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Two Portable Recombination Enhancers Direct Donor Choice in Fission Yeast Heterochromatin

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Abstract

Mating-type switching in fission yeast results from gene conversions of the active mat1 locus by heterochromatic donors. mat1 is preferentially converted by mat2-P in M cells and by mat3-M in P cells. Here, we report that donor choice is governed by two portable recombination enhancers capable of promoting use of their adjacent cassette even when they are transposed to an ectopic location within the mat2-mat3 heterochromatic domain. Cells whose silent cassettes are swapped to mat2-M mat3-P switch mating-type poorly due to a defect in directionality but cells whose recombination enhancers were transposed together with the cassette contents switched like wild type. Trans-acting mutations that impair directionality affected the wild-type and swapped cassettes in identical ways when the recombination enhancers were transposed together with their cognate cassette, showing essential regulatory steps occur through the recombination enhancers. Our observations lead to a model where heterochromatin biases competitions between the two recombination enhancers to achieve directionality.


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Introduction

Fission yeast cells switch mating type by directed recombination events where the information in the expressed mat1 locus is replaced with information copied from one of two silent loci, mat2 or mat3 (reviewed in [1]). The system allows investigating multiple facets of recombination, including effects of chromatin structure on recombination and mechanisms of donor choice; how is a particular DNA template selected for recombination when several are available in a cell?

The mat1, mat2, and mat3 loci are linked in the mating-type region (Figure 1). mat1 determines the mating type of the cell by expressing two divergent regulatory genes, Pi and Pc in P cells (mat1-P allele), Mi and Mc in M cells (mat1-M allele; [2]). Silent information for the P and M mating types is stored at respectively mat2 ~17 kb centromere-distal to mat1, and mat3 ~29 kb centromere-distal to mat1 [3]–[5]. The mating-type specific information at mat1, mat2 and mat3 is flanked by short homology boxes, the centromere-distal H1 box and the centromere-proximal H2 box [2]. Other elements are specific for mat2 and mat3 [2],[6],[7] (Figure 1). mat2 and mat3 are furthermore embedded in a ~20 kb heterochromatic domain that spans the mat2-mat3 interval and extends on both sides to inverted repeat boundaries [8],[9]. This domain has been studied extensively. It provides one of the best characterized model systems for how heterochromatin regions can be established and maintained. In this domain, histones are hypoacetylated, histone H3 is methylated at lysine 9 (H3K9me) in an RNA interference-dependent manner, and chromodomain proteins of the HP1 family are associated with the modified histones [8],[10]–[15]. The HP1-like chromodomain protein Swi6 interacts with numerous protein complexes believed to modulate heterochromatin formation, gene silencing and recombination, in ways that remain to a large extent undefined in particular regarding roles in recombination [14],[16]–[19].

Interconversions of the mat1 locus between mat1-P and mat1-M lead to mating-type switching (reviewed in [1]). The conversions are coupled to DNA replication which reaches mat1 from a centromere-distal origin [20],[21]. Switching is initiated by the introduction of a strand-specific imprint in the lagging strand, resulting from the incorporation of two ribonucleotides or a nick between the mat1 H1 homology box and the mating-type specific information [20],[22]–[28]. In the following rounds of DNA replication, the imprint is placed again on the chromatid made by lagging-strand synthesis, generating a lineage of imprinted, switchable cells [24],[29]. While lagging-strand synthesis propagates the imprinted mat1 locus in this lineage, leading-strand synthesis produces switched progeny (Figure 1B). At each division, leading-strand synthesis proceeds through the mat1 H1 homology box and stops at the imprint creating a single-ended double-strand break (DSB) or other recombigenic molecule with a free 3’end [25],[30]. The free 3’end invades the H1 box of one of the silent loci which is then used instead of mat1 as template for leading-strand synthesis [29],[31]. This heals the break. Resolution of the recombination intermediate occurs within the H2 homology box with the help of the Swi4/8 and Swi9/10 gene products, producing a switched mat1 locus [5],[32]–[36]. The newly-switched mat1 locus does not carry an imprint hence it does not...
switch at the following S phase, however the chromatin made by lagging-strand synthesis acquires an imprint and starts a new lineage of switchable cells.

A choice of information is made in all switchable cells such that either mat2-P or mat3-M is used as donor to replicate and convert mat1. At this step, mat2-P and mat3-M are not picked at random. Switchable mat1-M cells preferentially use mat2-P whereas switchable mat1-P cells use mat3-M [23],[37],[38]. Coupled with the mechanism of switching outlined above, these directed choices produce a reproducible pattern of mating-type switching where (1) one out of four grand-daughters of a newly-switched cell has a high probability of having a switched mating-type (80–90%; one-in-four rule) and (2) once a cell becomes switchable the probability of recurrent switches in its lineage is very high (80–90%; recurrent-switching rule; Figure 1C).

Previous studies have revealed the importance of donor location and chromatin structure in donor choice [39]–[42]. Strains in which the mat2 and mat3 contents were swapped from mat2-P mat3-M (h<sup>90</sup> configuration) to mat2-M mat3-P (h<sup>90</sup> configuration) switch inefficiently to the opposite mating-type [39]. Mutations in the chromodomain protein Swi6, the H3K9 methyltransferase Clr4, or the Clr4-complex subunits Clr7 and Clr8 have opposite effects on switching in the h<sup>90</sup> and h<sup>90</sup> mating-type regions indicating chromatin structure favors use of mat2 in M cells and use of mat3 in P cells [39],[42]. The phenotypes of these mutants suggest that unproductive homologous switching occurs in h<sup>90</sup> cells where mat1-M is converted by mat2-M and mat1-P by mat3-M instead of the productive heterologous switching occurring in h<sup>90</sup> cells.

