Abstract

A major goal of ageing research is the identification of genes which play a role in the process of ageing. This task is facilitated by the microarray technology, which enables genome-wide gene expression profiling. Bioinformatics methods are used to analyse microarray gene expression profiles and to determine gene functions and gene regulators by combining expression data with other types of biological data, e.g. annotations or genomic data.

In order to manage ageing-related gene data GiSAO.db has been developed. GiSAO.db is a web-based database system for storage and retrieval of information concerning **G**enes **i**nvolved in **S**enescence, **A**poptosis and **O**xidative stress. The database stores microarray gene expression data, annotation data, ortholog data and data of follow-up experiments. The web application is based on the Java EE framework and offers an intuitive user interface which simplifies data input and access. A mature authentication and authorization system is used to administrate user access rights.

Integrative data analysis has been performed on selected gene expression profiles stored in GiSAO.db to investigate mechanisms of ageing.

Gene expression patterns of various human ageing models have been compared to determine genes and pathways which are associated with oxidative stress induced senescence or other forms of senescence.

To identify regulators, functions and interactions of genes which are involved in UVB induced senescence, promoter analysis, pathway analysis and correlation analysis were conducted on corresponding gene expression profiles.

In conclusion, GiSAO.db assists researchers in the management of various types of data which are used to study genetic processes of ageing. Integrative data analysis has been performed to determine ageing-associated genes as well as pathways, potential regulators and interactions of these genes.

Keywords: ageing, microarrays, database, integrative data analysis