions (for a review, see Veenhuis & Harder, 1991). Recently, it was shown that peroxisomes are indispensable for growth of cells on methanol since they are essential in regulating the metabolic fluxes of formaldehyde, produced from methanol, over dissimi-
latory and assimilatory pathways. Moreover, they con-
fine the toxic byproduct of methanol oxidation, H₂O₂,
close to its site of synthesis where it is decomposed
efficiently by another peroxisomal enzyme, catalase
(Van der Klei et al., 1991b). Consequently, mutants of
H. polymorpha affected in peroxisome biogenesis/assembly (Cregg et al., 1990) are unable to utilize
methanol as sole carbon source.

Although much is known about the physiology, biochemistry and ultrastructure of H. polymorpha, and
classical genetic methods are well developed (Gleeson &
Sudbery, 1988), our present knowledge of the molecular
genetics is relatively poor. The main reason for this is
that genetic transformation methods for this yeast have
become available only recently. Furthermore, the trans-
formation protocols published so far are either delicate or
inefficient, or only successful when used with specific
strains (Gleeson et al., 1986; Roggenkamp et al., 1986;
Tikhomirova et al., 1988; Berardi & Thomas, 1990).
Studies at the molecular level have also been severely
hampered by the absence of efficient procedures for
plasmid integration, gene disruption and gene replace-
ment. These methods of gene manipulation have been
used in Saccharomyces cerevisiae and other fungi to
generate null mutants, to modify genes or their mode of
regulation, to clone and map genes and to stabilize
homologous and heterologous genes (for a review, see
Fincham, 1989). Although plasmid integrations by single
or double cross-over recombination events have been
reported recently (Sierkstra et al., 1991; Beburov et al.,
1990; Hodgkins et al., 1990; Sudbery et al., 1988;
Fellinger et al., 1991), at present no detailed analysis is
available of all the possible interactions between
transforming DNA and the H. polymorpha genome. Such
information would open new ways for exploring the
H. polymorpha genome. Furthermore, the availability of
a general integration strategy would offer the possibility
to routinely stabilize heterologous as well as homologous
genomes for gene expression purposes.

In order to improve the accessibility of H. polymorpha
for molecular genetics, we adapted the transformation
protocol described by Klebe et al. (1983) for S. cerevisiae,
for transformation of H. polymorpha. A number of
vectors was constructed which basically consist of a
pBR322 replicon, an antibiotic resistance marker for
E. coli and the S. cerevisiae LEU2 gene, which function-
ally complements the H. polymorpha leu1.1 mutation
(Gleeson et al., 1986). Here we report the high frequency
transformation and autonomous replication of these
plasmids and, when linearized within genomic se-
quences, their targeted integration into the genome with
varying frequencies. Integrations were consistent with
classical homologous single or double cross-over recom-
binations. Furthermore, evidence is presented for non-
recombinational repair of double-strand breaks in
transforming plasmid DNA.

Methods

Strains and plasmids. These are listed in Table 1.

Cultivation media and growth conditions. Escherichia coli strains were
grown in minimal M9 medium or rich LB medium (Sambrook et al.,
1989). When necessary, media were supplemented with ampicillin
(Ap; 100 μg ml⁻¹) or erythromycin (Em; 150 μg ml⁻¹). H. polymorpha
strains were grown on selective minimal YND, YNG or YNM media
[0.7% yeast nitrogen base without amino acids supplemented with 2% (w/v) glucose, 2% (v/v) glycerol or 0.5% (v/v) methanol, respectively] or
nonselective YPD medium [1% (w/v) yeast extract, 2% (w/v) peptone
and 2% (w/v) glucose].

(Bio)chemicals. Chemicals used were of analytical grade and, unless
stated otherwise, obtained from Merck. Restriction and DNA-
modifying enzymes were used as recommended by the manufacturers
(Boehringer Mannheim, Pharmacia and Biolabs).

