stop-PRISM integration allele in the rb1 tumor suppressor recapitulates developmental and cellular neural progenitor loss of function phenotypes

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Abstract

To simplify screening and genotyping of mutant embryos we generated a set of vectors for CRISPR/Cas9 targeted integration called pPRISM, which contain secondary markers that allow for simple visual genotyping (plasmids for Precise Integration with Secondary Markers). The plasmids are designed for integration using short homology arms as we reported previously (Wierson et al., 2019 bioRxiv). The stop-PRISM vectors have a cassette for transcriptional termination followed by a secondary marker for heart, lens or hatching gland-specific fluorescent reporter expression. Targeted integration into an early exon is predicted to cause early transcription termination and create a loss of function mutation. We isolated an *rb1-stop-PRISM-cmlc2:GFP* line and tested whether the integration allele behaved as a loss of function mutation in trans with our previously published 7 bp indel allele rb1/17is54. The gross morphology of rb1-stop-PRISM-cmlc2:GFP/rb1/17is54 trans heterozygotes is relatively normal, however the larvae fail to develop a swim bladder and are lethal, similar to rb1\(\Delta\)7is54\(\Delta\)7is54 homozygotes. To examine if the rb1-stop-PRISM*cmlc2:GFP* allele disrupts *rb1* function at the cellular level we used live embryo confocal imaging of H2A.F/Z:GFP chromatin in the developing optic tectum to follow neural progenitor cell cycle dynamics. At 5 dpf, *rb1-stop-PRISM-cmlc2:GFP/rb1*₂7is54 mutant neural progenitors re-enter the cell cycle and condense their chromatin. The cells then appear to arrest in prophase, and fail to align the chromosomes at the metaphase plate and progress through the cell cycle, as we previously found for $rb1\Delta7is54/\Delta7is54$ homozygotes (Schultz et al., 2018). PCR genotyping of the imaged embryos revealed the expected genotypes matched the observed phenotypes. Quantification of the neural progenitor mutant phenotype is in progress. Future analysis will compare phenotype and quantification data between our *rb1-stop-PRISM-cmlc2:GFP/rb1*₄7is54 trans heterozygotes and homozygous *rb1-stop-PRISM-cmlc2:GFP/stop-PRISM-cmlc2:GFP* embryos. Our results confirm integration of the pPRISM cassette can create loss of function mutations that recapitulate the phenotype of standard indels in the tumor suppressor *rb1*, both at the morphological and cellular level. stop-PRISM loss of function alleles will be useful genetic tools for rapid genotyping in combination with more complex edited alleles to study tissue or cell type specific gene function.

1. RB tumor suppressor regulates cell cycle entry, progression, and cell cycle exit

CDKN2/A inhibitor		
		G0 quiescence / differentiation
CDK4/6 kinase		Δ
NuRD/ HDAC1 RB	Mitosi	is G1 R point early gene
CHD RBBP4 E2F	T	t expression
	E2F target G2	S
JUHIHUHU	genes: Cell Cycle	
	Mitosis Cell Division	
	DNA replication	
neural progenitor c	•	
stem	progenitor	neuron
		XE
	$(\bigcirc) \longrightarrow \nearrow$	
Self-renev	Cell cycle	
	Differentiation	

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