

Evaluating the Effect of Promoter Strength on the Complementation of Deletion Mutants in *Synechocystis* sp. PCC 6803

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Introduction

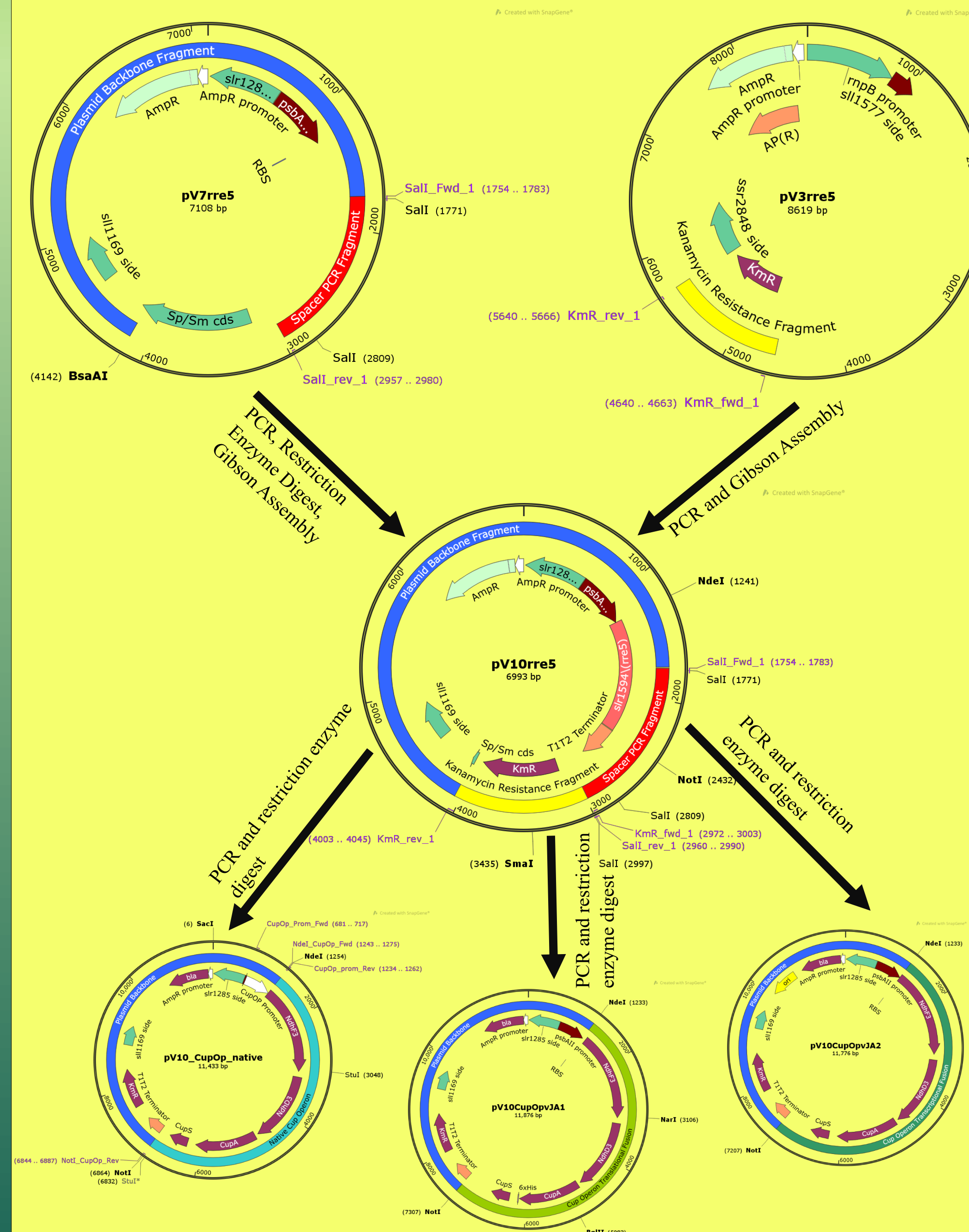
- The oxygen rich atmosphere we depend on was largely generated by numerous Cyanobacteria in the early stages of life on earth
- Cyanobacteria possesses unique CO₂ uptake systems, allowing them to efficiently scavenge inorganic carbon
- Cyanobacteria possesses an inorganic carbon concentrating mechanism including two CO₂ specific uptake systems. One is constitutive and one is low-CO₂ inducible. By limiting the CO₂ availability, the bacteria will express the inducible CO₂ concentrating mechanism to survive
- These systems are NDH-1₃, the inducible complex and NDH-1₄, the constitutive complex
- Previous work demonstrated we can complement deletions with the operon, however expression may not be optimal for future studies, and different expression systems produce different amounts of protein.