DNA techniques and transformation of E. coli. Large-scale and mini
preparations of plasmid DNA from E. coli were obtained by the
alkaline lysis method (essentially as described by Ish-Horowicz &

<table>
<thead>
<tr>
<th>Relevant properties</th>
<th>Source or reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>E. coli C600</td>
<td>Laboratory collection</td>
</tr>
<tr>
<td>H. polymorpha DH1 A16</td>
<td>Meissner et al. (1987)</td>
</tr>
<tr>
<td>H. polymorpha pHis</td>
<td>Hanahan (1983)</td>
</tr>
<tr>
<td>pHP7, pHIP1, pHIP3, pHIP11, pHRP2, pHIP111, pHIP112</td>
<td>Laboratory collection</td>
</tr>
</tbody>
</table>

Table 1. Strains and plasmids used in this study
Burke, 1979) or the boiling method (essentially as described by Holmes & Quigley, 1981), respectively. Plasmid DNA from *H. polymorpha*, used for retransformation of *E. coli*, was isolated as described by Hoffman & Winston (1987), including phenol/chloroform and chloroform extraction and a final ethanol precipitation step. Precipitated DNA was dissolved in 5 μl H₂O and dialysed against H₂O for at least 1 h, using a Millipore 0.225 μm filter. Chromosomal DNA was isolated from *H. polymorpha* essentially as described by Sherman et al. (1986). Total DNA of transformants was separated on Southern (1975); DNA probes were labelled using the random primed labelling kit from Boehringer Mannheim in combination with [α-32P]dATP from Amersham. Relative amounts of radioactivity according to the CaCl₂ procedure described by Sambrook et al. (1989). DNA was dissolved in 5 μl H₂O and dialysed against H₂O for at least used for retransformation of *E. coli*, was isolated as described by Burke, 1979) or the boiling method (essentially as described by Holmes & Quigley, 1981), respectively. Plasmid DNA from *H. polymorpha*, used for retransformation of *E. coli*, was isolated as described by Hoffman & Winston (1987), including phenol/chloroform and chloroform extraction and a final ethanol precipitation step. Precipitated DNA was dissolved in 5 μl H₂O and dialysed against H₂O for at least 1 h, using a Millipore 0.225 μm filter. Chromosomal DNA was isolated from *H. polymorpha* essentially as described by Sherman et al. (1986). Total DNA of transformants was separated on Southern (1975); DNA probes were labelled using the random primed labelling kit from Boehringer Mannheim in combination with [α-32P]dATP from Amersham. Relative amounts of radioactivity according to the CaCl₂ procedure described by Sambrook et al. (1989). DNA was dissolved in 5 μl H₂O and dialysed against H₂O for at least 1 h, using a Millipore 0.225 μm filter. Chromosomal DNA was isolated from *H. polymorpha* essentially as described by Sherman et al. (1986).

Southern blot hybridization analysis was performed essentially as described by Southern (1975); DNA probes were labelled using the random primed labelling kit from Boehringer Mannheim in combination with [α-32P]dATP from Amersham. Relative amounts of radioactivity according to the CaCl₂ procedure described by Sambrook et al. (1989).

**Results**

Transformation with circular plasmids lacking sequence homology with the *H. polymorpha* genome

Using the optimized transformation protocol, several independent transformation experiments were carried out with plasmids pHIP3 and its derivative pHIP1 (Fig. 1), which to our knowledge at that time did not contain any *H. polymorpha* autonomous replicating sequence (*HARS*). As a control, transformations were also performed with the replicating plasmid pHRP2 (Fig. 1), which contains the *HARS* sequence (Roggenkamp et al., 1986). Surprisingly, the plasmids pHIP1 and pHIP3 transformed the yeast with slightly higher frequencies than the replicating plasmid pHRP2 (Fig. 2). At an input of 1 μg plasmid DNA (per aliquot of competent cells), transformations by pHIP1 and pHIP3 resulted in approximately 5 × 10⁵ transformants, suggesting the establishment of the plasmids as autonomous elements in the host.

Conclusive evidence for autonomous behaviour was provided by three observations. Firstly, the plasmids could be rescued intact from *H. polymorpha* by electrotransformation of *E. coli* with total yeast DNA (results not shown). Secondly, segregational instability of the *Leu*⁺ phenotype was observed. After 40 generations of non-selective growth (YPD medium), 55–85% of the cells had lost the *Leu*⁺ trait. Thirdly, Southern hybridization analyses showed that the plasmids were maintained as multimers.

