liminary results lead us to conclude that dietary fatty acids do have an effect on the blood trancriptome, and that an unfavourable LA/ALA ratio could be related to a pro-inflammatory gene expression profile. Further analyses will be conducted to reveal the complex effects of the lipidome on the blood transcriptome.

P1–68

Proteomic approach to elucidate antimicrobial effect of *Papaver polychaetum* alkaloids

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Although bacteria have evolved numerous mechanisms to fight against antimicrobial agents, drug-resistant pathogens are on the rise. In the past few decades, this has led many research groups to medicinal plants for a search of novel antimicrobial agents. Long before mankind discovered the existence of microbes, the idea that certain plants had healing potential was well accepted and plants were used to treat common infectious diseases. The endemic plant *Papaver polychaetum*, from the genus of poppies, yields berberine as its major alkaloid. Berberine is a plant alkaloid with a long history of medicinal use in both Chinese and Ayurvedic medicine. It has demonstrated significant antimicrobial activity against different organisms including fungi and is relatively nontoxic to humans. However the antimicrobial mode of action of berberine is not clear. The aim of this work was to investigate the antimicrobial property of the alkaloid extract of the *P. polychaetum* against *E. coli* K12. For this purpose, proteomic approach was used which involved the selection of up and down regulated proteins on 2-dimensional polyacrylamide gels and their subsequent identification by MALDI-tof analysis. The common feature of the identified proteins was that they were DNA-binding. This approach enabled the elucidation of regulation of protein expression levels in the model microorganism *E. coli* K12 in the presence of the antimicrobial agent. The search for novel substances involves understanding of the molecular mechanisms of action of the drug/drug candidates and the related bacterial response. The results of this study will help to identify targets for future pro-drug design.

Further reading:

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P1–69

Computational analysis of 5′ and 3′ untranslated regions of breast cancer genes BRCA1 and BRCA2

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Untranslated regions (UTRs) are parts of the mature mRNA located before the start codon (5′ UTR) and after the stop codon (3′ UTR). They are transcribed with the coding region but they are not translated. Several regulatory roles have been assigned to the untranslated regions, including mRNA's localization and stability, and translational efficiency. These functions depend on the sequence and the structure of the UTR. BRCA1 and BRCA2 are the major hereditary breast/ovarian cancer predisposing genes and their mutations increase the risk of developing cancer. Interpretation of sequence variants found in genetic testing is the major concern for BRCA genes, especially for risk assessment in genetic counseling. From different repositories (dbSNP, BIC, kConFab), we collected BRCA1 and BRCA2 sequence variants that were found within 5′ and 3′ UTRs and we analyzed, using different on-line tools like UTResource and Transterm, their potential functional significance that could be expressed by disrupting or creating putative regulatory elements. As it is known that the function of non-coding RNAs (ncRNAs) greatly depends on their secondary structure, we analyzed how these non-coding sequence variants could have impact on the predicted secondary structure. By analyzing changes in the predicted secondary structures of the 5′ and 3′ UTRs from the patients with breast/ovarian cancer we tried to find out if this approach could be used for assessing clinical significance in cancer etiology.

P1–70

Phylogenetic and bioinformatic analysis of Glutathione S-Transferase Tau from Pinus brutia

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Glutathione S-Transferases (GSTs, EC.2.5.1.18) are widespread and complex enzyme superfamily that play important roles in detoxification and stress tolerance in plants. Plant GSTs are divided into four classes (Phi, Tau, Zeta and Theta), among which Tau is the most numerous one. It has been shown that plant Tau class GSTs could play essential roles in plant development and in buffering environmental and biotic stresses. Even, there are many studies on GSTs in plants, which have been focused generally on agricultural plants, there is no such an information considering the molecular characterization of GSTs in gymnosperms. The definition of detoxification enzymes like GSTs in perennial conifers, a large group of gymnosperms, is very important for their adaptations to several environmental stresses during their long lifespans. The present study reports the phylogenetic and bioinformatic analysis of GST gene (*Pb*GST-Tau) from a conifer, *Pinus brutia*, which is widely distributed in the north-eastern Mediterranean area, including Turkey. The *Pb*GST-Tau gene encodes a protein of 228 amino acid residues with a calculated molecular mass of 26.37 kDa. The sequence comparisons of *Pb*GST-Tau gene to other plant GST-Tau genes (*Pinus densata, Pinus tabulaeformis, Pinus yunnanennis, Oryza sativa japonica, Aegilops tauschii* and *Ginko biloba*) were performed at the amino acid level by using Bioedit programme. The phylogenetic tree was also constructed by using Neighbor-Joining/UPGMA method. The analyses indicated that *Pb*GST-Tau is placed with other three GSTs in Tau class from *Pinus tabulaeformis, Pinus densata* and *Pinus yunnanensis*, with 10.82%, 11.45% and 11.18% sequence diversity, respectively. The current difficulties for the comprehensive characterization of GST family in conifers originates from the insufficiency of comprehensive genome information on conifers in the literature. As the described members of the GST gene family in conifers are increased, the understanding for diversity and evolution of the GST classes would also be advanced.