The strand exchange taking place at H1 is likely to be a determining step in donor choice. The Swi2 and Swi5 proteins are believed to facilitate this step together with Rad22, the fission yeast RAD52 homolog [43] and Rhp51, the S. pombe RecA homolog [44],[45]. The imprint, detected as a chromosomal fragile site, is formed at mat1 in swi2 and swi5 mutants but a subsequent step in the conversion process fails [5]. Consistent with this step being strand-invasion at the donor loci Swi2 interacts physically with both Swi5 and Rhp51 [17] and Swi5 facilitates Rhp51-mediated strand exchange <i>in vitro</i> [46]–[49]. Combined with the observation that Swi2 interacts with Swi6 [17], the properties of Swi2 and Swi5 place these factors close to the point where donor selection takes place.

A model for the directionality of mating-type switching combining effects of chromatin structure and targeted recruitment of recombination proteins was proposed in [41] (Figure 1; referred to as 2004 model below). In this model, the search for a donor starts at mat2. If the Swi2/Swi5 recombination-promoting complex (RPC) is encountered at mat2, mat2 is used to convert mat1. If RPC is not at mat2, the search proceeds to mat3 and mat5, which is constitutively associated with RPC, is used to convert mat1. The constitutive association of mat3 and RPC observed in both P and M cells is proposed to occur through a DNA element named SRE [41] that we will call SRE3 below to reflect its proximity to mat3. RPC is localized at SRE3 in P cells – ensuring that mat3 is used in P cells - but spreads from SRE3 all the way to mat2 in M cells – ensuring that mat2 is used in M cells. Spreading of RPC from SRE3 to mat2 requires Swi6. A recent addition to the model proposes that the spreading is driven by a greater abundance of the Swi2 and Swi5 proteins in M cells resulting from the positive regulation of the <i>swi2</i> and <i>swi5</i> genes by the M-specific transcription factor Mc [50]. Alternatively, Mc might stimulate the production of a shorter form of Swi2 expressed in P cells through alternative promoter usage [51].

The directionality model summarized above [41] provides a framework for investigations of mating-type switching, although several critical steps in it have no documented mechanism. One unexplained feature is that the search for a donor should start at mat2. This step is important because it accounts for mat2 being used in M cells when Swi2/Swi5 is present at both mat2-P and mat3-M. The model proposes that a higher-order chromatin structure helps choosing mat2 by placing it near mat1 but how this occurs remains unknown. Another aspect of the model that has not been documented experimentally is the physical interaction between SRE3 and Swi2. This is also a crucial element because the model is centered on SRE3 being the sole entry point for Swi2 in the mating-type region, accounting for the observation that Swi2 was not detected in the mating-type region of SRE3-M strains by ChIP [41]. Here, we report further investigations on the directionality of mating-type switching bearing on these and other points. Our results challenge the notions that SRE3 is the sole entry point for Swi2, that Swi2 reaches mat2 by spreading from SRE3, and that the search for a donor starts at mat2. Instead, our results show that directionality requires two recombination enhancers, SRE2 and SRE3, whose ability to stimulate recombination in a cell-type specific manner is not tied to a specific location in the mating-type region. We present evidence that directionality results from competitions between SRE2 and SRE3, governed by cell-type specific chromatin structures.

## Results

SRE3-independent effects of Swi2 and Swi5 on the directionality of mating-type switching indicate the presence of a second recombination enhancer

The SRE3 element was described as the entry point at which the Swi2/Swi5 complex associates with the mating-type region [41]. Following this initial association, proposed to take place in both cell types, Swi2 could remain at SRE3 in P cells or spread to mat2 in M cells. Support for this mechanism is provided by ChIP experiments that failed to detect Swi2 anywhere in the mating-type region in strains lacking SRE3 [41]. We examined the model further through a simple genetic test. If the directed association of

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**Author Summary**

The state of chromatin, heterochromatin or euchromatin, affects homologous recombination in eukaryotes. We study mating-type switching in fission yeast to learn how recombination is regulated in heterochromatin. Fission yeast exists as two mating-types, P or M, determined by the allele present at the expressed mat1 locus. Genetic information for the P and M mating-types is stored in two silent heterochromatiic cassettes, mat2-P and mat3-M. Cells can switch mating-type by a replication-coupled recombination event where one of the silent cassettes is used as donor to convert mat1. Mating-type switching occurs in a directional manner where mat2-P is a preferred donor in M cells and mat3-M is preferred in P cells. In this study, we investigated factors responsible for these directed recombination events. We found that two portable recombination enhancers within the heterochromatiic region compete with each other and direct recombination in a cell-type specific manner. We also found that heterochromatin plays an important role in directionality by biasing competitions between the two enhancers. Our findings suggest a new model for directed recombination in a heterochromatiic domain and open the field for further studies of recombination regulation in other chromatin contexts.

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Figure 1. Mating-type region and mating-type switching in *S. pombe*. (A) Schematic representation of the mating-type region showing the expressed, switchable, *mat1* locus and the silent *mat2*-P and *mat3*-M donor loci. Elements are described in the text. (B) Model for the replication-coupled gene conversions of *mat1* responsible for mating-type switching. (C) Pedigree of switching. (D) 2004 model for the directionality of switching ([41]). The model proposes that SRE3 attracts the Swi2/Swi5 recombination complex to the mating-type region. Swi2/Swi5 remains localized near *mat3*-M in P cells, facilitating the use of *mat3*-M as a donor, and spreads over the entire mating-type region in M cells, facilitating the use of *mat2*-P. Use of *mat2*-P is favored over *mat3*-M when Swi2/Swi5 is present at both *mat2*-P and *mat3*-M (as in wild-type M cells) or in the absence of a functional directionality mechanism (as in SRE3Δ or swi2Δ cells).