Fig. 3 (lanes 1–4) shows the result of a Southern hybridization experiment in which both unrestricted and restricted DNA from a representative pHIP3 transformant (T2, grown for 40 generations in selective medium) was probed with pHIP3. Distinct hybridization signals (lane 2) above and below the position of unrestricted chromosomal DNA were observed. The higher signals matched with discrete bands visible on ethidium bromide-stained agarose gels. Digestion of total DNA with an enzyme (BglII; lane 3) having no recognition site for the plasmid DNA did not alter the position of these bands, whereas restriction with *NcoI* (lane 4), which linearizes pHIP3, shifted the signals completely to the position of linear pHIP3 (5.8 kb). These results clearly indicate that plasmid pHIP3 is maintained autonomously in *H. polymorpha* as a circular molecule. Similar results were obtained with pHIP1 (results not shown). Berardi & Thomas (1990) recently presented evidence for the existence of an *H. polymorpha* replicon-like sequence within or near the coding regions of the *S. cerevisiae* *LEU2* gene. Conceivably, this *S. cerevisiae*-derived *ARS* is responsible for the autonomous behaviour of plasmids pHIP1 and pHIP3 in *H. polymorpha*.

Further information about the fate of plasmid pHIP3 after transformation into *H. polymorpha* was obtained by Southern hybridization analyses of nine independent pHIP3 transformants (the analysis of five representative transformants is shown in Fig. 4). *BglII*-treated DNAs (lanes 1, 4, 7, 10, 13) mainly showed high-molecular-mass bands of varying lengths, indicating the presence of different multimeric forms of pHIP3 in the transformants. As expected, *NcoI* digestion of DNAs from the
Fig. 1. Physical maps of the *E. coli*- *H. polymorpha* shuttle vectors pHIP3 and pHRP2. Plasmid pHIP3 was constructed from plasmid pH7, consisting of the 1630 bp *Aha*III-*Aat*II fragment from pUC9 (nucleotides 2620–1570; Yanisch-Perron et al., 1985), the 960 bp *SacI*-CiaI fragment from pE194 (nucleotides 1940–2900; Horinouchi & Weisblum, 1982a) carrying the Em<sup>+</sup> gene and the 1030 bp *Hpa*II-MboI fragment from pC194 (nucleotides 975–2005; Horinouchi & Weisblum, 1982b) carrying a Cmr gene. Plasmid pHIP3 was constructed by insertion of the 2-2 kb SalI-XhoI fragment (sites were filled in) from YEpl3 (Broach et al., 1979), containing the *S. cerevisiae* LEU2 gene, into the *Stu*I site of pH7, thereby inactivating the Cmr gene. Plasmid pHIP1 is identical to pHIP3 except for the location of the LEU2 gene, which was inserted into the SalI site of pH7. Plasmid pHRP2 was constructed by inserting the LEU2-containing SalI-XhoI fragment from YEp13 (Broach et al., 1979) into *Stu*I- and *Sma*I-digested pHARSl (Roggenkamp et al., 1986), thereby inactivating the *URA3* gene. Complete sequences of plasmids pHIP3 and pHRP2 are available from the authors on request.

Fig. 2. Transformation of *H. polymorpha* A16 (leu1-1) with different plasmids. Cells were treated with different amounts of plasmid DNA (0.1, 1.0, 5.0 and 10.0 μg) using the optimized transformation protocol described in Methods. Transformation frequencies are mean values of at least three independent transformation experiments and are given as the total number of Leu<sup>+</sup> transformants obtained per 0.2 ml of competent cells. 〇, pHRP2; □, pHIP1; ▲, pHIP3; ■, pHIP1 linearized with *BamHI*.

Transformants (lanes 2, 5, 8, 11, 14) resulted in signals of the size of linear pHIP3, 5.8 kb. From this it can be concluded that the plasmids replicate as multimers, consisting of a variable number of monomers connected in a head-to-tail configuration. Three transformants (T2, T3 and T4) gave single bands, implying that they only contain intact copies of the plasmid. Two transformants contained additional bands smaller (T1: 3.7 kb, lane 2) or larger (T5: 7.0 kb, lane 14) than the original plasmid.

Restriction with *Asp718I* (lanes 3, 6, 9, 12, 15), which also linearizes pHIP3, resulted in a reverse situation: T1 showed a signal above (9.5 kb, lane 3) and T5 a signal below (1.1 kb, lane 15) the position of linear pHIP3. The
only structure that could account for the patterns of T1 and T5 is a multimer in which one of the monomers contains a deletion encompassing the Asp718i or the NcoI site, respectively. The sizes of the additional signals with T1 and T5 are consistent with deletions of 2.1 kb and 4.7 kb, respectively.

