

Adventures in PCR: The Impact of Alcian Blue Staining on Danio rerio Embryos.

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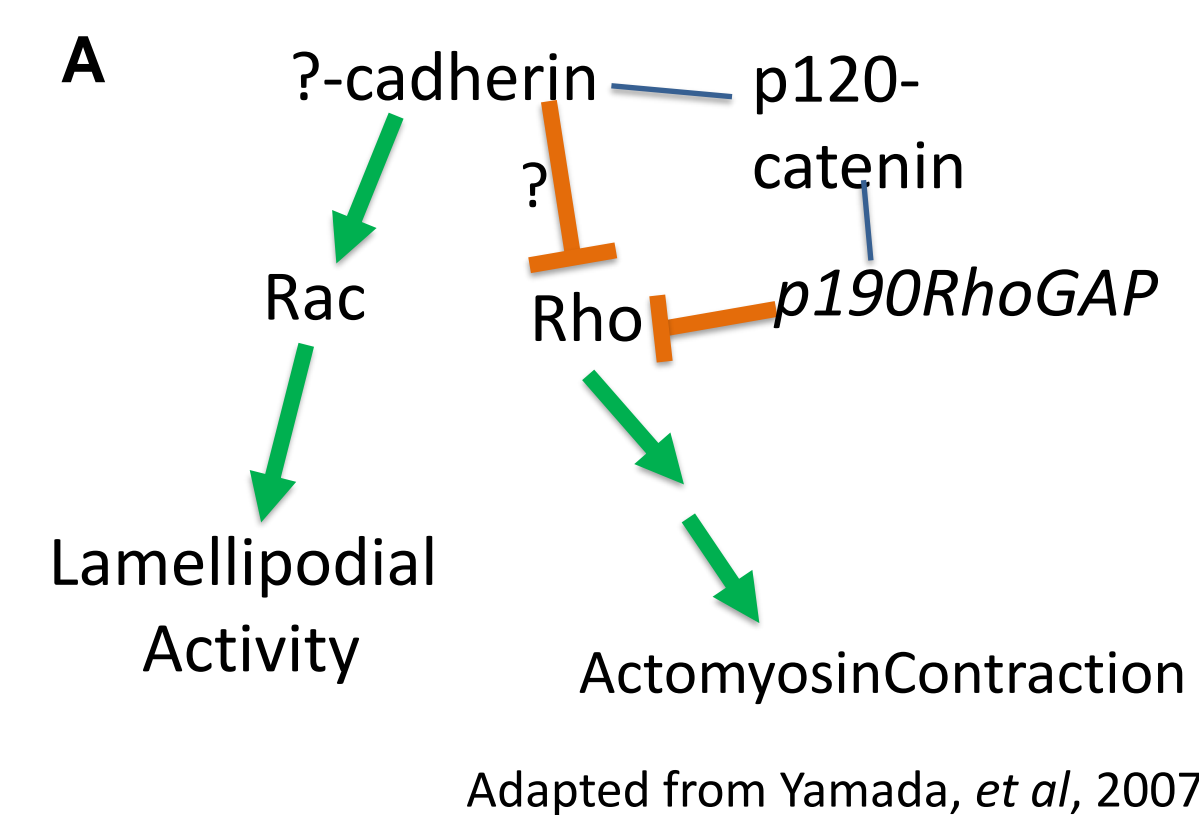
Abstract

p190RhoGAP(p190) is a member of the Rho family GTPase activating proteins, that have been shown to play a role in cytokinesis and play roles in cell proliferation. Studies have shown that *p190* plays various roles in nervous system development and defects are similar to defects seen in cell adhesion disorders. In conjunction with another research project examining the role of *p190RhoGAP* in jaw development via Alcian blue staining, this study set out to optimize genotypic verification of *p190* in zebrafish embryos. We used polymerase chain reaction (PCR) to amplify the *p190* genetic contributions in individual embryos followed by Restriction Fragment Length polymorphism (RFLP) analysis to distinguish between different genotypes of the *p190* gene; wild type(250 and 350b.p), mutant (600b.p), heterozygous (600, 350 and 250 b.p). Currently the common methods include single cell extraction at the 32-cell stage or head vs. tail dissections which are both technically challenging. While head vs tails extractions have been previously utilized in our lab, we sought to streamline this process to exclude embryo dissections. During the procedure, PCR optimization and trouble shooting had to be done prior to, determining if DNA samples would be viable for PCR when DNA extractions were done on previously dyed embryos. As a control we compare previously dyed embryos to tailed embryos that were non-dyed tail extractions. Our results indicate the Alcian blue staining did not have a notable impact on our genotypic verification when comparing the stained and non-stained embryos. Our data highlight the delicate nature of working with PCR on different embryo treatments which can halt forward progress in genotypic analysis of mutant embryos that may have subtle or late developing phenotypes.