Objectives

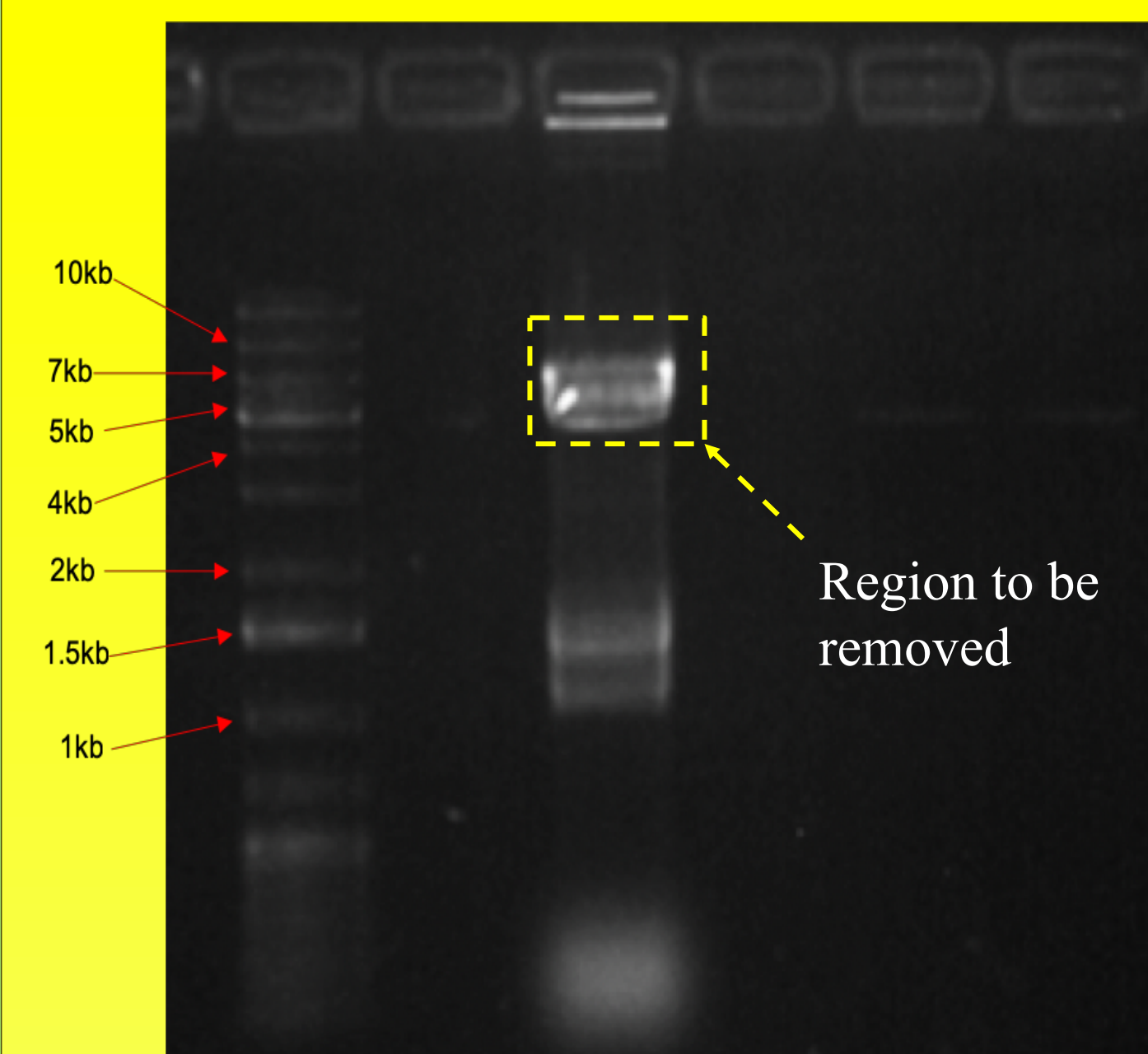
- The goal of our project is to develop a system for expressing NDH-1₃ operon in sufficient amounts for our future experiments
- The experiments here will test the effects of different gene expression control systems on the ability of deletion mutants complemented with the NDH-1₃ operon to grow in limiting CO₂

