

growing in harsh environments. Transcriptomic studies are usually conducted in a singular time, they do not provide any repetition across different seasons and frequently they encounter a high environmental variability because disturbing factors are frequently present. The identification of up- or down-regulated genes is often not enough to draw meaningful biological conclusions because it is hard to assign a clear role to each gene/protein belonging to specific signaling networks in host responses. Meta-analysis of transcriptomic data will discover commonalities and differences among differentially modulated genes and will allow screen which genes are good candidates for validation studies on gene-gene and protein-protein interaction networks. These analyses will allow delivering key knowledge on how a particular factors affect plant molecular responses to difficult environmental conditions. Meta-analysis of transcriptomic data represents a powerful tool to discover new candidate genes usable in marker-assisted selection. The objective of this work is to identify specific and common genes, proteins, gene sets, pathways linked to both abiotic and biotic stress resistances among key crops. The identification of genes involved in different stresses will improve diagnosis of an early "stress state" in response to stresses. Here, we will show results obtained by several meta-analysis of RNA-seq data related to plant responses to biotic and abiotic stresses. Common genes across species and type of stress usually encode key transcription factors, proteins involved in stress signaling and signal transduction, hormone-related pathways and other key gene categories have been identified. These analyses will help in monitoring stressed plants to start early specific management procedures for each stress and develop more sustainable therapeutic strategies through a fine-tuning of plant physiological responses.

TAXONOMIC DIVERSITY AND FUNCTIONAL TRAITS OF NEMATODE ASSEMBLAGES IN INTERTIDAL HABITATS ALONG ADRIATIC SEA COAST, ALBANIA

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Numerous studies have highlighted the importance of free-living nematodes in qualitative assessments of benthic ecosystems. Nematodes are considered as one of the most appropriate groups that best fulfills the characteristics of the indicator organisms. Recently, they are proposed as suitable for ecological quality evaluation of marine ecosystems, according to the Water Framework Directive (WFD). This study presents composition and structure of free-living marine nematode assemblages in five estuarine intertidal habitats along Adriatic Sea. Nematode assemblages from different sites are analyzed in term of diversity, life strategies and trophic structure, attempting to assess the anthropogenic pressure flowing from rivers into the estuaries, based on the state of nematode community succession. The comparison of different assemblages points out differences in taxonomic diversity and functional traits. The nematode assemblages were characterized by low trophic diversity and dominance of opportunistic genera, reflecting low ecological status.

EPIGENETIC PROFILING AND THERAPEUTICS IN LIVER DISEASE

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Epigenetic trait represents a stably heritable phenotype resulting from changes in a chromosome without alterations in the DNA sequence. Epigenetics modifications occur through strongly interlaced processes including DNA methylation, histone modifications, ncRNAs based mechanisms able to influence the gene expression. Disease susceptibility depends on a complex interplay between the individual genetic profile and epigenetic modulations do to aberrant DNA methylation and histone modification patterns caused by environmental stresses that may help to explain why identical twins do not always get the same disease. In Hepatocellular Carcinoma epigenetically induced genes were mapped to pathways driving cellular transformation, tumor growth and metastasis, while epigenetically repressed genes mapped to apoptosis, cell adhesion, and cell cycle progression. On the other hand, HBV and HCV viruses are recognized as drivers of epigenetic changes related to the persistence of liver cancer risk after Sustained Virologic Respond to antiviral treatment of HCV. On the other hand, the association between nutrition, epigenetic modifications and metabolic disease is well established. In murine models a diet depleted of methyl donors, able to induce DNA hypomethylation, is related to steatosis development and genome-wide association studies in humans shown a general tendency to demethylation of genes associated with Non Alcoholic Fatty Liver Disease. The knowledge of epigenetics alterations in liver disease shows clinical and translational implications regarding variation in disease phenotype, better risk stratification for disease progression, development of new diagnostic/prognostic biomarkers and development of new drugs. Finally, lifestyle modification strategies seems to be useful to prevent unhealthy epigenetic traits development.

LOCALIZATION AND LEVELS OF HSP60 IN TISSUE SAMPLES OF NORMAL AND PATHOLOGICAL HUMAN STOMACH

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Heat shock proteins (HSP) are a family of proteins produced by cells in response to a stress condition, the increase in the concentration of these proteins does not only occur in relation to the stimulation of high temperature, but following a large number of stimuli such as infections, inflammatory cytokines, biomechanical forces, UV rays and heavy metals. The HSP are differentiated according to their molecular weight. The HSPs also perform important "non-canonical" functions in fact they are involved in various biomolecular cell mechanisms, such as DNA replication, gene expression, cell differentiation furthermore many studies have shown the relationship between chaperone activity and carcinogenesis. The purpose of the following experimental work was to evaluate, through immunohistochemistry and immunofluorescence, the localization and the expression levels of HSP60 and inflammatory markers (CD3, CD20, CD68) within biopsy samples of gastric mucosa of gastritis (mild to moderate), hyperplastic polyps and adenocarcinoma with a medium degree of differentiation (G2). The different biopsy specimens were selected from the archives of the Biotechnology Laboratory of Institute Euro-Mediterranean of Science and Technology (IEMEST). All selected adenocarcinoma samples were characterized by a