p190RhoGAP and PCR genotyping

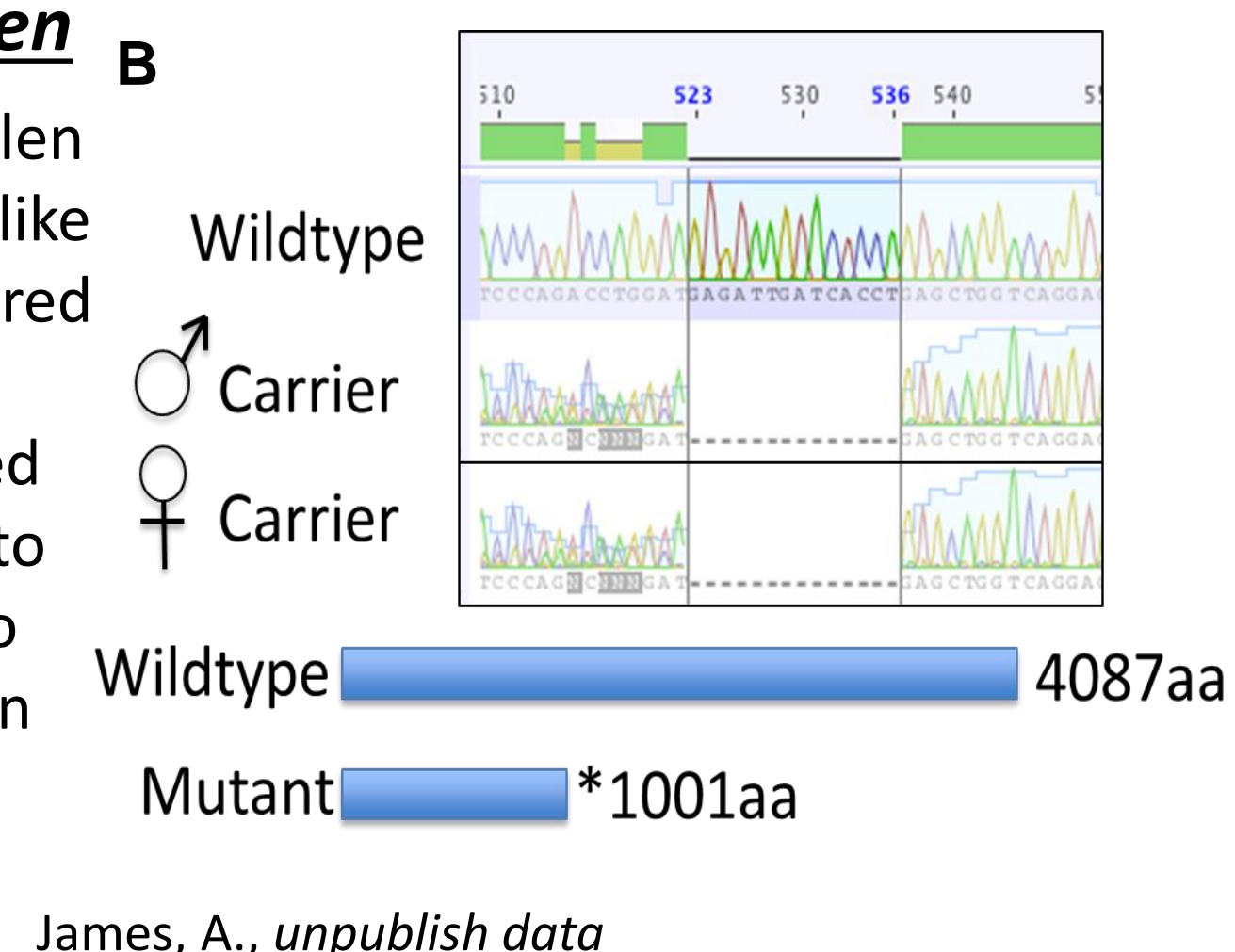
p190RhoGAP

Rho Gaps are a protein domain of GTPase activating proteins which can alter actin arrangements when responding to extracellular signals. *p190RhoGAP* is a Rho regulator that can play a mirid of roles in development, from the nervous system to playing a role in eye development. Deficiencies in Rho Gaps have been shown to have terrible morphogenetic results similar to those described in cases of cell adhesion mediators.