To determine the approximate copy number of the plasmids in H. polymorpha, the original probe from the Southern blot shown in Fig. 3 lanes 1-4 (transformant T2) was removed and the blot was reprobed with a fragment consisting of approximately 1 kb of pHIP3 (Cm moiety) and 1 kb of H. polymorpha genomic DNA (part of the AO gene). Densitometric scanning of the signals representing linear pHIP3 and the genomic fragment (Fig. 3, lane 7) revealed an approximate copy number of 6 (plasmid copies per genome equivalent).

Targeted integration of plasmids in the H. polymorpha genome

In order to examine the possibility of integrating plasmids in the H. polymorpha genome at defined sites, three plasmids were constructed (Fig. 5a). Plasmid pHIP11, carrying a 0.8 kb internal part of the H. polymorpha AO gene, is expected to integrate in the AO coding region by a single cross-over recombination event (also called 'homologous additive integration'; Hinnen et al., 1978), thereby disrupting the AO gene (Fig. 5b). Plasmid pHIP112, carrying the homologous amine oxidase gene (AMO) downstream of the AO promoter (2.3 kb region) and in addition a 0.7 kb fragment covering the 3' end of the AO gene, was designed to replace the complete AO structural gene by a double cross-over recombination event (Fig. 5d). Finally, plasmid pHIP111, carrying the H. polymorpha AO promoter on a 2.3 kb fragment, was expected to integrate in the AO promoter region in an additive way, thereby leaving the AO coding region intact and placing the plasmid-borne AMO under control of one of the copies of the AO promoter (Fig. 5f).

In S. cerevisiae (Orr-Weaver et al., 1981) linear ends of homologous sequences are recombinogenic and are used to target plasmids to specific sites on the genome. To test this for H. polymorpha, plasmids were linearized within the regions homologous to the yeast genome (integration boxes). Plasmid pHIP11 was linearized (BglII) in the middle of its 800 bp integration box, pHIP112 was cut at the BamHI site, thereby exposing its 2.3 and 0.7 kb integration boxes, and pHIP111 was cut at the SphI site, thereby creating recombining regions of 0.5 and 1.8 kb. In all three cases, linearization of the plasmids increased the transformation frequency approximately 10-fold, resulting in frequencies of approximately 10^6 transformants per μg DNA. To determine the frequency of targeted integration of pHIP11 and pHIP112, which should lead to disruption of the AO gene, transformants were screened for their inability to utilize methanol as sole carbon source. As shown in Table 2, 1 and 3% of the linear pHIP11 and pHIP112 transformants, respectively, displayed a Mut^- (methanol utilization defective) phenotype, whereas no Mut^- phenotype was observed...
Fig. 5. (a) Physical maps of integrating plasmids pHIP11, pHIP111 and pHIP112 and the structure of the relevant part of the *H. polymorpha* chromosome. Plasmid pHIP11 was constructed by insertion of the 800 bp EcoRV-BglII fragment of the *AO* gene (nucleotides 22-823; Ledeboer et al., 1985) into BamHI- and SmaI-digested pHIP1. Plasmids pHIP111 and pHIP112 are derivatives of plasmid pTZ19R (Mead et al., 1986). pHIP111 was constructed by insertion of the 2.2 kb *SalI*-*XhoI* fragment (*XhoI* site filled in) from YEpl3 (Broach et al., 1979), containing the *S. cerevisiae* LEU2 gene into *SalI*-HindIII (HindIII site filled in) cleaved pTZ19R, resulting in plasmid pTZ19LEU. Subsequently, two fragments were simultaneously inserted into *BamHI*-SacI-digested pTZ19LEU: (i) a 2.2 kb *BamHI*-HindIII fragment containing the *AO* promoter region (Ledeboer et al., 1985) in which the *AO* translation initiation codon was replaced by a HindIII site by means of site-directed mutagenesis; and (ii) a 2.2 kb *HindIII*-SacI fragment containing the *H. polymorpha* amine oxidase (AMO) gene (nucleotides -18 to +2138; Bruinenberg et al., 1989). Plasmid pHIP112 was constructed by insertion of a 0.7 kb *BglII*-XbaI fragment (*BglII* site filled in) covering the 3' region of the *AO* gene (nucleotides 1904 to 2604; Ledeboer et al., 1985) into *SalI*-SacI (SalI site filled in) cleaved pHIP111. Complete sequences of plasmids pHIP11, pHIP111 and pHIP112 are available from the authors on request. (b-f) Chromosomal structures resulting from homologous recombination. (b) Chromosomal structure resulting from 1 x cross-over recombination of one copy of pHIP11 within the genomic *AO* gene. (c) Chromosomal structure resulting from 1 x cross-over recombination of three copies of pHIP11 within the genomic *AO* gene. (d) Chromosomal structure resulting from 2 x cross-over recombination of pHIP112 with the flanking regions of the genomic *AO* gene (gene replacement). (e) Chromosomal structure resulting from 2 x cross-over recombination of pHIP112 with the flanking regions of the genomic *AO* gene (gene replacement), followed by 1 x cross-over recombination of an additional plasmid copy. (f) Chromosomal structure resulting from 1 x cross-over recombination of one copy of pHIP111 within the promoter region of the genomic *AO* gene. Small arrowheads (△ or ▽) indicate *NcoI* cleavage sites, kb values indicate the sizes of the *NcoI* fragments detected in Southern hybridization analyses with an internal *AO* probe (xxxxx) or a recombinant probe homologous to the *AO* promoter region (*pAO*) and the plasmid-borne *LEU2* gene (xxxx). The box with vertical hatching represents the region downstream of the *AO* gene. 'AO' and 'AO' indicate 5'- or 3'-deleted *AO* regions, respectively. Small open boxes in (c) represent duplicated 'AO' regions. Different chromosomal structures are not drawn to scale.
among transformants resulting from circular plasmid DNA. These results emphasize the significance of linearizing the plasmids within their integration boxes. They also suggest that, analogous to S. cerevisiae, plasmids can be targeted to specific sites in the genome of H. polymorpha by linearization within homologous regions. When the Mut+ transformants were grown on glycerol, conditions which partially derepress AO synthesis, no alcohol oxidase activity could be detected in these cells, confirming disruption of the AO gene. This was corroborated by Southern hybridization analysis (Fig. 6) of total DNAs isolated from untransformed yeast (A16), two pHIP11 transformants (11a and b) and two pHIP112 transformants (112a and b). DNAs were digested with NcoI, hybridized first with an internal fragment of the AO gene, indicated as xxxxxxx in Fig. 5) or a recombinant probe homologous to 1.5 kb of the AO promoter region and 1.1 kb of the plasmid-borne LEU2 gene (panel b, indicated as xxxxx in Fig. 5). Lanes 4, 5, 9, 13 and 14 contained molecular mass markers which did not hybridize with the probes used.

