



CALIFORNIA STATE SCIENCE FAIR 2016 PROJECT SUMMARY

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| Name(s) Suraj K. Anand | Project Number J0502 |
| Project Title Conserved Regions of Coagulation Factors III, VIII, and XII's Percent, Location, and Function in Diverse Species | |
| <p style="text-align: center;">Abstract</p> <p>Objectives/Goals The objective of this study is to locate and quantitate the conserved regions of Coagulation Factors III, VIII, and XII across diverse species as well as to discover the functions of major polypeptides located in the conserved regions.</p> <p>Methods/Materials Laptop computer with access to the Internet. Websites and databases used include NCBI, T-coffee, Clustal Omega, and Prosite. Sequences of the Coagulation Factors III, VIII, and XII of diverse species were found and aligned with the human sequence using computer databases and programs. Created Java program to obtain the number and percent of amino acids conserved. Major, important polypeptides and their functions were then searched for in the protein.</p> <p>Results The closer related the species was to Homo sapiens, the more conserved the amino acid sequence of the factor was. Compared to humans, mammals had 50-80% of the amino acids sequences of Coagulation Factors III, VIII, and XII conserved; reptiles scored between 30-50% of the Coagulation Factors conserved whereas fish only had about 25% of the amino acid sequence identical. Another major trend was that when the whole sequence was tested for polypeptides, only the conserved regions contained major known functional polypeptides. For example, in Coagulation Factor VIII (Figure 5) the Multicopper Oxidases Signature was found in the first half of the first conserved region.</p> <p>Conclusions/Discussion These results provide scientists with a roadmap of the highly conserved regions of the Coagulation Factors III, VIII, and XII. For patients that have unknown mutations that cause hemophilia, scientists can look at this roadmap to find the likely location of the undiscovered mutation. This data will also allow scientists to discover new important polypeptides because major polypeptides are present in conserved regions. By studying the conserved regions that have no known major polypeptides present, one can likely discover new functional polypeptides. These results concur with Natural Selection.</p> | |
| Summary Statement I located and quantitated the conserved regions of the Coagulation Blood Factor proteins across diverse species and showed that important functional polypeptides are located in conserved regions. | |
| Help Received I formulated and completed my experiment myself. Some of the ideas I used came from a website called science buddies. The tools and databases used were from the National Center for Biotechnology Information (NCBI). | |