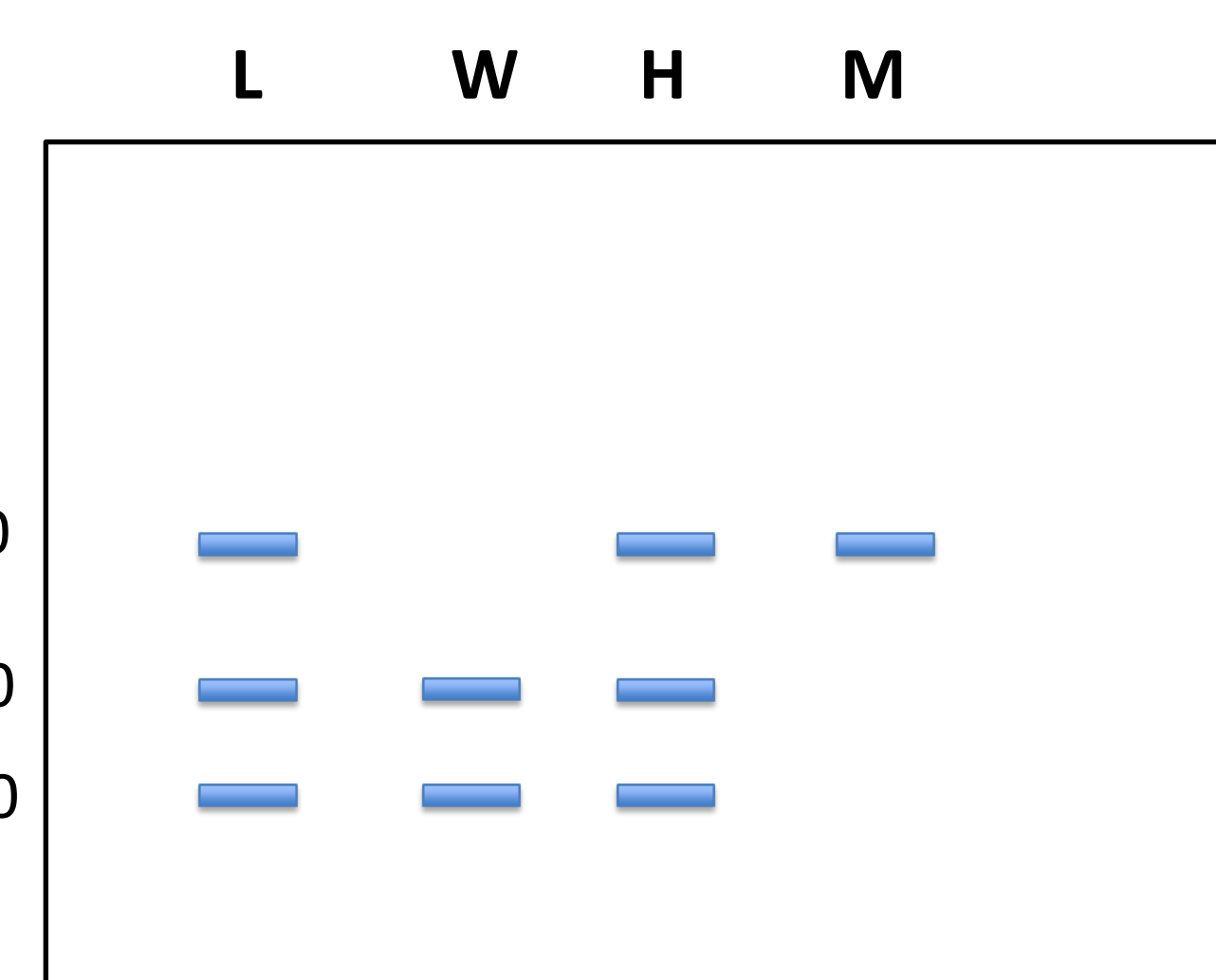
p190RhoGAP Talen

When looking at *p190RhoGAP*, fish with a *p190* Talen cut site were used. Talen (Transcription activation- like effector nucleases). Talen enzymes can be engineered by using TAL effector DNA binding domain to a nuclease that can cut DNA strands. This can be used to find specific proteins or genes and make cuts into specific strands. Zebrafish were then engineered to have a *p190* cut site and breed with non *p190* Talen fish to have the Heterozygous offspring.