As expected, hybridization of DNAs from 112a and 112b with the AO probe (Fig. 6a, lanes 11 and 12) showed no signals, indicating replacement of the AO gene by the plasmid. This was confirmed by reprobing the DNAs with the pAOX/LEU2 probe. Bands of approximately 6.5 and 5.9 kb appeared (Fig. 6b, lanes 11 and 12), which is consistent with the gene-replacement structure depicted in Fig. 5e. In addition, 112a showed a band of 2.9 kb, which is at the same position as the 2.9 kb pHIP112 fragment visible in lane 3. This additional fragment can be explained by the chromosomal structure depicted in Fig. 5e. This structure could result from a gene-replacement recombination followed by a single cross-over recombination of an additional (recircularized) plasmid copy.

Since site-specific integration of pHIP11 leaves the AO gene intact, integrations could not be screened by a Mut+ phenotype, and therefore had to be analysed directly by Southern blot hybridization analysis. Out of nine transformants analysed, two showed identical hybridization patterns consistent with single cross-over recombinations within the AO gene as depicted in Fig. 5b. In addition, DNA from 11a (lane 7) showed a band of 6.7 kb, at the same position as linear pHIP11 (lanes 1 and 15), indicating tandem integrations of pHIP11 (Fig. 5c). Reprobing the DNAs with the pAOX/LEU2 probe further confirmed the chromosomal structures of 11a and 11b; only the bands representing linear pHIP11 and the chromosomal fragment covering the AO 5' region reappeared (Fig. 6b, lanes 7 and 8). The relative density of the band representing linear DNA in case of 11a indicates tandem integration of three plasmid copies.

