1. Introduction

IPRO 318 is entitled Novel New Drug Targets. The objective for this IPRO is to determine specific proteins that are involved in disease pathology. The team will investigate diseases and their protein sequences in order to determine their function and whether it is suitable for drug targeting. The information collected will be created into an informational website that can be used in further IPRO semesters. With the analyzed data the team will begin testing several relevant sequences to determine drug targeting.

2. Background

This IPRO is relatively new and there was little done before this semester. At the start of the project background information was given on the history and methodology of protein sequences in drug research. This gave the team time to become acclimated to the project. The research team was also given a compiled list of several diseases and their protein sequences; as this list was incomplete and unorganized the team recompiled the list. The team is now starting anew with its research and experiments.

3. Purpose

There are multiple objectives and goals the team has set forth this semester:

- Research diseases and their respective protein sequences.
- Compile all the data into an organized database.
- Analyze the data to determine several protein sequences of relevance.
- Begin experimentally testing several protein sequences.
- Develop a logbook of the experiments done and the results including pictures.
- Create detailed information for continuing IPROs to resume testing.

The most important objective for the Fall 2006 team is to create a useable database of the diseases linking them to their protein sequences.

There is currently no sponsor for IPRO 318.

4. Methodology

Work Breakdown

1. Bench Work Team
    A. Protein Expression Team
    B. Yeast Two-Hybrid Team
2. Research Team
    A. Web Design
    B. Database Design

The Yeast Two-Hybrid Team was able to culture yeast and determine protein-protein interaction within the yeast cells.

The Protein Expression Team was able to successfully isolate 4 hypothetical proteins arbitrarily named H1, H2, H3, and H4.

The Web Design Team created a website with information on the IPRO and its members. It also includes the database that was created by the other team.

The Database Team compiled a list of over 2000 known genetic diseases and their associated protein and gene numbers.

5. Assignments

Team Member Assignments

Team Leader: Lindsey Polich
Protein Expression Team: Amit Kamdar, Ronak Desai, Tengchuan Jin.
Yeast Two-Hybrid Team: Joshua Marell, John Knox, Floriann Stankovich, Vrudhdhi Patel
Web Design: Martina Dolejs
Database Team: Lindsey Polich, Calvin Wu, Hyunsuk Kim
Project Plan: Lindsey Polich
Midterm Report: Lindsey Polich
Poster: Calvin Wu, Hyunsuk Kim, Vrudhdhi Patel
Final Paper: Amit Kamdar, Lindsey Polich, John Knox, Floriann Stankovich
Power Point Presentation: Lindsey Polich, Ronak Desai, Amit Kamdar
Presentation: Ronak Desai, Lindsey Polich, Tengchuan Jin

6. Obstacles

The team as a whole has found that the most difficult problem to overcome is understanding the project fully. While most of the IPRO team consists of students with majors based in biology, the task set to the team is relatively new material. In order to overcome this obstacle the team sat with the IPRO professor and the Teaching Assistant and learned more about the process in which the IPRO is based. The team now completely understands the procedures and processes and is coming to handle them with more expertise after some practice.

Another problem the team has had to overcome is a lack of funding for the IPRO. IPRO 318 is not sponsored by a company and is in need of money for the materials needed in the lab. In order to complete the tasks set forth the Professor has generously allowed the team to use some of the resources from his other lab courses, but for the IPRO to continue successfully, more materials are needed.

The bench-work team has also had some trouble with the procedures because it is very tedious and time consuming. Each run of the procedure takes at least a week were the yeasts have to be grown. During this time it is hard to continue any work as the yeasts grown are needed for the next step in the process. This problem has been overcome by developing a cycle so that while one set of yeast is being grown another has just finished.

The last problem that the IPRO has encountered is in regards to the research team. The team at first was having trouble compiling the data into a useable source because the gene and protein numbers that were associated with the disease were not matching the numbers in the primary source. Through much tedious compiling the research team was able to match the numbers to its disease.

7. Results

Key milestones expected	Milestone data expected	Task Completion
Construction of entry clone for 318-H1	End of September	completed
Construction of entry clones for 318-H2 and 318-H3	End of October	completed
Construction of 318-H1 bait clone	Early October	completed
Construction of 318-H2 and 318-H3 bait clones	End of November	In progress
Two-hybrid screen of 318-H1	Early October	completed
Bacteria/yeast expression of 318-H1	End of October	completed
Construction of 318-H2 and 318-H3 expression clones	End of November	In progress
Database structure finalized	End of October	completed
Expended database on the web	End of November	Pending completion of test version
Website test beta version finalized	End of October	completed

The IPRO has a whole has accomplished several of the tasks set forth at the beginning of this semester.

The research team has successfully gathered and organized the data that will make up the website for this IPRO. There are more than 200 genes and proteins with more than 100 diseases making up the database for the research team. The team has been able to put the data together in order to make it easier to read and understand. They have also begun to discuss the web site layout determining the aesthetics for the page.

The Bench-work team that is in charge of the yeast two hybrids has now had practice in the procedure and was able to successfully procure useable yeast culture for the project.

The Bench-work team responsible for the protein-expression has also had practice in the techniques and procedures that are required for this part of the project, but has yet to make any significant progress toward the final outcome desired for the project. As this team's work is dependent on the yeast two-hybrid team, it is first necessary for the other team to finish their tasks before moving ahead.

As far as deliverables are concerned with the project, the team has yet to discuss the poster and power point presentation for IPRO day; and is currently more intent on procuring results from the lab. The website design has been started as it is an integral part of the IPRO's final goals.

All the work that has been done by the three teams is being documented in lab notebooks for reference by future IPRO's.

8. Recommendations

Our recommendations for the future IPRO is to be aware of the time delays in the lab portion of this IPRO. Culturing yeast and running several experiments is very time consuming and has a huge effect on the results of this IPRO. In the future we would like to see completion of the final version of the database and more work done on the hypothetical proteins isolated this semester.

9. References

www.ncbi.nlm.nih.gov/

10. Acknowledgments

Dr. Y. Zhang