Methods

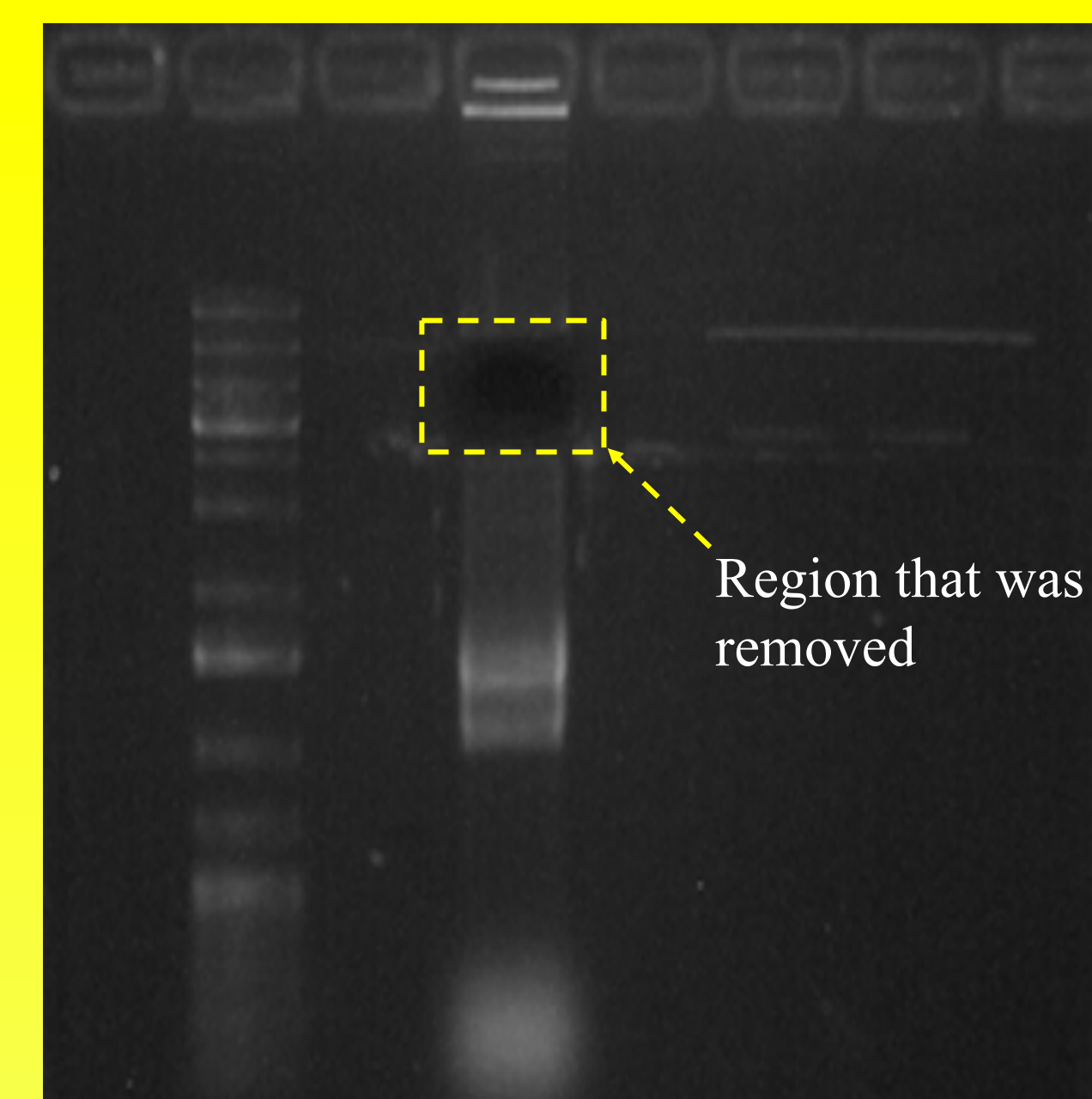
We began our experiment by constructing a new plasmid that contains antibiotic resistance (pV3) and a backbone fragment (pV7). We then created 3 different complementation plasmids each with different promoters in order to analyze promoter strength. The 3 promoters include native promoter, transcriptional fusion non-native promoter, and translational fusion.



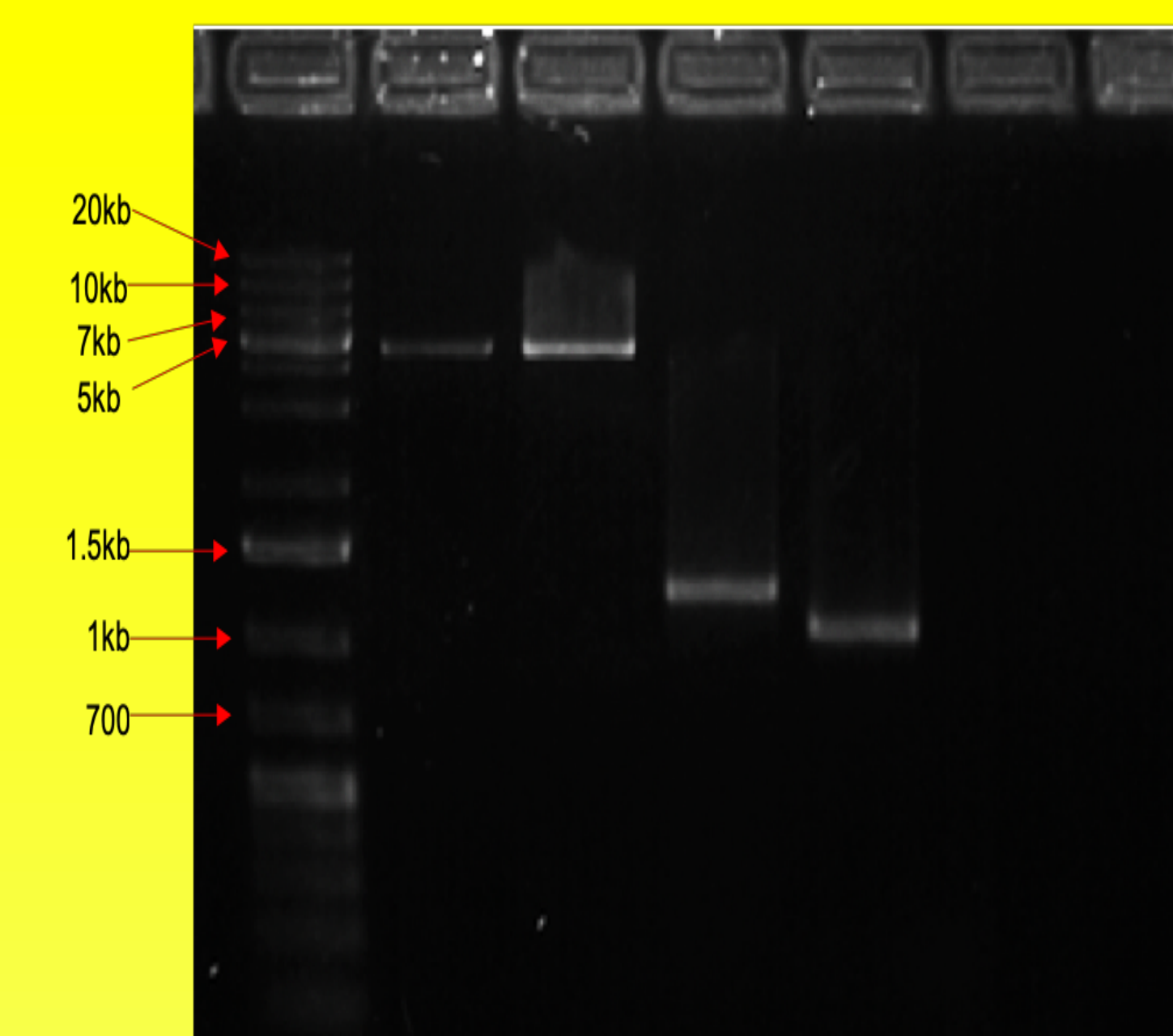
Methods (continued)



