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Identification of Mirror Repeats within the SWI 6 Gene of Saccharomyces cerevisiae

Gargi[1], Vikash Bhardwaj[2], Namrata[3]
[1]*Research Scholar*
[2]*Associate Professor, Department of Zoology, Baba Mastnath University, Rohtak, Haryana, India,*
[3]*Research Scholar*

Abstract
The SWI6 gene in Saccharomyces cerevisiae, also known as Switching Deficient 6, encodes a protein essential for the formation and function of the SBF complex (Swi4/Swi6 complex), a critical regulator of the cell cycle. SWI6 plays a pivotal role in facilitating the G1-to-S phase transition by partnering with the transcription factor Swi4 to activate the expression of genes necessary for DNA replication and cell division. Through its involvement in chromatin remodeling and transcriptional activation, SWI6 ensures proper cell cycle progression, particularly in the initiation of DNA synthesis. Mutations or defects in SWI6 disrupt the cell cycle, resulting in cell cycle arrest and impaired cellular proliferation. This study highlights the fundamental role of SWI6 in the regulation of cell division and provides insights into the molecular mechanisms controlling genetic stability in eukaryotic cells through the analysis of mirror repeats using the FASTA–Parallel Complement–BLAST (FPCB) method. To analyze SWI6's sequence and functional homology, we applied the FPCB FASTA–Parallel Complement–BLAST method, facilitating the identification of conserved motifs. Additionally, our research investigates mirror repeats in the SWI6 gene, exploring their potential impact on genetic stability and sequence evolution.

Keywords: SWI6, Saccharomyces cerevisiae, mirror repeats, Switching Deficient 6, cell cycle, FPCB .SWI6, Saccharomyces cerevisiae, mirror repeats, Switching Deficient 6, cell cycle, FPCB .

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Introduction
Saccharomyces cerevisiae, also known as baker's yeast, is a widely used model eukaryotic organism that has been thoroughly researched in cell biology, genetics, and molecular biology. This unicellular organism offers a simplified yet highly informative system to study basic biological processes that are conserved across all eukaryotes, including humans. Due to its well-characterized genome, rapid growth, and ease of manipulation, *S. cerevisiae* has become a cornerstone in molecular and cell biology research. Many cellular processes in yeast are directly comparable to those in higher organisms, making it an invaluable tool for studying complex biological mechanisms in a simplified context.

One of the most fundamental and universally conserved processes in all eukaryotic cells is the cell cycle. The cell cycle refers to the series of events that lead to cell division and the replication of the cell's genetic material. In *S. cerevisiae*, as in all eukaryotes, the cell cycle is divided into distinct phases: G1, S, G2, and M. These phases are meticulously regulated to ensure that each step-in cell division is accurately completed before the next phase begins. The cell cycle in yeast is controlled by a network of genes and proteins, many of which are conserved across higher organisms, allowing *S. cerevisiae* to serve as an effective model for the study of cell cycle regulation in more complex eukaryotes, including humans.

In the cell cycle, the G1-to-S phase transition is one of the most critical steps. This transition ensures that the cell is ready for DNA replication, which is essential for the accurate division of genetic material. The regulation of this transition is orchestrated by several complexes, one of the most important being the Swi4/Swi6 complex (SBF). The Swi4 protein, along with its cofactor SWI6, plays a central role in activating genes that are required for DNA replication, thus propelling the cell from G1 into S phase. The precise regulation of this transition is crucial for the maintenance of genomic stability and the prevention of cell cycle errors that can lead to genomic instability or cell death.

The SWI6 gene is a key player in this process. SWI6 encodes a protein that is necessary for the formation and function of the SBF complex. This complex acts as a transcriptional activator, ensuring that the genes required for DNA replication are expressed at the appropriate time in the cell cycle. In addition to its role in transcriptional regulation, SWI6 is also involved in chromatin remodeling, a process that is essential for making DNA accessible for replication. Without SWI6, the cell is unable to transition from G1 to S phase, leading to cell cycle arrest and impaired cell proliferation. The precise function of SWI6, as well as its interactions with other proteins and complexes in the cell cycle, is critical for understanding not only cell division but also broader mechanisms of cellular growth and genetic stability.