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Swi2 with the mating-type region is abolished in SRE3A cells the mating-type bias in SRE3A cells should not be altered by deletion of swi2.

In S. pombe, the efficiency of mating-type switching can be estimated by staining sporulated colonies with iodine vapors. Efficiently-switching strains produce colonies that are stained darkly by iodine vapors because they contain many spores while poorly-switching strains produce lightly-stained colonies [52]. The predominant mating-type in cell populations can be further determined by quantifying the content of mat1 by Southern blot or PCR. In addition, we developed here a reporter system in which M cell express YFP and P cells express CFP allowing typing individual cells with a fluorescence microscope (Figure 1D). Sporulated SRE3A colonies were stained lightly by iodine and colonies did not stain at their junctions indicating preferential use of one donor (Figure 2B). Southern blotting, competitive PCR, and fluorescent typing all showed that SRE3A cells contain predominantly the mat1-P allele (P:M = 82:18 by Southern blot; P:M = 88:12 by cell count; Figure 2; competitive PCR not shown). The SRE3A strain used for these analyses was made in our laboratory [7] hence these results confirm the observations in [41] with an independent strain and support the conclusion of these authors that mat2-P is the preferred donor in SRE3A cells.

We assessed the effect of deleting swi2 in both wild-type h90 cells and SRE3A cells (Figure 2). Iodine staining indicated that deletion of swi2 severely affected switching efficiency in both backgrounds: h90 swi2A and SRE3A swi2A cells formed streaky colonies staining at their junctions showing that cells are predominantly of the M mating-type in some colonies and predominantly of the P mating-type in other colonies (Figure 2B). We measured P:M ratios in nine independent cultures of respectively h90 swi2A; h90 swi2A; SRE3A swi2A; and SRE3A swi2A by Southern blot (Figure 2C). While all h90 swi2A cultures had balanced P:M ratios and all SRE3A swi2A cultures were predominantly of the P mating-type, large fluctuations in P:M ratios were observed in h90 swi2A and SRE3A swi2A cultures. The strong phenotypic variability observed in h90 swi2A cultures disagrees with the report [41] that h90 swi2A cells contain predominantly mat1-P and that the switching pattern of h90 swi2A cells is indistinguishable from switching in h90 SRE3A cells. Further, the clear phenotypic differences we observed between SRE3A swi2A (P>M in all colonies; 81% P cells averaged over 9 cultures) and SRE3A swi2A strains (variegated phenotype; 40% P cells averaged over 9 cultures) is not predicted in [41]. Similarly, we observed culture-to-culture variations with, if any, a bias towards M cells in h90 swi5A cultures (72% M cells averaged over 9 cultures; Figure S1) in contrast to [50] who found that h90 swi5A cells are predominantly P. As for the deletion of swi2*, deletion of swi5* abrogated the preferential use of mat2-P in SRE3A cells (Figure S1). We conclude that the RPC is necessary for the efficient and preferential choice of mat2-P in SRE3A cells. Since this represents a situation where RPC cannot reach mat2-P by spreading from SRE3, this result does not support the spreading model and suggests instead that other DNA element(s) or factors attract Swi2 and Swi5 independently of SRE3.

Chromosomal deletions adjacent to mat2-P impair switching, defining the SRE2 recombination enhancer

While systematically introducing deletions in the mating-type region we found that a set of nested deletions on the centromere-distal side of mat2-P affected switching, defining a ~500 bp element adjacent to the H1 box, SRE2. Deletion of SRE2 caused a pronounced switching defect (Figure 3). Sporulated SRE2A colonies were stained very lightly by iodine vapors and they did not stain at their junctions; a Southern blot testing mat1 content in nine independent cultures indicated a large predominance of M cells in all cultures; and the existence of a strong bias towards M cells was also supported by fluorescence microscopy (Figure 3). Identical phenotypes were obtained when SRE2A colonies were seeded from P or M spores confirming efficient asymmetric switching favoring mat3-M (data not shown). The location of SRE2 relative to mat2 is similar to the location of SRE3 relative to mat3 but no extensive sequence similarities were noted between SRE2 and SRE3. Both elements are A-T rich (73% for SRE2 and 72% for SRE3 over 492 bp). The authors of a recent study [51] noticed like us that a deletion adjacent to mat2-P prevented efficient use of mat2-P however the study did not characterize the element further. Several observations reported below argue against deletion of SRE2 simply preventing use of mat2 as a donor. They suggest instead that SRE2 regulates donor choice.

As for the strains examined above, deleting swi2* affected switching in SRE2A cells. Two types of sporulated colonies were observed following iodine staining, light colonies with a few dark streaks containing mostly M cells, and more rare darker colonies containing a greater proportion of P cells (Figure 3; 30% M cell averaged over nine colonies). Deletion of swi5 produced a similar phenotype (77% M cell averaged over nine colonies; Figure S1; Southern blot quantifications are summarized in Figure S2). These phenotypes are consistent with mat3-M remaining a preferred donor in SRE2A cells even when RPC is not present in the cells. This again fails to support the 2004 model, where mat2-P is the preferred donor when RPC is not present due to higher-order chromatin structure. Alternatively, SRE2 might be responsible for the higher-order structure postulated by the model.

We investigated the association of Swi2 with parts of the mating-type region by ChIP (Figure S3). In unswitchable mat1-M cells, where mat2-P is perhaps poised for switching, Swi2 was detected at mat2-P and at SRE2 as previously reported [41]. In our experiments, Swi2 was also detected at these locations in SRE3A cells consistent with an SRE3-independent mode of recruitment to the mating-type region. This recruitment appeared facilitated by SRE2 since the association of Swi2 with mat2 was reduced in SRE2A cells (primer pairs 44, 46 and ‘SRE2A’ in M cells, Figure S3).