Agarose gel stained with gel green. Digestion of backbone product (blue). Backbone is shown as the larger and brighter band

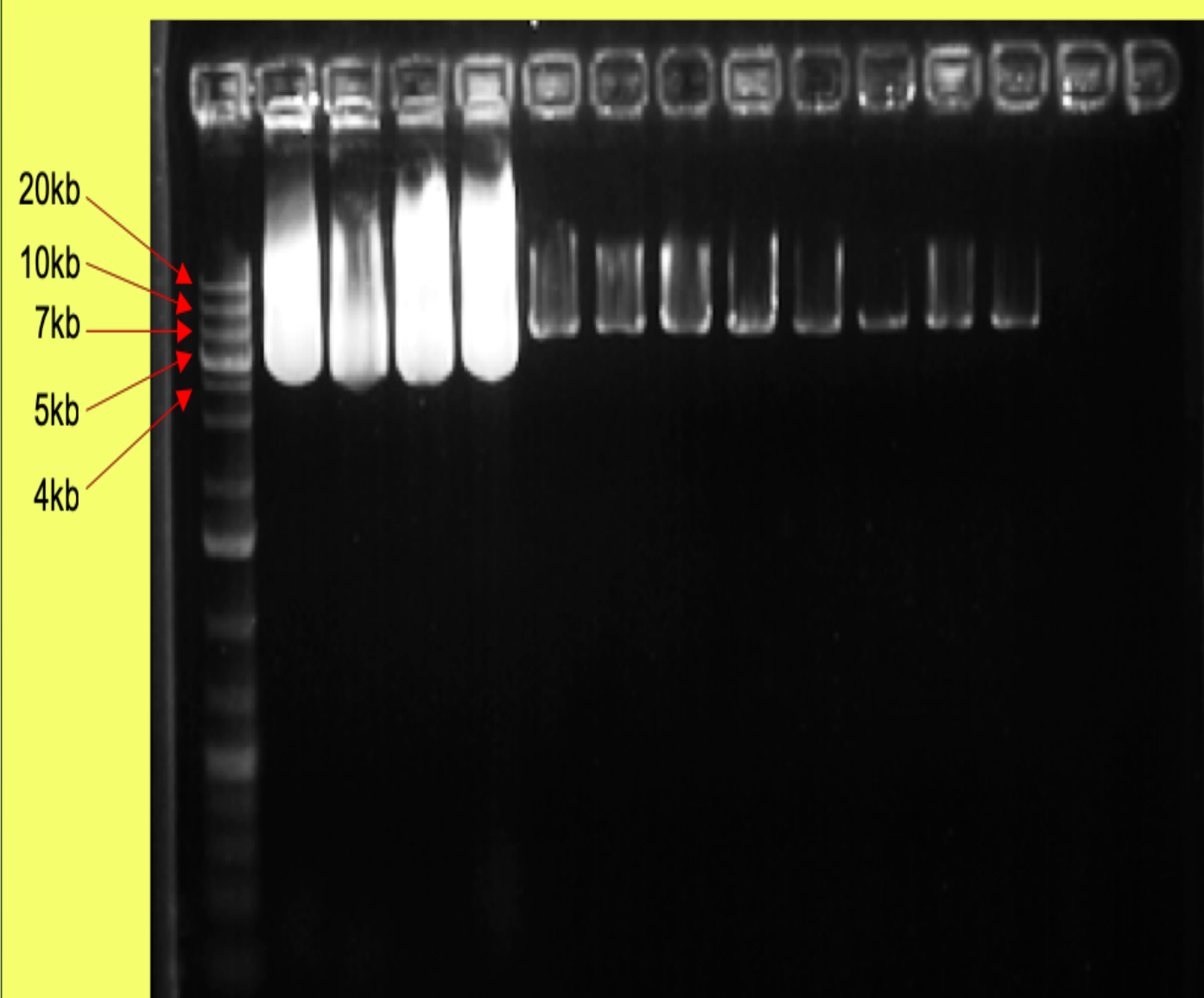


Agarose gel demonstrating the backbone product being cut out



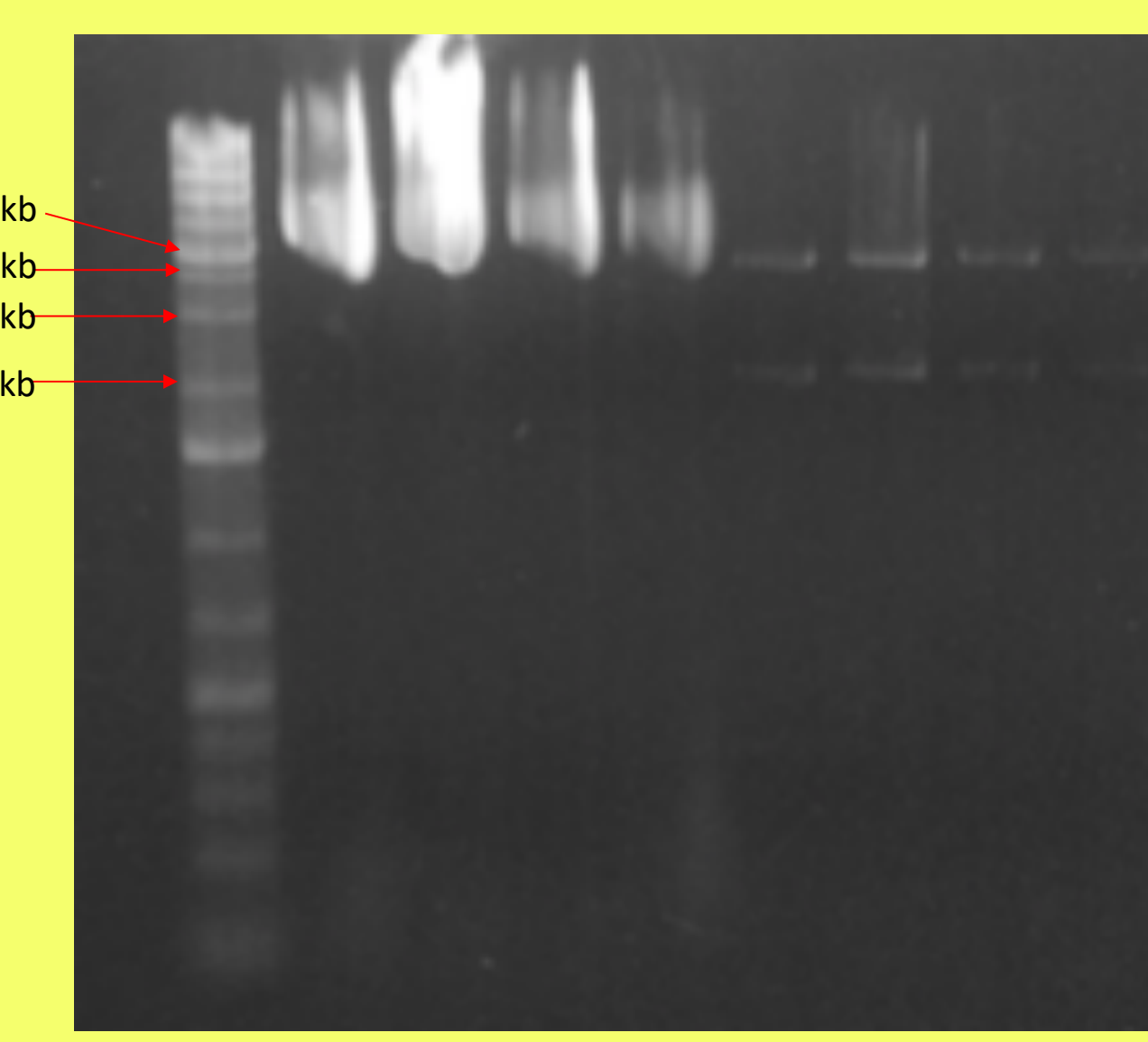
Agarose gel stained with gel green. PCR used to clone out Kanamycin Cassette (yellow) from pV3, spacer (red), and restriction digestion to provide the pV7 backbone (blue)

- Lane 1 & 2 : pV7 backbone
- Lane 3: Spacer Fragment
- Lane 4: Kanamycin Cassette