The importance of SWI6 extends beyond the regulation of the cell cycle. Recent studies have highlighted the potential role of mirror repeats in the SWI6 gene sequence. Mirror repeats are sequences of nucleotides that are arranged in a palindromic fashion, where one strand of DNA mirrors the sequence of the complementary strand. These motifs are found in many eukaryotic genomes and may have important biological functions. Mirror repeats have been implicated in various genetic phenomena, including DNA replication, recombination, and genetic instability. The presence of mirror repeats in the SWI6 gene suggests that these structures may play a role in regulating its expression and possibly influence the stability of the gene during cell division. The study of these mirror repeats could provide valuable insights into how DNA sequence features influence gene function and genome stability.

Figure 1a: Role of SWI 6 in cell cycle.

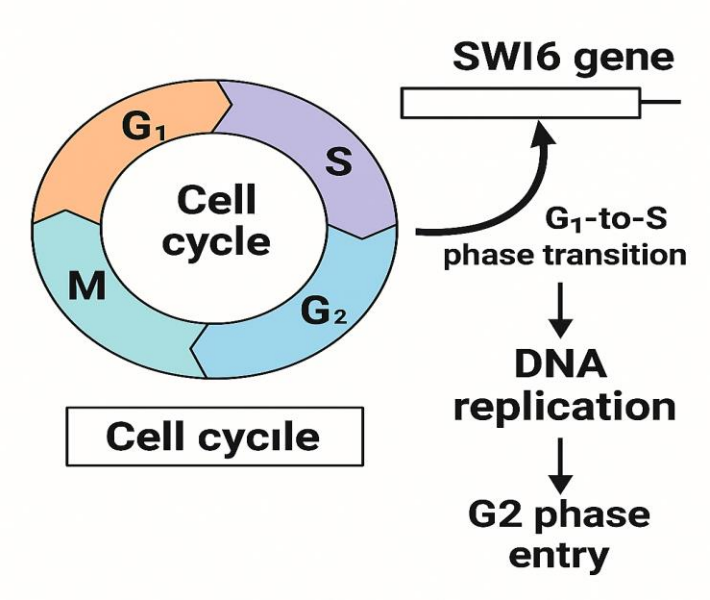
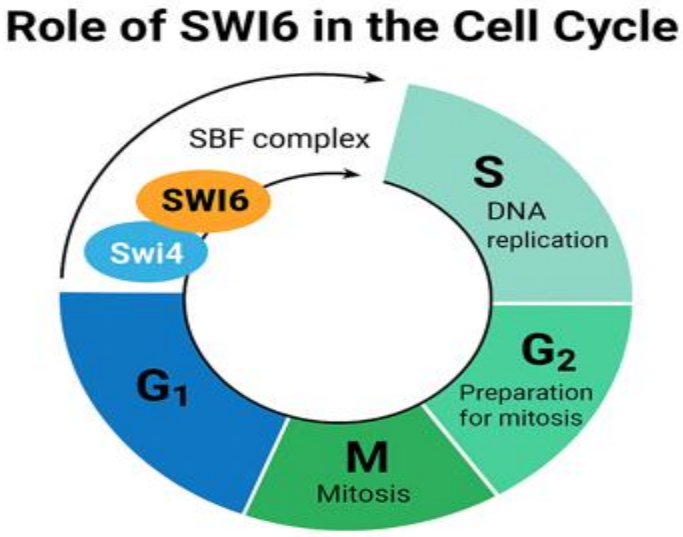


Figure 1b: Role of SWI 6 in cell cycle.



Understanding the role of mirror repeats in the regulation of SWI6 is a key focus of this research. By exploring these motifs, we aim to uncover how they might contribute to the genetic regulation of the cell cycle, particularly in relation to the SWI6 gene and its critical role in the G1-to-S phase transition. To investigate the potential functional significance of these mirror repeats, we will employ two advanced computational methods. First, we will utilize the FPCB FASTA–Parallel Complement tool, a powerful method for identifying conserved sequence motifs and comparing the SWI6 gene with homologous genes across gene. This tool will allow us to detect mirror repeats and other sequence features that might influence the function of the SWI6 protein.

Additionally, we will use NCBI BLAST (Basic Local Alignment Search Tool) to analyze the SWI6 gene sequence. This method will help us understand how the SWI6 gene has evolved across gene, providing insights into the functional significance of its mirror repeats and their potential role in maintaining genetic stability. Through this comprehensive analysis, we hope to gain a deeper understanding

of the SWI6 gene, its regulation of the cell cycle, and the possible contributions of mirror repeats to the stability and function of the gene.