Fig. 6. Southern hybridization analyses of DNAs from chromosomally engineered strains. NcoI-digested DNAs of E. coli-derived plasmids pHIP11 (lanes 1, 15), pHIP112 (lane 2), pHIP112 (lane 3), H. polymorpha strain A16 (lane 6), transformants 11a and 11b (lanes 7, 8), 111 (lane 10) and 112a and 112b (lanes 11, 12) were hybridized with an internal part of the AO gene (panel a; 1260 bp PvuI-NdeI fragment of the AO gene, indicated as xxxxxx in Fig. 5) or a recombinant probe homologous to 1-5 kb of the AO promoter region and 1.1 kb of the plasmid-borne LEU2 gene (panel b, indicated as xxxxx in Fig. 5). Lanes 4, 5, 9, 13 and 14 contained molecular mass markers which did not hybridize with the probes used.
Table 3. Transformation of H. polymorpha with linearized plasmids

<table>
<thead>
<tr>
<th>Plasmid used</th>
<th>Location of linearizing cut</th>
<th>No. of transformants</th>
<th>Relative frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>pHIP1</td>
<td>Circular</td>
<td>620</td>
<td>1-0</td>
</tr>
<tr>
<td></td>
<td>BamHI (5')*</td>
<td>9800</td>
<td>15-7</td>
</tr>
<tr>
<td></td>
<td>NcoI (5')*</td>
<td>9500</td>
<td>15-1</td>
</tr>
<tr>
<td></td>
<td>SalI (5')*</td>
<td>8800</td>
<td>14-1</td>
</tr>
<tr>
<td></td>
<td>PsiI (5')*</td>
<td>7100</td>
<td>11-5</td>
</tr>
<tr>
<td></td>
<td>SmaI (blunt)*</td>
<td>5800</td>
<td>9-4</td>
</tr>
<tr>
<td></td>
<td>Asp718i (5')*</td>
<td>LEU2</td>
<td>6400</td>
</tr>
<tr>
<td></td>
<td>EcoRV (blunt)*</td>
<td>LEU2</td>
<td>4100</td>
</tr>
<tr>
<td>pHIP11</td>
<td>Circular</td>
<td>310</td>
<td>1-0</td>
</tr>
<tr>
<td></td>
<td>BhgII (5')*</td>
<td>AO region</td>
<td>4600</td>
</tr>
<tr>
<td></td>
<td>NcoI (5')*</td>
<td>Vector</td>
<td>5600</td>
</tr>
</tbody>
</table>

* Type of DSB (blunt ends, 3’ or 5’ overhanging ends).

The above results clearly show that DSB in plasmid regions bearing no homology with chromosomal DNA are efficiently repaired in H. polymorpha. To determine whether this also occurs in the case of DSB at sites having homology with chromosomal DNA, and whether this takes place without interaction with the homologous chromosomal locus, linearized plasmid pHIP11 was used to transform strain A16 at a DNA input of 0.1 µg. Transformation frequencies with pHIP11 linearized (BglII) within the 0.8 kb region homologous to the genomic AO gene were not increased as compared to pHIP1 linearized within its nonhomologous vector region (NcoI; Table 3), suggesting that the BglII cut is repaired without interaction with the homologous region on the chromosome. Physical evidence for non-recombinational DSB repair was provided by Southern hybridization analysis of DNAs from eight linear pHIP11 transformants (Fig. 7). These transformants were all Mut+, indicating that pHIP11 had not integrated in the AO gene. DNAs from four BglII- and four NcoI-linearized pHIP11 transformants were digested with BglII or NcoI. Hybridization with pHIP11 revealed that one out of four plasmid DNAs obtained from pHIP11-BglII transformants contained an intact BglII site and three of four plasmid DNAs obtained from the pHIP11-NcoI transformants contained an intact NcoI site. This value of 50% precise repair is not significantly different from the 68% precise repair of DSB within the LEU2 gene. Restriction of the plasmids lacking either the BglII or the NcoI site with NcoI or BglII, respectively, resulted in signals at the position of linear intact pHIP11, indicating only small rearrangements encompassing the lost restriction site.
Discussion

In this paper we describe an optimized method for plasmid-mediated transformation of the methylotrophic yeast *H. polymorpha* and a successful strategy for targeted plasmid integration. Although plasmid transformations and plasmid integrations have been reported for *H. polymorpha* by several authors (Gleeson et al., 1986; Roggenkamp et al., 1986; Tikhomirova et al., 1986; Berardi & Thomas, 1990; Sierkstra et al., 1991; Beburov et al., 1990; Hodgkins et al., 1990; Sudbery et al., 1988; Fellinger et al., 1991), no detailed analysis was available of the possible interactions between transforming DNA and the *H. polymorpha* genome. Because this information would greatly enhance the possibilities for genetic engineering of *H. polymorpha*, this study aimed to perform such an analysis.