SRE2 and SRE3 direct donor choice independently of their location

A deletion reducing the use of a donor cassette is not on its own evidence that the deletion removed a directionality element. We explored the possibility that SRE2 and SRE3 are genuine directionality elements by engineering h90 cells. The donor loci are mat2-M mat3-P in the h90 mating-type region [39]. The cassette contents are precisely exchanged between the H2 and H1 homology boxes placing mat2-M near SRE2 and mat3-P near SRE3. This arrangement results in inefficient switching to the opposite mating-type ([39]; Figure 4). The h90 strain provides a useful tool to study directionality since it allows designing experiments in which the tested outcome is improved switching rather than loss of switching. We tested whether swapping SRE2 and SRE3 in h90 cells improved heterologous switching.

Figure 4 shows that h90 cells with swapped elements exhibited mating-type very efficiently and produced populations with equal proportions of P and M cells. Their sporulated colonies were undistinguishable from h90 colonies. Their mat1 content examined by Southern blot was evenly balanced and fluorescence microscopy confirmed equal proportions of P and M cells in colonies (Figure 4). Conversely h90 cells with swapped SRE elements switched mating-type poorly, produced mainly mat1-M cells as h90 cells with unswapped elements do, and formed colonies very
similar to $h^{oo}$ colonies (Figure 4). Together these experiments show that the PSRE2 MSRE3 combination (whether mat2-PSRE2 mat3-MSRE3 in wild-type $h^{oo}$ cells with native elements or mat2-MSRE3 mat3-PSRE2 in $h^{oo}$ cells with swapped elements) leads to balanced use of the two cassettes while the PSRE3 MSRE2 combination (whether mat2-PSRE2 mat3-PSRE3 in $h^{oo}$ cells with native elements or mat2-PSRE2 mat3-MSRE2 in $h^{oo}$ cells with swapped elements) leads to inefficient heterologous switching. We conclude

Figure 2. SRE3-independent effects of Swi2 on donor choice. (A) Representation of the mating-type region showing the probe (Ddel-NsI fragment) and restriction sites used for the Southern blots in (C). (B) Iodine staining of sporulated colonies with indicated genotypes. Dark staining reflects efficient switching. Light staining indicates a switching defect that can be either asymmetric towards a preferred mating-type (no staining at colony junctions) or inefficient in both directions (staining at colony junctions). (C) Southern blots of genomic DNA digested with Ddel and hybridized to the Ddel-NsI probe shown in (A), for nine independent cultures of $h^{90}$ swi2$: 968 (1–9); $h^{90}$ swi2$: TP133 (10–18); SRE3 swi2$: TP75 (19–27); SRE3 $swi2$: TP157 (28–36). (D) Quantification of mat1 content estimated from the Southern blots shown in (C), P/(P+M) ratios are plotted as % P cells. (E) Independent measurement of cell type ratios by fluorescence microscopy using a dual reporter system, YFP under control of the M-specific mfm3 promoter and CFP under control of the P-specific map2 promoter. M cells are yellow and P cells cyan. $h^{90}$ swi2$: TP220; SRE3 swi2$: TP270. Cell counts from fluorescence microscopy are presented in Table S3. Effects of Swi5 on donor choice are presented in Figure S1. All Southern blot quantifications are summarized in Figure S2.

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from these observations that SRE2 and SRE3 behave as directionality elements responsible for the balanced heterologous switching observed in \( h^{90} \) cells. P cells select the cassette adjacent to SRE3 while M cells select the cassette adjacent to SRE2 and SRE2 and SRE3 can both be recognized ectopically when their location relative to \( mat1 \) has been swapped.

Asymmetries

Should SRE2 and SRE3 be the sole determinants of directionality and should their action be fully symmetrical, \( h^{09} \) cells with native SRE elements and \( h^{90} \) cells with swapped SRE elements would engage in futile cycles where \( mat1-P \) selects \( mat3-PSRE3 \) (in \( h^{09} \) cells with swapped elements) and \( mat1-M \) selects \( mat2-MSRE2 \) (in \( h^{90} \) cells with swapped elements; Figure 4). Two types of colonies would be formed, one type containing predominantly P cells, the other predominantly M cells. This is not what is observed. Both \( h^{09} \) cells with native elements and \( h^{90} \) cells with swapped elements form populations where M cells predominate (Figure 4) indicating preferential choice of the cassette adjacent to SRE2. The fact that the bias is towards the \( MSRE2 \) cassette in both cases even though the \( MSRE2 \) cassette occupies different locations in the two strains shows that a preponderant cause for the bias is location independent.

The mechanisms responsible for directionality are likely to fail occasionally, allowing the ‘wrong’ donor to be selected. We reasoned that a small error rate would not have a strong impact on the overall composition of \( h^{90} \) cell populations, but the same error rate could have more profound consequences in \( h^{90} \) populations because the mistakes would lead to changes in mating-type that would subsequently be stably propagated through homologous switching. We modeled a situation where P cells use predominantly SRE3 to select a donor for switching, while M cells select predominantly SRE2 (Figure 4). We allowed a low occurrence of mistakes in both cell types, where P cells occasionally use SRE2 (20% of attempted switches) while M cells use SRE3 more rarely (10% of attempted switches). As expected such a bias leads to an accumulation of M cells in both \( h^{90} \) cells with native elements and \( h^{90} \) cells with swapped elements supporting the hypothesis that aberrant choices contribute to the preponderance of M cells in these strains. We note that in addition to SRE2 being more promiscuous than SRE3, the cassette content in the \( MSRE2 \) combination might facilitate use of \( MSRE2 \) over PSRE3 in P cells.

