## Two new multi-purpose multicopy *Schizosaccharomyces pombe* shuttle vectors, pSP1 and pSP2

Guillaume Cottarel, David Beach, Ulrich Deuschle\*

Howard Hughes Medical Institute, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY 11724, USA

Received: 2 November 1992 / Accpted: 22 November 1992

Abstract. Plasmids pSP1 and pSP2 are two new *Schizosaccharomyces pombe ars1* multicopy vectors with the *Saccharomyces cerevisiae LEU2* and *URA3* genes as selectable markers. They are derivatives of *S. cerevisiae* integrative plasmids. These plasmids allow classical molecular genetic techniques, such as mutagenesis, nest-ed deletions and sequencing, to be performed directly.

Key words: Autonomously replicating sequence – Recombinant DNA – Nested deletions – Mutagenesis – Schizosaccharomyces pombe

Although S. pombe molecular genetics has been possible for more than a decade (Beach and Nurse 1981), little has been done to improve the cloning and manipulations of its DNA. Initially, genes of S. pombe have been cloned using S. cerevisiae-Escherichia coli shuttle vectors bearing the 2-um autonomously replicating sequence (ars) for replication: pDB248 (Beach and Nurse 1981), pDB262 (Beach et al. 1982a), pDB248' (Beach et al. 1982b), YEp13 (Broach et al. 1979), and pWH5 (Wright et al. 1986). In contrast to common belief these 2-µm-based vectors do not behave as real high-copy plasmids in S. pombe (Heyer et al. 1986). The region that functions as an ars in S. pombe does not include the complete replication origin that functions in S. cerevisiae (Gaillardin et al. 1983; G. C. unpublished data) and not all 2-µm-based plasmids transform S. pombe at high frequency.

The isolation and characterisation of ars sequences that promote high transformation efficiency (Losson and Lacroute 1983; Maundrell et al. 1988) was crucial for the design of multicopy plasmids such as pFL20 (Losson and Lacroute 1983), pIRT2 (Hindley et al. 1987), pON163 and pDW232 (Weilguny et al. 1991).

Correspondence to: G. Cottarel

We designed two versatile S. pombe vectors by introducing the S. pombe ars1 element into the integrative S. cerevisiae plasmids pRS305 and pRS306 (Sikorski and Hieter 1989). These two constructs carry the LEU2 (pRS305) or URA3 (pRS306) gene within the NdeI site of PRSS56 (Sikorski and Hieter 1989), a chimeric plasmid constructed from pBluescribe and pBluescript (Stratagene; Sikorski and Hieter 1989). These plasmids contain the f1 phage origin of DNA replication for the production of single-stranded DNA in vivo, the T3/T7 phage promoters for the in-vitro synthesis of RNA, and a large polylinker region in the alpha fragment of the LacZ gene allowing the blue/white color screen of recombinants. Nested deletions of inserts can be performed (Henikoff 1984, 1990) and single-stranded DNA can be prepared for sequencing (Sanger et al. 1977). The S. cerevisiae LEU2 and URA3 genes complement S. pombe mutants carrying the leu1 and ura4 alleles respectively. The 1.2-kbp EcoRI ars1 DNA fragment from S. pombe (Losson and Lacroute 1983) was filled in with T4 DNA polymerase in the presence of dATP and dTTP and introduced into the AatII sites of pRS305 and pRS306 which were blunted with the exonuclease activity of the T4 DNA polymerase in the presence of dCTP (Sambrook et al. 1989). The derivatives were named pSP1 and pSP2 respectively (plasmid S. pombe) (Fig. 1). Although the ligation of a blunt AatII site to a blunt EcoRI site should recreate an EcoRI site, these sites are not present in pSP2 probably due to a fortuitus nucleotide misincorporation during the blunt-ending reaction. Therefore, EcoRI is unique and in the cloning area of pSP2, while pSP1 carries three sites. The natural NdeI site in S. pombe ars1 was removed by a fill-in reaction (D.B., unpublished data) prior its use in the construction of these vectors. As a consequence NdeI is not present in pSP1 and is unique in the URA3 fragment of pSP2. The structure of the plasmids is available through compilation of the components from computer database.

Both vectors transform *S. pombe* at high efficiency and have been used successfully to subclone various genes (Matsumoto and Beach 1991; G. C. unpublished

<sup>\*</sup> Present adress: Basel Institute for Immunology, Grenzacherstrasse 487, CH-4005 Basel, Switzerland

548



Fig. 1. Structure of the pSP1 and pSP2 vectors. The unique restriction sites are shown. The T3 promoter resides upstream of the KpnI(not shown in pSP1) and transcription proceeds toward the SacI site; the T7 promoter resides upstream of the SacI site and initiates transcription in the opposite direction. Ap, ampicillin resistance

data), generate nested deletions in DNA fragments as large as 7.5 kbp (Henikoff 1984) for identification of the complementing region by direct transformation of yeast, and for DNA sequencing (G. C., unpublished results).

Acknowledgements. G. C. acknowledges the support of the Fondation Simone et Cino del Duca.

## References

- Beach D, Nurse P (1981) Nature 290:140-142
- Beach D, Durkacz B, Nurse P (1982a) Nature 300:706-709
- Beach D, Piper M, Nurse P (1982b) Mol Gen Genet 187:326-329
- Broach JR, Strathern JN, Hicks JB (1979) Gene 8:121-133
- Gaillardin C, Fournier P, Budar F, Kudla B, Gerbaud C, Heslot H (1983) Curr Genet 7:245-253
- Henikoff S (1984) Gene 28:351-359



 $\beta$ -lactamase gene; *LEU2*, *S. cerevisiae*  $\beta$ -IPM dehydrogenase gene; *URA3*, *S. cerevisiae* orotidine-5'P decarboxylase gene; *LacZ*,  $\beta$ -galactosidase gene; *LacI*, Lac repressor gene; *ori*, ColE1 origin of replication;  $f1^+$ , f1 origin of replication; *ars1*, *S. pombe* autonomously replicating sequence previously deleted of its *NdeI* site

- Henikoff S (1990) Nucleic Acids Res 18:2961-2966
- Heyer W-D, Sipiczki M, Kohli J (1986) Mol Cell Biol 6:80-89
- Hindley J, Phear G, Stein M, Beach D (1987) Mol Cell Biol 7:504-511
- Losson R, Lacroute F (1983) Cell 32:371-377
- Matsumoto T, Beach D (1991) Cell 66:347-360
- Maundrell K, Hutchinson A, Shall S (1988) EMBO J 7:2203-2209
- Sambrook J, Fritsch EF, Maniatis T (1989) Molecular cloning: a laboratory manual. Cold Spring Harbor Laboratory, Cold Spring Harbor, New York
- Sanger F, Nicklen S, Coulson AR (1977) Proc Natl Acad Sci USA 74:5463-5467
- Sikorski RS, Hieter P (1989) Genetics 122:19-27
- Weilguny D, Prætorius M, Carr A, Egel R, Nielsen O (1991) Gene 99:47-54
- Wright A, Maundrell K, Heyer W-D, Beach D, Nurse P (1986) Plasmid 15:156-158

Communicated by R. Rothstein