FUNCRYPTA - a systems biology approach to understand anhydrobiosis

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TARDIGRADES = WATER BEARS

- first described by the german pastor J.A.E. Goeze (1773)
- occur over the whole world in a variety of habitats within marine, freshwater and terrestial ecosystems
- water bears are a phylum of small invertebrates, related to the Arthropods [1]
- their body size ranges in length from 0.05 - 1.2 mm
- they have capability to enter a reversible state known as anhydrobiosis [2]

ANHYDROBIOSIS & FUNCRYPTA AIM

- first observed and described by Antony van Leewenhoek (1702)
- defined as a state in which metabolism is not detectable as a response to desiccation [3]
- tardigrades in this state shows no visible signs of life - "Dead but still alive"
- the aim of project is to understand the mechanism of anhydrobiosis, investigation of genes, enzymes and their product that enable tardigrades to survive extreme environmental conditions

PROTEOMICS

- identification of induced proteins with following methods:

  proteome map, 2D-DIGE, ICPL, mass spectrometry

Fig. 1: Two-dimensional gel electrophoresis, proteome map of tardigrades

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POTENTIAL APPLICATION

- long-term storage and preservation of cell, tissue, food and macromolecules
- metabolic pathway components responsible for dessication tolerance
- extending shelf life of protein-based drugs and enzymes
- stabilization of macromolecules, cells, tissues and even intact plants and animals

GENOMICS

- construction of two standard (active / inactive) & four normalized cDNA libraries (active / inactive / intermediate stages) (Fig. 2)
- native libraries are being Sanger sequenced, normalized libraries sequenced by pyrosequencing
- expression profiling and comparison of different stages via cDNA microarrays
- identification of candidate gene by representational difference analysis (optional arraying of RDA products) [4]

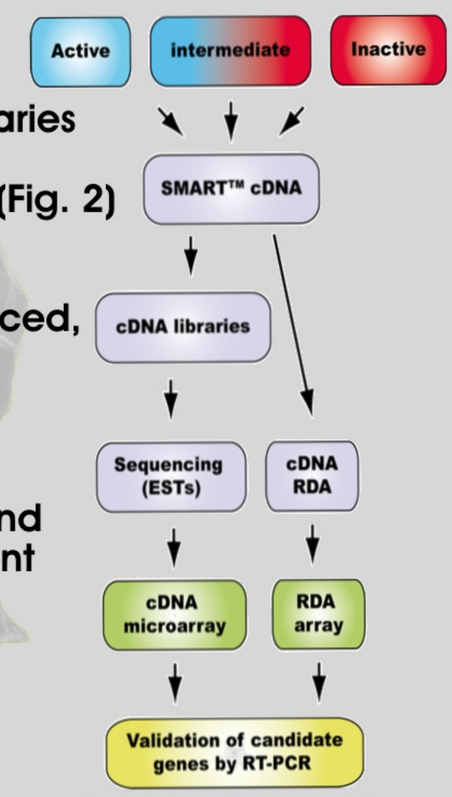

Fig. 2: Schematic representation of the genomics subproject

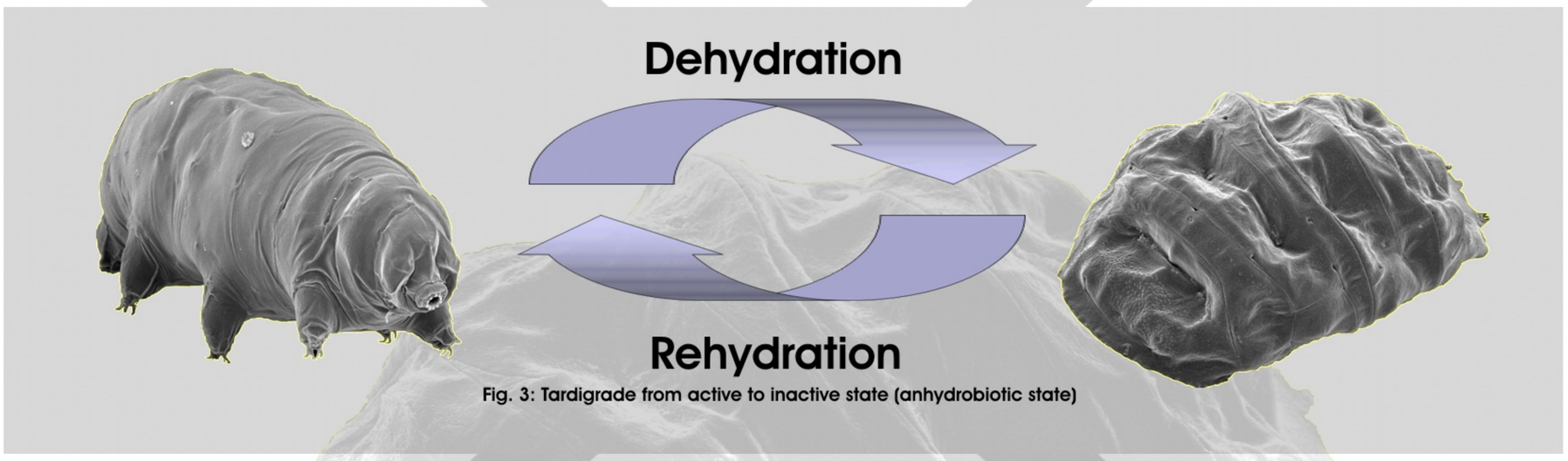

Fig. 3: Tardigrade from active to inactive state (anhydrobiotic state)

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ZOOLOGY / PHYSIOLOGY

- physiogical investigations to validate and quantify identified genes and proteins with the following methods: qRT-PCR, FISH,RNAi, functional assays
- provider of culture

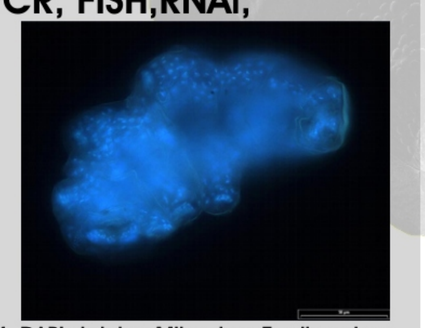

Fig. 4: DAPI staining Milnesium Tardigradum

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BIOINFORMATICS

- drawing up mathematical models to predict dynamic cellular changes between the active and cryptobiotic stages of tardigrades

Fig. 5: Tardigrade Analyzer web interface

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