SRE2 and SRE3 enhance recombination in both cell types

As a way of testing the extent to which P cells can use SRE2 we replaced SRE3 with SRE2 (\( mat2-PSRE2 \) \( mat3-MSRE2 \) strain referred to as \( 26 \text{SRE2} \)). The \( 26 \text{SRE2} \) strain switched mating-type efficiently as judged from its dark iodine staining and balanced ratio of P and M cells (Figure 5). \( 26 \text{SRE2} \) populations contained 48% P cells according to Southern blot, 56% P cells according to microscopy. The phenotype of the \( 26 \text{SRE2} \) strain shows that P cells are proficient in the use of the SRE2 element in \( mat3-MSRE2 \) otherwise P cells would accumulate in the population of \( 26 \text{SRE2} \) cells. To illustrate this further SRE2 \( D \) colonies are shown near the \( 26 \text{SRE2} \) strain for comparison in Figure 5.
Recombination Enhancers Regulate Donor Choice

A

\[ h_{09} \] swapped elements

\[ h_{90} \] swapped elements

B

\[
\begin{array}{cccccc}
\% P_{\text{cells}} \\
1 & 2 & 3 & 4 & \text{Mean} & 5 & 6 & 7 & 8 & \text{Mean} & 9 & 10 & 11 & 12 & \text{Mean} & 13 & 14 & 15 & 16 & \text{Mean} \\
0 & 25 & 50 & 75 & 100 & 26\% \\
25 & 50 & 75 & 100 & 50\% \\
25 & 50 & 75 & 100 & 49\% \\
25 & 50 & 75 & 100 & 33\% \\
\end{array}
\]

C

\[
\begin{array}{cccc}
16\% P : 84\% M \\
48\% P : 52\% M \\
54\% P : 46\% M \\
27\% P : 73\% M \\
\end{array}
\]

D

\[
\begin{array}{cccccc}
h_{09} \text{ swapped SREs} \\
1 & 2 & 3 & 4 \\
5 & 6 & 7 & 8 \\
\end{array}
\]

\[
\begin{array}{cccccc}
h_{90} \text{ swapped SREs} \\
9 & 10 & 11 & 12 \\
13 & 14 & 15 & 16 \\
\end{array}
\]

E

\[
\begin{array}{cccc}
h_{09} \text{ swapped elements or } h_{90} \\
\text{SRE2} \\
\text{mat1-P} & 20\% & \text{SRE3} & 80\% \\
\text{SRE2} \\
\text{mat1-M} & 90\% & \text{SRE3} & 10\% \\
\end{array}
\]

\[
\begin{array}{cccc}
P/(P+M) \\
# \text{ generations} \\
0 & 5 & 10 & 15 & 20 \\
0 & 0.2 & 0.4 & 0.6 & 0.8 \\
0 & 0.2 & 0.4 & 0.6 & 0.8 \\
\end{array}
\]

\[
\begin{array}{cccc}
P/(P+M) \\
# \text{ generations} \\
0 & 5 & 10 & 15 & 20 \\
0 & 0.2 & 0.4 & 0.6 & 0.8 \\
0 & 0.2 & 0.4 & 0.6 & 0.8 \\
\end{array}
\]
in the next section where $h^{90}$ swi6 and $2 \times SRE2$ swi6 strains clearly differ from each other. Similarly we replaced SRE2 with SRE3 (mat2-PSRE3 mat3-MSRE3 strain referred to as $2 \times SRE3$). The $2 \times SRE3$ strain produced a mixture of P and M cells which shows that M cells can use SRE3, however with a bias towards M cells (Figure 5). $2 \times SRE3$ populations contained 23% P cells as estimated from Southern blot, 25% estimated from microscopy. Together with the results presented above for the $2 \times SRE2$ strain these ratios indicate that M cells are not as proficient at using mat2-PSRE3 as P cells are at using mat3-MSRE2. In summary SRE2 can stimulate recombination of donor loci with mat1 efficiently not only in M cells but also in P cells whereas SRE3 is more active in P cells than in M cells. The ability of each element to function in both cell types shows that these elements are not strictly dependent on cell-type-specific factors to stimulate recombination.

**Figure 4. SRE2 and SRE3 mediate directionality ectopically.** (A) Schematic representation of mat2-mat3 region and iodine staining of strains with transposed cassette contents or SRE elements. The M mating-type information is in yellow; the P information in light blue; SRE2 in dark blue; SRE3 in red. Light iodine staining indicates poor switching in strains where cassette contents and recombination enhancers are uncoupled. Swapping the recombination enhancers in $h^{90}$ cells restores switching efficiency to wild-type level. (B) Quantification of mat1 content as in Figure 2 for four independent cultures of each strain. $h^{90}$: PG19 (1–4); $h^{90}$ with swapped elements: TP38 (5–8); $h^{90}$: 968 (9–12); $h^{90}$ with swapped elements: TP39 (13–16). (C) Cell-type quantification by fluorescence microscopy as in Figure 2E. The strains were, from left to right: TP262, TP263, TP220, TP265. (D) Blots used for the quantifications in (B). (E) Computer simulations of P/(P+M) ratios in growing cultures started from P or M cells, when SRE2 and SRE3 are chosen at the rates indicated on the left. A small difference in the rates at which SRE2 and SRE3 are ‘wrongly’ used (dotted lines; 20% and 10% respectively) leads to unbalanced mating-type ratios and might contribute to the biases observed in $h^{90}$ cells and $h^{90}$ cells with swapped elements. doi:10.1371/journal.pgen.1003762.g004