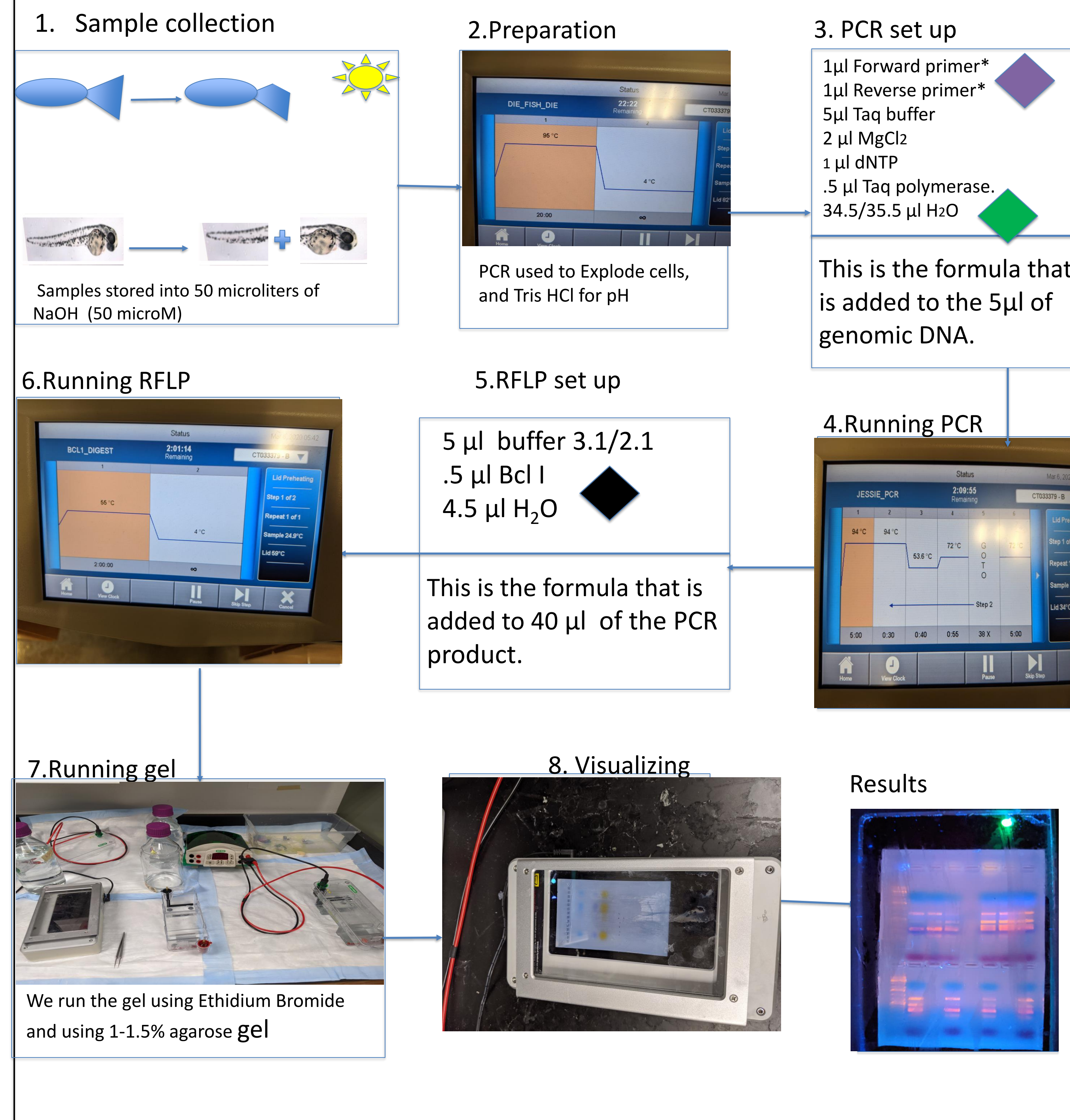


Wild type vs. heterozygous vs. mutant.