The findings of this research have broader implications for understanding cell cycle regulation, genomic stability, and the potential role of DNA sequence motifs in regulating essential cellular processes. Furthermore, exploring the role of mirror repeats in SWI6 could provide new insights into the molecular mechanisms underlying genetic instability, which has implications for cancer and other diseases characterized by cell cycle dysregulation.

Materials and Methods

The coding DNA sequence (CDS) of the SWI6 gene from *Saccharomyces cerevisiae* was obtained in FASTA format from publicly accessible databases, including the Saccharomyces Genome Database (SGD). These resources provided well-annotated and curated genomic sequences essential for subsequent bioinformatics analysis. To identify mirror repeats, a strand-specific reverse complement of the CDS was generated using the Reverse Complement Tool available on Bioinformatics.org. This tool generated a "parallel complement" that maintains the original strand orientation, as opposed to the conventional reverse complement typically used in base-pairing analyses. The original sequence was then compared to its parallel complement using the BLASTN tool (Basic Local Alignment Search Tool for nucleotides) available through the NCBI BLAST portal. Alignments were manually examined to identify regions where the nucleotide sequence appeared in reverse order in both the query and subject sequences, which were then annotated as mirror repeats. To enhance sensitivity in detecting high-similarity regions, the Mega BLAST option was also employed. This methodology formed part of the FASTA–Parallel Complement–BLAST (FPCB) pipeline, a manual bioinformatics approach designed to identify symmetric sequence motifs. The identified mirror repeats were further analyzed for their distribution within the gene, including their location, length, and symmetry characteristics. Only motifs exhibiting true reverse symmetry, without complementary base-pairing, were considered as mirror repeats. The resulting data were cataloged for further analysis to explore the potential regulatory or structural roles of the mirror repeats within the SWI6 gene.

Result and Discussion

The SWI6 gene, located on chromosome 12 of *Saccharomyces cerevisiae*, spans a total length of 2.41 kb and plays a pivotal role in regulating the cell cycle, particularly in controlling the transition from the G1 phase to the S phase. SWI6 is a key component of the SBF complex (Swi4/Swi6 complex), which regulates the initiation of DNA replication and ensures the orderly progression of the cell cycle. Proper function of SWI6 is critical for maintaining genomic stability, and any mutations or defects within this gene can result in cell cycle arrest and impaired cellular proliferation. In this study, we focused on identifying and analyzing mirror repeats in the SWI6 gene to understand their potential roles in the regulation and structural integrity of the gene during the cell cycle.

Mirror Repeats Distribution

Our bioinformatics analysis identified a total of 40 mirror repeats across the five segments of the SWI6 gene. The gene was divided into five distinct segments, each approximately 500 base pairs (bp) in length, except for the final segment (2001-2412 bp), which was shorter due to the total length of the gene. The mirror repeats were distributed across these segments, with varying frequencies of perfect and imperfect mirror repeats. The following observations were made based on the distribution of mirror repeats:

1. 1st Segment (1-500 bp): This segment contained a total of 9 mirror repeats, including 8 perfect and 1 imperfect repeat. The perfect repeats ranged in length from 7 to 11 bp, with the longest perfect repeat measuring 11 bp. The imperfect repeat in this segment was associated with two spacers, with a total length of 17 bp. The high number of perfect repeats suggests that this region may play a critical role in structural and regulatory functions, potentially affecting the accessibility of the gene to transcription factors involved in the G1-to-S phase transition.
2. 2nd Segment (501-1000 bp): In this segment, we identified 12 mirror repeats, comprising 10 perfect and 2 imperfect repeats. The length of the perfect repeats ranged from 7 to 10 bp, with the longest perfect repeat being 10 bp. The imperfect repeats were associated with six spacers and had a total length of 25 bp. The presence of imperfect repeats, interspersed with perfect repeats, suggests a dynamic regulatory role in gene expression and chromatin structure, which may contribute to the regulation of SWI6 during the cell cycle.
3. 3rd Segment (1001-1500 bp): This segment contained 9 mirror repeats, including 7 perfect and 2 imperfect repeats. The perfect repeats ranged in length from 7 to 11 bp, with the longest measuring 11 bp. The imperfect repeats, associated with four spacers, had a total length of 19 bp. This segment, like the previous two, exhibited a combination of perfect and imperfect repeats, suggesting that these motifs may be important for maintaining the structural integrity of the gene while regulating its expression during cell cycle progression.
4. 4th Segment (1501-2000 bp): In the fourth segment, we identified 7 mirror repeats, including 6 perfect and 1 imperfect repeat. The perfect repeats ranged from 7 to 10 bp, with the longest being 10 bp. The imperfect repeat in this segment was associated with eight spacers and had a total length of 30 bp. The longer length of the imperfect repeat in this segment suggests that these repeats may have a more significant role in modulating gene function and maintaining chromatin stability, especially given their location near critical regulatory regions involved in DNA replication.

