PATTERNS AND PREDICTIONS FROM DOLPHIN (*Tursiops truncatus*) DIFFERENTIAL GENE EXPRESSION.

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The use of cDNA microarrays in functional genomics approaches, especially in an organism like the dolphin where the knowledge base is small, can greatly accelerate both novel gene discovery and the study and understanding of molecular physiological responses, in both controlled experimental situations and in wild populations. In this study, the transcriptome analysis of 20 wild dolphin blood samples from different geographical locations in U.S. waters (Charleston, SC and Indian River Lagoon, FL) has been conducted using a species-specific peripheral blood leukocyte (PBL) cDNA microarray. Total RNA extracted from blood leukocytes of wild dolphins was analyzed to investigate such variables as sex, location, age, health status and environmental stress. Two different machine learning approaches were used: Artificial Neural Networks (ANN) and Support Vector Machines (SVM), and different sets of genes were used as classifiers. In such supervised learning methods, the algorithm uses transcriptional profiles from samples of known classification to predict the classification of new samples. Here we show the results from ANN for the prediction of the "location" (Charleston, SC and Indian River Lagoon, FL) confirmed by SVM and cluster analysis, a more traditional microarray analysis approach. The results show that such gene expression analysis can provide insight into the natural history and physiological status of wild dolphins.