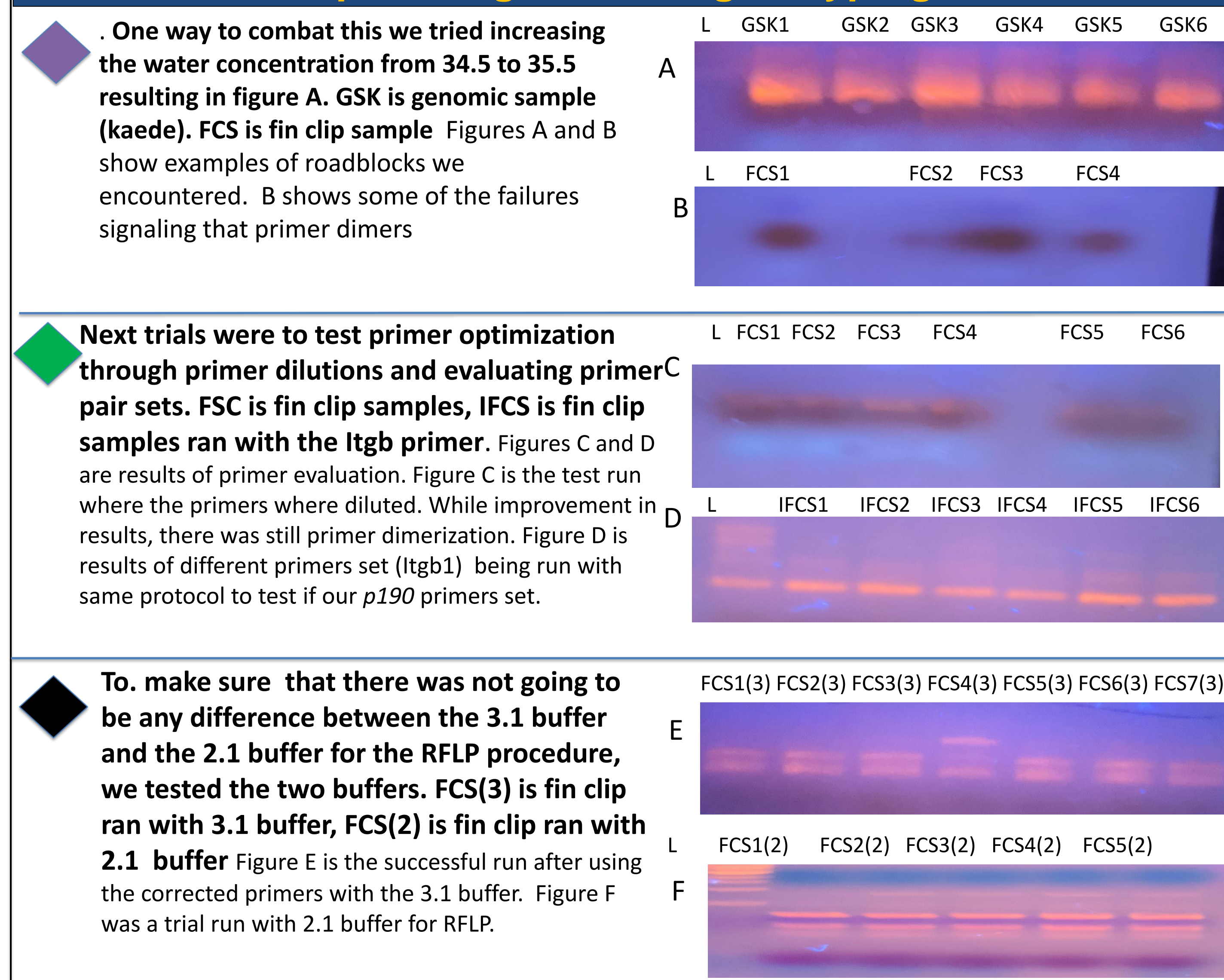
When using gel electrophoresis to visualize the genotyping, there are three possible outcomes. First is wild type where there is a cut in the band making two bands at 350 and 250 b.p long. The mutant is left uncut leaving a band 600 b.p long. The heterozygous genotype is categorized with having cuts and non-cuts resulting with all three bands. L is the ladder, W is expected wild type, H is expected heterozygous, and M is mutant.