The main advantage of our protocol over other protocols for transformation of *H. polymorpha* (Gleeson et al., 1986; Roggenkamp et al., 1986; Tikhomirova et al., 1986; Berardi & Thomas, 1990) appeared to be its reproducibility. Very recently, a transformation protocol much resembling our protocol has been shown to be applicable to a variety of yeast species including *S. cerevisiae* and *Schizosaccharomyces pombe* (Dohmen et al., 1991). Using our protocol and the replicating plasmid pHRP2 (contains the *HARSI* sequence; Roggenkamp et al., 1986), we were able to obtain highly reproducible transformation frequencies of $2 \times 10^3$ transformants per μg plasmid DNA. Recently, the use of this protocol and vector pHRP2 allowed us to generate *H. polymorpha* gene libraries in mutant strains which are impaired in the assembly of functional peroxisomes (Cregg et al., 1990).

Two genes involved in peroxisome assembly were successfully isolated from these gene libraries (P. Haima and others, unpublished results).

Surprisingly, transformation of *H. polymorpha* strain A16 with plasmids pHIP1 and pHIP3 lacking the *HARSI* sequence resulted in approximately twofold higher frequencies. This is probably due to the presence of an active *H. polymorpha* replicon-like sequence within or near the coding regions of the *S. cerevisiae LEU2* gene (Berardi & Thomas, 1990). ARS activity conferred by the *S. cerevisiae LEU2* gene fragment has also been detected in *Pichia pastoris* (Cregg et al., 1985). Autonomous behaviour of the plasmids was confirmed by the observation that plasmids could be rescued intact from the yeast by retransformation of *E. coli* with total yeast DNA and by the instability of the Leu+ trait under non-selective conditions. Southern hybridization analyses revealed that the plasmids replicated as multimers consisting of monomers in a head-to-tail configuration at an approximate copy number of 6 (monomers per genome equivalent). Two out of nine transformants analysed appeared to contain multimers in which one of the monomers contained a deletion. The nature of this structural instability is as yet unknown. Possible explanations include slipping of the recombination mechanism responsible for yielding multimers or structural instability of the multimeric plasmid forms. Plasmid multimerization was observed in *H. polymorpha* by Tikhomirova et al. (1986) and in *Sch. pombe* by Sakaguchi & Yamamoto (1982), and was shown to enhance the mitotic stability of the plasmids. Conceivably, plasmid multimerization is responsible for the relatively high mitotic stability of the pHIP plasmids in...
H. polymorpha under non-selective growth conditions (frequency of plasmid loss is 55–85% per 40 generations) as compared to the stability of plasmids containing HARS1 and HARS2 sequences (plasmid loss for pHARS1 and pHARS2 amounts to 98% per 10 generations; Roggenkamp et al., 1986). A high degree of plasmid multimerization might also offer an explanation for the occurrence of stable phenotypes with multi-copy tandem arrangements of plasmid sequences as observed by Roggenkamp and coworkers in H. polymorpha pHARS1 and pHARS2 transformants (Roggenkamp et al., 1986; Janowicz et al., 1991). Although the authors favour multi-copy integration of the plasmids in the genome, the possibility of multimeric autonomous plasmids cannot be ruled out. Detailed Southern hybridization analyses of these stable transformants should clarify this point.

Targeted integration with plasmids pHIP11 and pHIP112 by single or double cross-over recombinations, respectively, was only observed with plasmids linearized within the regions homologous to the yeast genome (integration boxes). From this it may be concluded that, analogous to S. cerevisiae (Orr-Weaver et al., 1981) and P. pastoris (Cregar & Madden, 1987), linear ends of homologous sequences are recombogenic. However, targeted integration of circular plasmids has also been observed in H. polymorpha (Sierkstra et al., 1991), indicating that linear homologous ends are not obligatory for targeted integration. Occasionally, we also observed targeted integration of circular plasmids containing large integration boxes, but integration was always less efficient as compared to linear plasmids (K. N. Faber & P. Haima, unpublished results). This resembles the situation in S. cerevisiae, where the integration frequency of circular replicating plasmids is always less than 1% (Orr-Weaver et al., 1983).

Southern hybridization analyses revealed chromosomal structures which were consistent with classical single and double cross-over recombinations. Both single-copy and multi-copy tandem integrations (two and three copies) were observed. The chromosomal structure of one of the pHIP112 transformants was consistent with a $2 \times$ cross-over integration followed by $1 \times$ cross-over integration of an additional (recircularized) plasmid copy. Recently, these combinations of $1 \times$ and $2 \times$ cross-over integrations have also been reported for P. pastoris (Romanos et al., 1990).