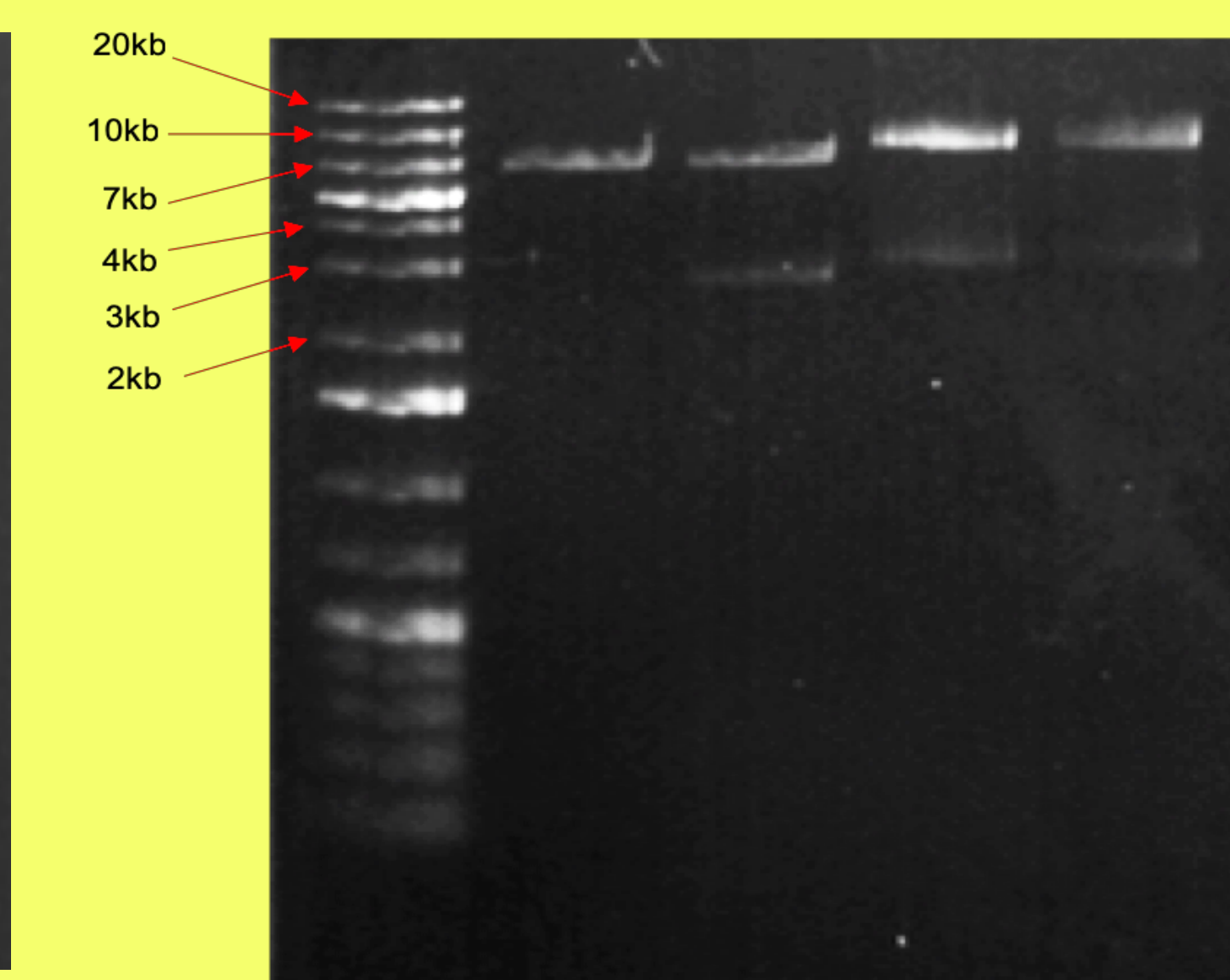


Agarose gel stained with gel green.

- Lane 1-4: raw plasmid, each isolated from a single colony
- Lane 5-12: checking activity of restriction enzymes that will be used to test each of the four isolates