**Figure 5. SRE2 and SRE3 can stimulate recombination in both cell types.** (A) Iodine staining of strains with the indicated mating-type regions (M: yellow; P: light blue; SRE2: dark blue; SRE3: red) shows that SRE2 stimulates recombination at mat3 when it is substituted for SRE3 (2×SRE2 strain) and that SRE3 stimulates recombination at mat2 when it is substituted for SRE2 (2×SRE3 strain), albeit less efficiently. The strains were, from left to right: SP837, TP75, TP126, TP8, TP303. (B) Fluorescence microscopy and (C) quantification of mat1 content by Southern blot confirm balanced donor use in 2×SRE2 cells showing that P cells use SRE2 (TP273 and TP126 strains). (D–E) Same analyses as (B–C) for 2×SRE3 (TP313 and TP303 strains) indicate that M cells are not fully proficient in the use of SRE3 and accumulate in 2×SRE3 populations. doi:10.1371/journal.pgen.1003762.g005
Effects of chromatin — mechanisms of recombination enhancement by SRE2 and SRE3

A remarkable aspect of mating-type switching is that the donor loci are in heterochromatin. We asked whether and how the ability of the SRE elements to stimulate recombination was affected by heterochromatin through epistasis analyses using cells lacking the chromodomain protein Swi6.

Deletion of swi6 in \(^{ho}\) or \(^{ho}\) cells with native or swapped elements radically altered donor choice (compare Figure 4 and 6). Populations of \(^{ho}\) cells or \(^{ho}\) cells with swapped elements went from balanced P:M ratios (49% and 50% P resp.) to containing predominantly M cells (87% and 84% resp.). Conversely the M bias in populations of \(^{ho}\) cells or \(^{ho}\) cells with swapped elements was abrogated by swi6Δ. In all cases, the changes reflected that use of the cassette adjacent to SRE2 was greatly decreased in favor of the cassette adjacent to SRE3 following deletion of swi6Δ, as indicated in Figure 6. These phenotypes show that Swi6 biases donor choice towards the cassette controlled by SRE2, or away from the cassette controlled by SRE3, whether the cassette contains the P or M information, and whether it is located at \(mat2\) or \(mat3\).

Reduced selection of SRE2 in \(^{ho}\) swi6Δ cells depended on the presence of SRE3 in the same cells. No change in preferred donor was observed in \(^{ho}\) SRE2Δ cells following deletion of swi6Δ, SRE2 kept being used (compare SRE3A in Figure 2 to SRE3A swi6Δ in Figure 6; \(mat1\)-P predominates in both). This indicated that SRE2 could stimulate recombination at \(mat2\)-PSRE2 in the absence of Swi6 when SRE3 was not present. Very inefficient switching in SRE2Δ SRE3A swi6Δ cells confirmed that the selection of mat2-PSRE2 in SRE2A swi6Δ cells depended on SRE2 (Figure 6; inefficient switching in the SRE2A SRE3A swi6Δ strain produces colonies staining at their junctions and large fluctuations in P:M ratios). Similarly, use of mat3-MSRE3 in SRE2A swi6Δ cells required SRE3 (compare SRE2A swi6Δ with SRE2A SRE3A swi6Δ in Figure 6). In summary these phenotypes show that both SRE2 and SRE3 can stimulate recombination in the absence of Swi6. Competitions between the two enhancers drive donor selection both in the absence and presence of Swi6. In the absence of Swi6 SRE3 is preferred over SRE2. When present, Swi6 biases donor selection towards SRE2.

Discussion

Some forms of recombination occur with an extraordinary efficiency in heterochromatin as illustrated by fission yeast mating-type switching. In mating-type switching, a euchromatic locus, \(mat1\), undergoes productive recombinogenic interactions with a heterochromatic partner in every other dividing cell. Not only are these recombination events frequent, they are also exquisitely fine-tuned such that a specific donor is selected for each conversion of \(mat1\). Our work identifies small, portable, DNA elements responsible for donor choice and provides new insights into the mechanisms responsible for the directionality of switching. Some of our observations differ from previous reports [41,50]. We discuss here these discrepancies and use our findings to build a new model for the directionality of mating-type switching.

The SRE elements direct donor choice ectopically

Cells in which the silent-cassette contents are swapped (\(^{ho}\)) switch mating-type inefficiently, indicating cells fail to choose heterologous donors when the donors are not at their endogenous location [39]. Here, we find that a crucial aspect of donor location is proximity of the donors to their respective recombination enhancers, SRE2 and SRE3. The determining role of SRE2 and SRE3 in donor selection was revealed by the high efficiency of switching in \(^{ho}\) cells when the SRE elements were swapped concomitantly with the contents of \(mat2\) and \(mat3\) (Figure 4). Heterologous donors could be found efficiently even when they were not at their endogenous location, provided the coupling with their cognate recombination enhancers was maintained.

The fact that \(^{ho}\) cells with swapped SRE elements switch well has strong implications for the 2004 model. The 2004 model is a two-component model integrating effects of donor positioning relative to \(mat1\) (in the model the recombinogenic DSB at \(mat1\) encounters \(mat2\) before it encounters \(mat3\)) and presence of RPC (the first RPC-associated donor encountered is used; Figure 1). In \(^{ho}\) cells with swapped elements a search starting at \(mat2\) would encounter SRE3 first. SRE3 being the proposed nucleation site for RPC, constitutively associated with RPC in both cell types, \(mat2\)-MSRE3 should be selected preferentially in both cell types which is clearly not the case. Our observations show instead that M cells choose SRE2 and P cells choose SRE3 when these elements are present, independently of their location.

One way of reconciling the portability of the SRE elements with the 2004 model is to propose that SRE2 is responsible both for the higher-order chromatin structure that brings \(mat2\) close to \(mat1\) in this model and also for directing the spreading of Swi2 away from SRE3 in M cells. While such roles for SRE2 should be envisioned and tested, other observations we made suggest that Swi2 does not reach \(mat2\) by spreading from SRE3.