Despite the linearization within the integration boxes, only a minority of our plasmid constructs integrated at the homologous site in the genome (integration frequencies amounted to 1, 3 and 22% for pHIP11, pHIP112 and pHIP1111, respectively). This appears very akin to the situation in S. cerevisiae, in which integration frequencies of linearized replicating plasmids can vary from 6 to 50% (Orr-Weaver et al., 1983). The observed differences in integration frequencies of plasmids pHIP11, pHIP112 and pHIP111 might be due to differences in the length of the integration boxes. We observed that by increasing the length of the pHIP11 integration box from 800 to 1260 bp, the integration frequencies were approximately doubled (P. Haima & G. J. Swaving, unpublished results). Alternatively, integrations might occur with variable frequencies at different loci, as has been observed with S. cerevisiae (Orr-Weaver et al., 1981) and Sch. pombe (Grimm & Kohli, 1988). In the cases in which no targeted integration was found, we observed intact autonomous plasmids. Apparently, the DSB in these plasmids had been repaired without recombination with the homologous site on the genome. This view was strengthened by the observation that DSB in nonhomologous plasmid regions were repaired as efficiently as in homologous plasmid regions. In both cases, linearization increased the transforming activity of the plasmids up to 15-fold as compared to circular plasmids. Homology-independent DSB repair has been observed before in H. polymorpha (Gleson et al., 1986), S. cerevisiae (Orr-Weaver et al., 1981, 1983; Orr-Weaver & Szostak, 1983; Kunes et al., 1985; Perera et al., 1988) and Sch. pombe (Grimm & Kohli, 1988). A striking difference from our observations is that these authors never observed a stimulating effect of plasmid linearization on transformation frequencies; in S. cerevisiae in fact the opposite was often observed, namely that linearization had a strong negative effect on plasmid transformation frequencies (Orr-Weaver et al., 1981). A possible explanation for this discrepancy may be that linear plasmid molecules are more efficiently internalized in our transformation system. This could represent a characteristic feature of either the host H. polymorpha or the transformation procedure.

Non-recombinational DSB repair was precise in 68% of the cases of linearization within the coding region of the LEU2 gene of plasmid pHIP1 and 50% in the case of BglI- and NcoI-linearized pHIP11. In those cases in which DSB repair was not precise, plasmids contained small rearrangements encompassing the lost restriction site. Comparable data were reported for S. cerevisiae: up to 50% of the transformants resulting from non-recombinational DSB repair contained deleted plasmids (Orr-Weaver & Szostak, 1983; Kunes et al., 1985).

The plasmid integration strategy for H. polymorpha presented in this study involves the use of replicating plasmids containing recombinogenic DSB within H. polymorpha genomic sequences. Since integration of these plasmids can be achieved by either single or double cross-over recombinations, it can be used as a strategy to routinely stabilize genes for gene expression purposes and to modify or inactivate genes of interest. Recently we
successively applied this integration strategy to modify the amine oxidase gene (K. N. Faber and others, unpublished). However, plasmid integration efficiency is relatively low (1–22%), due to efficient repair of DSB in \textit{H. polymorpha} and the presence of an active \textit{H. polymorpha} replication origin within the \textit{S. cerevisiae}-derived \textit{LEU2} fragment. A possible way to enhance the efficiency is to use a stabilizing procedure, which involves growing the transformants for 50–100 generations in non-selective medium and subsequently selecting for segregants still showing the transformant phenotype (Roggenkamp et al., 1986). By use of such stabilizing procedures, Sierkstra et al. (1991) succeeded in obtaining 50% targeted integration of a circular replicating plasmid in \textit{H. polymorpha}. The main disadvantage of this method is that in all the other cases (50%) the plasmid integrated at nonhomologous loci. Using the above stabilizing procedure for integration of pH1P111, we observed up to 80% nonhomologous integrations (K. N. Faber, unpublished). Therefore, the use of non-replicating plasmids is probably the most attractive way to obtain high frequencies of homologous recombination. The construction of such suicide plasmids is likely to be very valuable in order to further increase the efficiencies of targeted integration in \textit{H. polymorpha}.

We thank Martin Bokrantz and Jim Cregg for helpful discussions and Anton Nolle for photography. Peter Haima was supported by Unilever Research Laboratories, Vlaardingen. Klaas Nico Faber was supported by the Netherlands Technology Foundation (STW), which is subsidized by the Netherlands Organization for the Advancement of Pure Research (NWO).

References