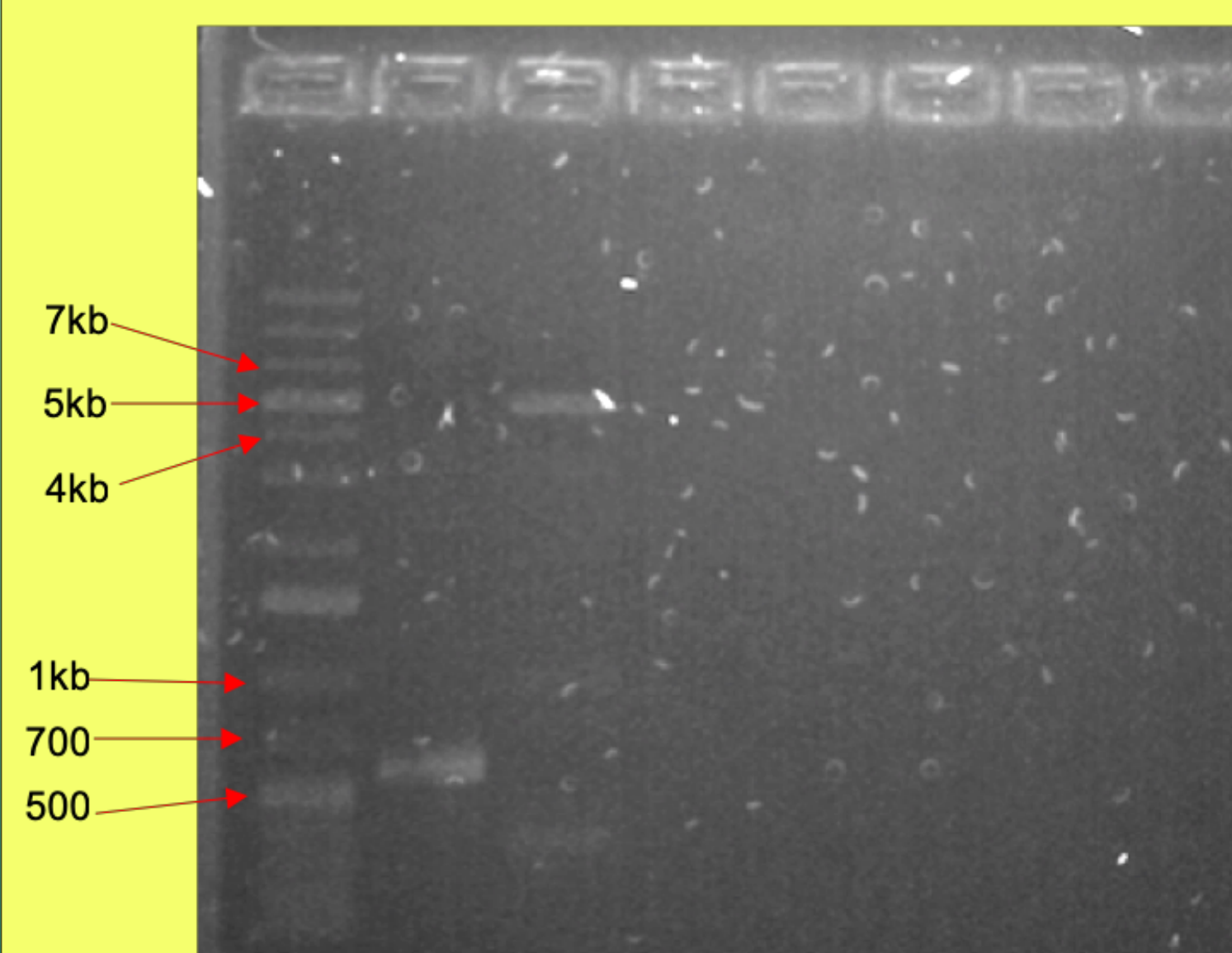


Agarose gel stained with gel green. Demonstrating correct construction of pV10. All fragments are presented in the gel



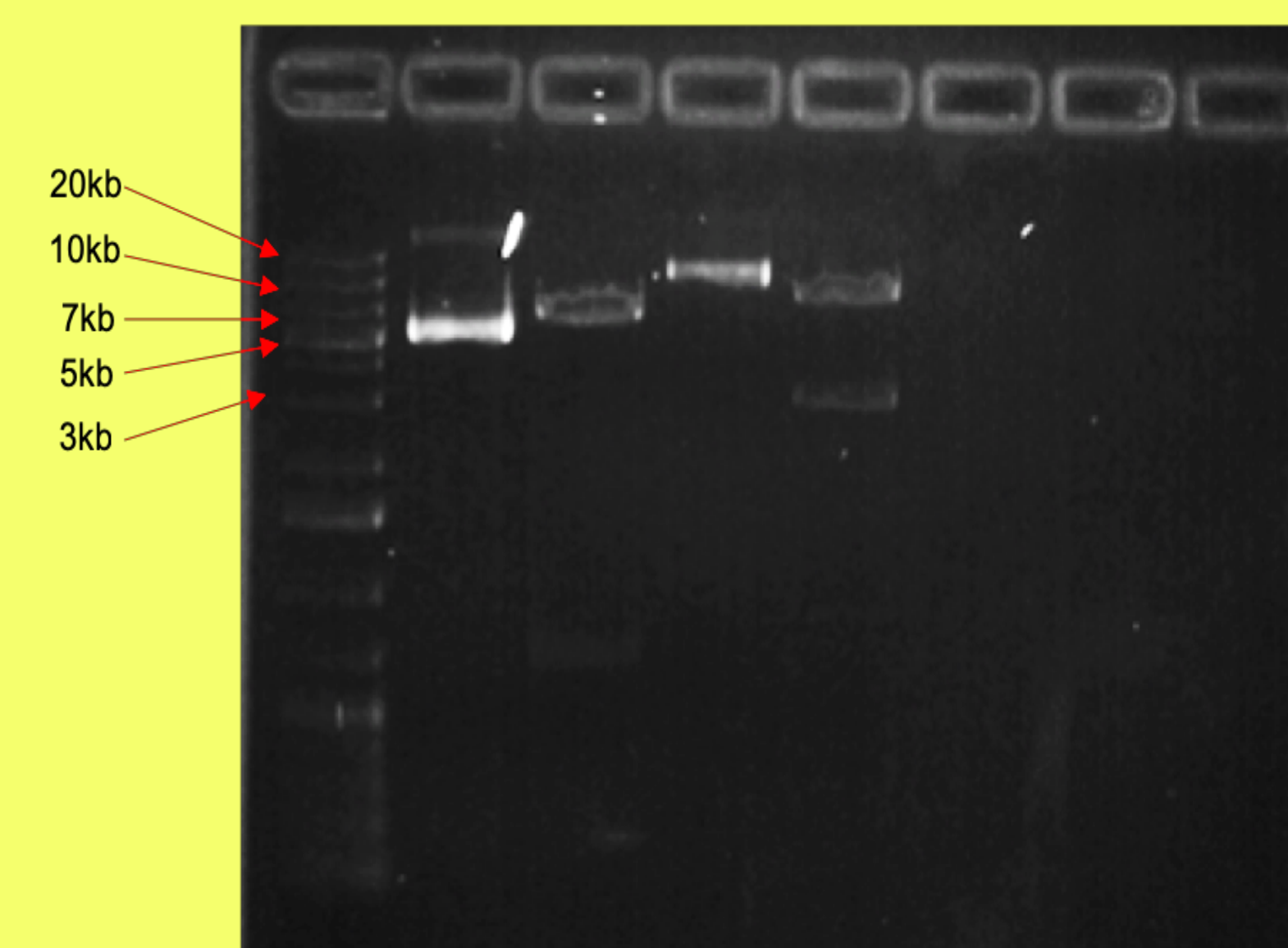
Agarose gel stained with gel green.