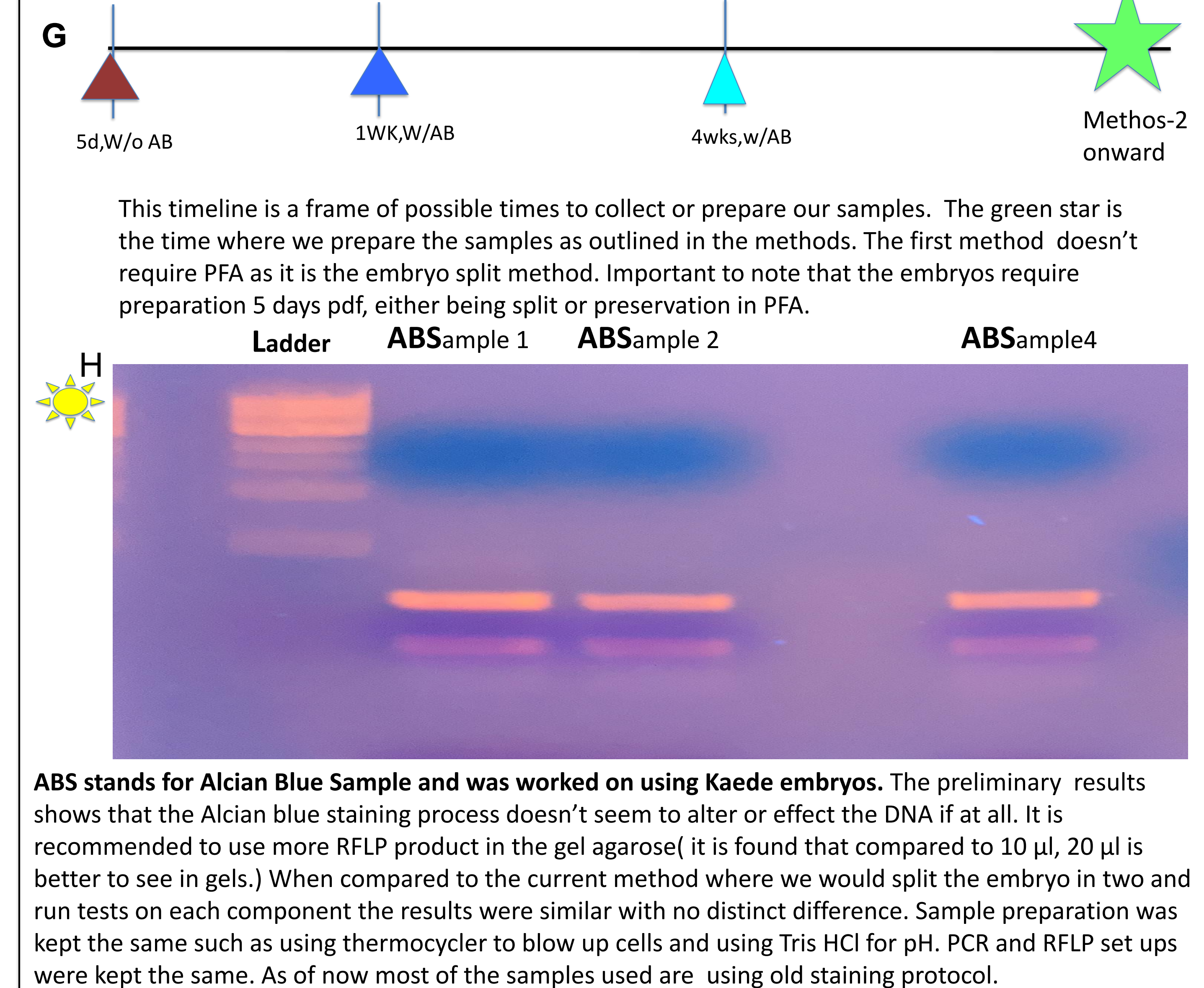
Methods- PCR , RFLP, Gel Electrophoresis



Optimizing PCR and genotyping



p190RhoGAP and Alcian Blue Results



Conclusions

- PCR has shown to have many steps that be considered when optimizing. We recommend evaluating the primers first, examining if it is the correct sequence and that it is diluted.
- The lab also found that there is little difference between the two water concentrations once primers were corrected. That said the higher dosages was helpful step in right direction and seemed to help with showing some results.
- The two buffers seem to work identically and didn't seem to have much difference.
- We were able to find that the Alcian blue staining did not impd or effect the samples. Going forward rather than having to harvest cells from a cell in the initial hours, or having to split embryos, we could just go forward with our staining and still use the samples and check their genotyping.

Future Directions

- Going forward we would use these protocols to help provide genotyping data in other studies to help provide data for consideration.
- We would also like to test and see if it is possible to use this protocol for other procedures, such as whole mount immunofluorescence, to streamline and optimize genotyping of samples by removing harvesting at the initial step of experiments.

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