RPC Catalyzes asymmetric switching in situations where RPC was not previously detected by ChIP and in the absence of SRE3

ChIP experiments reported in previous publications have detected large, cell-type specific variations in the association of RPC with the mating-type region [41,50]. RPC was detected over the entire mat2-mat3 interval in M cells but the association was restricted to SRE3 in P cells [41]. In cells lacking SRE3, RPC was not detected at all [41]. While these strikingly differential associations hint to some relevance for directionality, how the associations lead to the selection of a specific donor is not straightforward. RPC associations do not on their own determine which cassette will be used since the association of RPC with SRE3 is cell-type independent. Here, we found that RPC catalyzes switching even in situations where RPC was not previously detected by ChIP [41] and in the absence of SRE3. In our experiments, the pronounced bias towards the P mating-type displayed by SRE3A cells was abolished in SRE3A swi2A cells and in SRE3A swi5A cells, showing RPC is necessary for the preferential use of \(mat2\)-P in SRE3A cells (Figure 2 and Figure S1). Not only is this epistatic relationship not predicted by the 2004 model—the model predicts that the SRE3A swi2A double mutant should switch like SRE3A—but the 2004 model specifically relies on swi2A and SRE3A cells having identical phenotypes, which is also contradicted by our results (Figure 2).

Based on our genetic evidence we suggest that ChIP has failed to detect interactions between Swi2 and the mating-type region that are relevant to directionality. Difficulties in detecting the association of Swi2 with the mating-type region might be due to the fact that Swi2 is not an abundant protein, that relevant interactions occur in a short window of the cell cycle, or to the fact that ChIP experiments have been conducted in switching-defective cells lacking elements at \(mat1\) that might participate in directionality as indicated in [24]. Unlike [41], we observed that in M cells Swi2 remained associated with \(mat2\)-P and SRE2 in the absence of SRE3 (Figure S3). A core feature in the 2004 model is that Swi2 spreads from SRE3 to \(mat2\) in P cells. Spreading of a protein along
Figure 6. Chromatin structure regulates the relative efficiency of the SRE2 and SRE3 recombination enhancers. (A–B) Same analysis as in Figure 4A–B, for swi6Δ strains. Grey boxes indicate preferred donors according to Southern blot quantification. SRE3 is preferred over SRE2 independently of cassette content and location in the four swi6Δ strains examined. A comparison with the swi6Δ strains displayed in Figure 4A–B shows the overriding effect of Swi6 on enhancer choice. (C–D) Same analysis as in Figure 5, for swi6Δ strains. SRE2 and SRE3 can each promote recombination in swi6Δ strains. When only one enhancer is present, or when two enhancers of the same kind are present, Swi6 has little effect on donor choice. Isolate 1 and 8 for the SRE3.1 swi6Δ strain had rearranged mating-type regions and were not taken into account for the analysis.

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the chromatin fiber can be difficult to distinguish from other mechanisms that might lead to the same final associations. Binding at multiple sites might give the appearance of spreading from one of the sites. Here, we suggest that Swi2 does not have to spread from SRE3 to facilitate switching at SRE2.

Effects of chromatin on the ability of SRE2 and SRE3 to stimulate recombination

We observed that both SRE2 and SRE3 can stimulate recombination in the absence of Swi6. While populations of SRE2A swi6Δ cells were predominantly M and populations of SRE3A swi6Δ cells were predominantly P these biases were lost in populations of SRE2A SRE3A swi6Δ cells (Figure 6C–D) showing SRE3 stimulates recombination with mat2-M in SRE2A swi6Δ cells and SRE2 stimulates recombination with mat2-P in SRE3A swi6Δ cells. We furthermore observed that competitions between SRE2 and SRE3 take place in swi6Δ cells when both elements are present. While SRE3A swi6Δ populations were predominantly P (Figure 6C–D), reflecting choice of SRE2, k90 swi6Δ populations were predominantly M (Figure 6A-B), reflecting choice of SRE3, from which we conclude that SRE3 outcompetes SRE2 in k90 swi6Δ cells. The switching phenotypes of k90 swi6Δ; k90 with swapped elements swi6Δ; and k90 with swapped elements swi6Δ cells all show that SRE3 is preferred over SRE2 in swi6Δ cells when both elements are present (Figure 6A–B).

Swi6 exerts major effects on mating-type switching through SRE2 and SRE3. Comparing Figure 4 and Figure 6A–B shows that Swi6 tilts the relative efficiency of the two elements, allowing SRE2 to be preferred over SRE3 in M cells. We suggest that this effect is key to directionality. Several lines of evidence have established that heterochromatin differs in the mating-type region, as is the case in M cells, SRE2 is more efficient in its adjacent H1 box than SRE3.

In the proposed model SRE2 and SRE3 compete to capture the free DNA end generated at mat1. When Swi6 and associated factors are in comparatively low abundance in the mating-type region as is the case in P cells, SRE3 stimulates recombination at its adjacent H1 homology box more efficiently than SRE2. When Swi6 and associated factors are in greater abundance in the mating-type region, as is the case in M cells, SRE2 is more efficient than SRE3.