5. 5th Segment (2001-2412 bp): The final segment of the SWI6 gene contained 3 mirror repeats, consisting of 2 perfect and 1 imperfect repeat. The perfect repeats were relatively short, ranging from 7 to 8 bp, with the longest being 8 bp. The imperfect repeat, associated with two spacers, had a total length of 14 bp. Although fewer mirror repeats were observed in this segment, the presence of imperfect repeats with spacers suggests that this region may play a role in fine-tuning gene expression and maintaining genomic stability during later stages of the cell cycle.

Types of Mirror Repeats

Mirror repeats can be classified into perfect and imperfect repeats based on their symmetry. Perfect mirror repeats are symmetric sequences that are identical when reversed and aligned, while imperfect mirror repeats show some degree of mismatch in the reversed sequence, indicating a potential regulatory role rather than a structural one.

- Perfect Mirror Repeats: These repeats exhibit perfect symmetry, with no mismatches in the nucleotide sequence when compared to the reversed version. The length of the perfect repeats in the SWI6 gene ranged from 7 to 11 bp, with the longest perfect repeat found in the 1st and 3rd segment, measuring 11 bp. These perfect mirror repeats are likely involved in stabilizing the gene's structure and ensuring the precise regulation of its expression during the G1-to-S phase transition, where the initiation of DNA replication is critical.
- Imperfect Mirror Repeats: These repeats showed some mismatch between the query and subject sequences, indicating their potential involvement in regulatory functions such as chromatin remodeling or gene expression control. The imperfect repeats were observed throughout the gene, often interspersed with perfect repeats. The imperfect mirror repeats were associated with spacers, which could suggest that these motifs contribute to the flexibility and fine-tuning of SWI6 gene regulation during the cell cycle. The length of the imperfect repeats ranged from 7 to 30 bp, with the longest being 30 bp in the 4th segment.

Potential Functional Implications

The identification of mirror repeats, particularly in the regions associated with the G1-to-S phase transition, suggests that these motifs may play an important role in the regulation of SWI6 gene expression and function. Mirror repeats are known to contribute to various DNA functions, including DNA replication, genetic recombination, and chromatin remodeling. In the context of SWI6, the mirror repeats could serve as structural elements that facilitate the activation or repression of the gene's expression during critical points of the cell cycle.

Moreover, the presence of imperfect mirror repeats interspersed with perfect repeats suggests that these motifs may enable SWI6 to fine-tune its expression. This flexibility in gene regulation could be essential for the precise timing of DNA replication and other cell cycle processes. Given that SWI6 is a central component of the SBF complex, which controls the initiation of DNA replication, these mirror repeats may assist in the orchestration of SWI6 activity, ensuring its proper function during cell cycle progression.

Figure 2: The bar graph shows the count of perfect and imperfect mirror repeats for each segment of the SWI6 gene. The pie chart provides a breakdown of the total number of perfect and imperfect repeats across all segments.