- Lane 3: pV10V1 (translational fusion digested with PST1)
- Lane 4: pV10V2 (transcriptional fusion digested with PST1)



Agarose gel stained with gel green. PCR

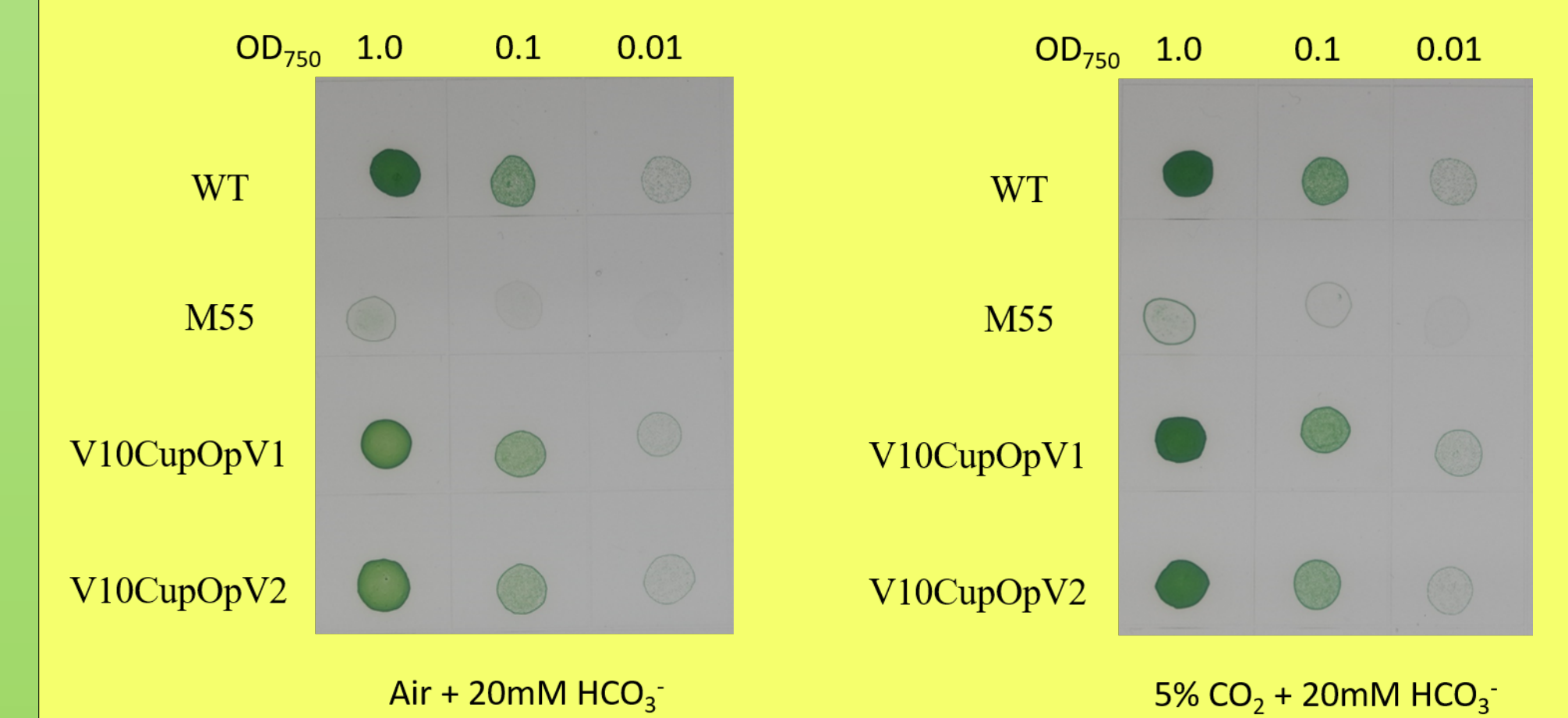
- Lane 1: Native CupOp promoter
- Lane 2: Entire CupOp



Agarose gel stained with gel green.

- Lane 1 & 2: pV10 re 5
- Lane 3&4: pV10 digested with diagnostic restriction enzymes (Assembled version is shown in the gel to the left)

Results



- A series of spot assays were completed in order to demonstrate the phenotypic characteristics of each complement versus the WT and M55 (negative control)
- The spot assays shown above analyzed 2 different promoters, pV10CupOpV1 (transcriptional fusion) and pV10CupOpV2 (translational fusion)
- Results were not recorded for the native promoter due to contamination issues
- Growth was compared under two conditions, 5% CO₂ and Air
- No significant change in growth was noted between the promoters and growth conditions

Conclusion

- The growth in air phenotype was restored in both complementation strains
- The differences between the promoters had no effect on the growth in air phenotype
- Either strain could be used to study NDH-1₃ complexes further.

Future Research

- Repetition of spot assay with the native promoter for further analysis
- Deeper analysis of the carbon concentrating mechanism
- Analyze this expression system with the same set of genes in various organisms

Acknowledgments

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