Several mechanisms can be envisioned for how SRE2 and SRE3 might facilitate strand invasion at their adjacent H1 box in a chromatin-dependent manner. SRE2 and SRE3 might have an intrinsic ability to facilitate D-loop formation as suggested by their low melting temperature (predicted from 72–75% AT content and data not shown). Indeed, evidence has been presented that SRE2 can form a heteroduplex with DNA adjacent to the mat1 H1 box [33]. Swi6 could modulate the ability of SRE2 and SRE3 to stimulate strand-invasion at H1 through changes in chromatin structure. Swi6 binds to nucleosomes methylated at H3K9 and it oligomerizes. The association of Swi6 with chromatin per se might constrain the topology of DNA around H1 and the SRE elements in a way that would alter D-loop induction by the SRE elements and depend on the concentration of Swi6. Other, non mutually-exclusive effects of SRE2 and SRE3 could be through the positioning of nucleosomes. Swi6 might induce the local sliding or displacement of nucleosomes through one of its associated ATP-dependent chromatin remodeling complexes (RSC, Ino80, FACT; [18],[19]) thereby altering the ability of a recombination enhancer to increase H1 accessibility. Finally, direct interactions might take place between the recombination enhancers and recombination factors such as Swi2 as suggested in the case of Swi2 and SRE3 [41]. Directionality would occur if SRE3 had a higher affinity for Swi2 than SRE2 but a lower peak efficiency than SRE2 when stimulating recombination in the context of heterochromatin. At low concentration of Swi2, SRE3 but not SRE2 would be associated with Swi2, promoting invasion of its adjacent cassette. At high concentrations of Swi2, SRE2 would not only be associated with Swi2 but it would use its associated Swi2 more efficiently than SRE3, leading to preferred choice of SRE2 over SRE3. Low association of Swi6 and Swi2 in the mating-type region of P cells would promote invasion of the SRE3-adjacent cassette. High association of Swi6 and Swi2 in the mating-type region of M cells would promote invasion of the SRE2-adjacent cassette.

How pre-existing chromatin structures affect recombination and DSB repair is poorly understood in spite of a great relevance for the maintenance of genome integrity in all eukaryotes. Competitions between donors for gene conversions [55],[56] and regional, cell-type specific, control of recombination [57]–[59] were observed in S. cerevisiae similar to what we observed here. Indeed, much of our knowledge on the effects of chromatin on recombination was acquired using S. cerevisiae [59]–[61]. Our characterization of the fission yeast SRE elements opens the field for further in vivo and in vitro studies of recombination regulation in other chromatin contexts.

Model for the directionality of mating-type switching

We propose a simple model for the directionality of mating-type switching that takes into account our observations (Figure 7). This model is an alternative to models where the recombination enhancers favor cell-type specific interactions between the donor loci and mat1 through DNA looping but it is not incompatible with looping models.
Materials and Methods

Standard procedures were used to construct and examine *S. pombe* strains. The details of the strain constructions, Southern blots and microscopy are presented in Text S1 (Extended experimental procedures). Strain genotypes are listed in Table S1 and oligonucleotide sequences in Table S2.

Supporting Information

Figure S1  Effects of *Swi5* on donor choice. The content of *mat1* was estimated by quantifying Southern blots as in Figure 2, for nine independent cultures of the indicated strains. (A) shows that deletion of *swi5* results in culture-to-culture fluctuations, with a general bias towards M cells. The strains were *h90 swi5*+: TP138 (1–9); *h90 swi5*Δ: TP138 (10–18). (B) shows that deletion of *swi5*+ abrogates the preferential use of *mat2-P* in *SRE3*Δ cells. The strains were *SRE3*Δ*swi5*+: TP75 (1–9); *SRE3*Δ*swi5*Δ: TP150 (10–18). (C) shows that deletion of *swi5*+ causes some culture-to-culture variation in *SRE2*Δ cells, with a general bias towards M cells. The strains were *SRE2*Δ*swi5*+: TP8 (1–9); *SRE2*Δ*swi5*Δ: TP149 (10–18).

Figure S2  Summary of *mat1* content in wild-type and mutant strains.

(TIF)

Figure S3  Effects of *SRE2* and *SRE3* on the association of *Swi2* with the mating-type region. The association of *Swi2* with the mating-type region was assayed using strains with a 13myc tag at the C-terminus of *Swi2*. (A) Schematic overview of the silent mating-type region indicating where *Swi2* binding was measured. (B) Quantification of ChIP experiments performed with stable P (*mat1-P*17::LEU2; upper panel) or M (*mat1-M*1mt-0; lower panel) strains harboring *SRE2A* or *SRE3A* as indicated. The primer pairs used were as in [41] except for primers at *SRE2A* and *SRE3A*, designed to replace respectively primer pair 46 and 69. Enrichments of *Swi2* in the regions of interest were calculated relative to *act1*. For these regions, the distribution of *Swi2* in wild-type cells was similar to previously published data [41] with a globally more pronounced association of *Swi2* in M cells than in P cells. Unlike [41], *Swi2* was detected at *mat2* in M cells (primers: 44, 46) in both the presence and absence of *SRE3*. This indicates that *Swi2* can be attracted to the mating-type region independently of...
The association of Swi2 with mat2 depended on SRE2 (primers: 44, SRE2Δ). (C) Pictures of gels quantified in B. Non-saturated images were used for the quantification. The P strains were: WT: SPA237; SRE2 Δ: TP366; SRE2 Δ: TP197. The M strains were: WT: TP186; SRE2 Δ: TP367; SRE2 Δ: TP192.

Table S1 Strain table.

Table S2 Oligonucleotide sequences.

Table S3 Cell counts from fluorescence microscopy.

References


Text S1 Extended experimental procedures.

Acknowledgments

We thank Ferran Azorin for strains with the *sre2Δ::kanR* and *sre3Δ::kanR* alleles [54] and the Riken Bioresource Center for the pDUAL2-HFC1- and RDB6118 50/E05 plasmids.

Author Contributions

Conceived and designed the experiments: GT. Performed the experiments: TJ JVH GT. Analyzed the data: TJ GT AT LRH. Wrote the paper: GT TJ. Did initial experiments leading to discovery of SRE2: LRH.

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