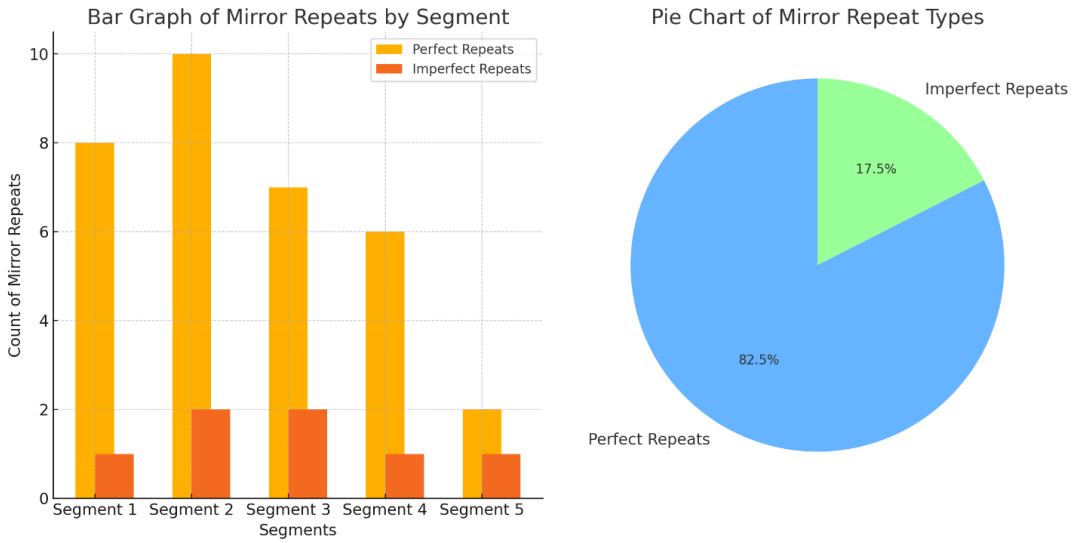


Table 2: Displays the number of mirror repeats, their positions, lengths, and types of the SWI6 gene.

Symbol/Gene ID	Gene regions (bps)		Location of mirror repeats Query start Query end sit		Length (bps)	Type of mirror repeats
SWI6 YLR182W SGDID: S000004172	1-500bp	369	ACCAGAAAACAAGACCA	385	17	Imperfect mirror
		385	AAAAGTGAAAA	395	11	Perfect with one spacer
		425	TTAATAATT	433	9	Perfect with one spacer
		10	GAAGAAG	16	7	Perfect with one spacer
		56	CACTCAC	62	7	Perfect with one spacer
		86	TCCTCCT	92	7	Perfect with one spacer
		179	AAAGAAA	185	7	Perfect with one spacer
		183	AAATAAA	189	7	Perfect with one spacer
		343	GAAGAAG	349	7	Perfect with one spacer
	501-1000bp	309	ATAATGACAGCAGTAATA	326	18	Imperfect mirror
		288	AAGAAATGCCTACATCCCTTAATAA	312	25	Imperfect mirror
		353	CAACAACAAC	262	10	Perfect
		255	CATTCTTAC	263	9	Perfect with one spacer
		355	ACAACAACA	363	9	Perfect with one spacer
		86	AGCGGCGA	93	8	Perfect
		337	AGGGGGGA	344	8	Perfect
		22	TGAGAGT	28	7	Perfect with one spacer
		221	GTAAATG	227	7	Perfect with one spacer
		307	TAATAAT	313	7	Perfect with one spacer
		440	GTAGATG	446	7	Perfect with one spacer
		464	TTACATT	470	7	Perfect with one spacer
	1001-1500bp	294	AACGAAAAAGAAAGCAA	310	17	Imperfect mirror
		329	GGAAAGAAAGG	339	11	Perfect with one spacer
		185	CATTATTAC	193	9	Perfect with one spacer
		291	ACTAACGAAAAAGAAAGCA	309	19	Imperfect mirror

		467	ATTAGATTA	475	9	Perfect with one spacer
		140	TTTAATTT	147	8	Perfect
		371	GATAATAG	378	8	Perfect
		126	TATTTAT	132	7	Perfect with one spacer
		264	AAACAAA	270	7	Perfect with one spacer
	1501-2000bp	391	GAAGAAGAAG	400	10	Perfect
		393	AGAAGAAGA	401	9	Perfect with one spacer
		176	TAATTAAT	183	8	Perfect
		227	ATGAAACAGTGCAATAT AA--TGAGAAATTA	255	30	Imperfect mirror
		373	AATTTAA	379	7	Perfect with one spacer
		447	TGAAAGT	453	7	Perfect with one spacer
		334	TTGAAAG	340	7	Perfect with one spacer
	2001-2412bp	384	AAGATTTTTTAAAA	397	14	Imperfect mirror
		210	TAACCAAT	217	8	Perfect
		301	AAATAAA	307	7	Perfect with one spacer

Conclusion

In conclusion, this study underscores the significant role of mirror repeats within the SWI6 gene of *Saccharomyces cerevisiae* and their potential contribution to the regulation and structural integrity of the gene during the cell cycle. Our analysis identified a total of 40 mirror repeats distributed across five distinct segments of the gene, with 33 perfect and 7 imperfect repeats occurring in varying frequencies. While much remains unknown about the specific roles of these mirror repeats, further research will be essential to uncover their precise functions and mechanisms in regulating gene expression and chromatin structure.

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