جامعة بيرزيت
BIRZEIT UNIVERSITY

EMBO European Molecular Biology Organization

EMBO Young Investigators

"Frontiers in Molecular Biology and Biomedicine"

Workshop

Sponsored by:

The Faculty of Science, Department of Biology and Biochemistry, Birzeit University

and

The Young Investigator program of the European Molecular Biology Organization

March 20th and 21st, 2010

Abstracts

Birzeit University, Palestine

BIRZEIT UNIVERSITY

EMBO European Molecular Biology Organization

EMBO Young Investigators

Workshop

"Frontiers in Molecular Biology and Biomedicine"

March 20th and 21st, 2010

Birzeit University, Palestine

Organizing Committee:

Birzeit University	***EMBO***
Dr. Simon Kuttab	Dr. Buzz Baum
Dr. Ahed Abdulkhaliq	Dr. Karim Labib
Dr. Khaled Swaileh	
Dr. Jamil Harb	
Dr. Johnny Stiban	

جامعة بيرزيت
BIRZEIT UNIVERSITY

EMBO European Molecular Biology Organization

EMBO Young Investigators

"Frontiers in Molecular Biology and Biomedicine"
Workshop
Sponsored by:

The Faculty of Science, Department of Biology and Biochemistry, Birzeit University
and
The Young Investigator program of the European Molecular Biology Organization

March 20th and 21st, 2010

Birzeit University, Palestine

Saturday March 20th	
8:30 - 9:00	**Registration**
9:00 - 9:30	Welcome Birzeit & EMBO Dr. Adnan Yahya VP for Academic Affairs Dr. Buzz Baum, EMBO Dr. Simon Kuttab, Dean Faculty of Science
Session 1: chair, Dr Ahed Abdulkhaliq	
9:30 -10:30	Lecture: **Buzz Baum**, Department of Cell and Developmental Biology, University College, London **"From genetic information to physical form"**
10:30-10:50	Research Talk: **Johnny Stiban**, Department of Biology & Biochemistry, Birzeit University, Palestine. **"Initiation of apoptosis in cancer cells by post-translational modifications of ceramide producing enzymes"**
10:50-11:10	**Break**
Session 2: chair, Dr. Emilia Rappocciolo	
11:10-12:10	Lecture: **Elena Levashina**, Cell and Molecular Biology Institute, Strasbourg. **"Molecular approaches to Malaria"**

12:10-12:30	Research Talk: **Sabri M. Naser,** Department of Biology & Biotechnology, An-Najah National University, Palestine. **"Molecular identification of lactic acid bacteria *Enterococcus*, *Lactobacillus*, and *Streptococcus* based on pheS, rpoA and atpA multilocus sequence analysis (MLSA)"**
12:30 -1:00	Meeting with President & VP for Academic Affairs
1:00 - 2:00	**Lunch**
Session 3: chair, Dr. Johnny Stiban	
2:00-2:20	Research Talk: **Buzz Baum,** Department of Cell and Developmental Biology, University College, London. **"Preparing for division - in normal and cancer cells"**
2:20-2:40	Research Talk: **Elena Levashina,** Cell and Molecular Biology Institute, Strasbourg **"Mosquito complement-like system and its role in mosquito immune responses"**
2:40-3:00	Research Talk: **Yacoub Ashhab and Mahmoud Al-Saheb** Palestine Polytechnic University, Hebron, Palestine. **"Transcriptional profiling of segmental genomic duplication".**
3:00-3:15	**Break**
Session 4: chair, Dr. Sabri Naser	
3:15-3:35	Research Talk: **Wa'el Qara'een,** Department of Physics, Birzeit University, Palestine. **"Investigating the Dynamic Transition in proteins using recurrence quantification Interval analysis"**
3:35- 3:55	Research Talk: **Henry Jaqaman,** Department of Physics, Birzeit University, Palestine. **"A computer vision program for the detection of large numbers endocytosis pits in fluorescent microscopy"**
3:55-4:45	Students meeting & Discussion
6:30-	**Dinner in Ramallah**
Sunday March 21st	
Session 5: chair, Dr. Mahmoud A. Srour	
9:00–10:00	Lecture: **Karim Labib,** Patterson Institute for Cancer Research, Manchester. **"How cells copy their chromosomes and avoid genetic diseases"**
10:00-10:20	Research Talk: **Hani al Ahmad,** Department of Biology and Biotechnology, Al-Najah National University, Palestine. **"Tandem Mitigation Technology for Reducing Risks of Transgene Flow from Genetically Modified Plants.**

10:20-10:40	Research Talk: **Imad Matook**, Department of Biology, Al-Quds University, Palestine. **"H19 RNA encounters oncogenic properties and may serve as anti-tumor target"**
10:40-11:00	**Break**
Session 6: chair, Dr. Khaled Swaileh	
11:00-12:00	Lecture: **Petr Svoboda,** Institute of Molecular Genetics, Prague. **"RNA silencing - small but mighty RNAs"**
12:00-12:20	Research Talk: **Karim Labib,** Patterson Institute for Cancer Research, Manchester. **"Genome instability and the eukaryotic replisome"**
12:20-1:30	**Lunch**
Session 7: chair, Dr. Hani Al-Ahmad	
1:30-2:30	Lecture: **Nesrin Ozoren,** Department of Molecular Biology and Genetics, Boğaziçi University. Istanbul. **"The innate immune system: first line of defense"**
2:30-2:50	Research Talk: **Petr Svoboda,** Institute of Molecular Genetics, Prague. **"Rebooting the genome after fertilization"**
2:50-3:05	**Break**
Session 8: chair, Dr. Imad Matook	
3:05-3:25	Research Talk: **Mahmoud A. Srour,** Department of Medical Laboratory Science, Al-Quds University, Palestine. **Hepatitis B virus genotypes and pre-core/core-promoter mutations in Palestinian patients with chronic HBV infection**
3:25-3:45	Research Talk: **Nesrin Ozoren,** Department of Molecular Biology and Genetics Boğaziçi University. Istanbul. **"Inflammation and apoptosis"**
3:45-4:30	Students discussions & closing session

1. **Dr. Buzz Baum,** Department of Cell and Developmental Biology, University College, London

"From genetic information to physical form"

A complex animal is generated from a simple fertilised egg containing a single diploid genome. This process is one of the most miraculous events in biology. Work over the last 30 years has revealed many of the genes involved in both patterning and tissue morphogenesis during animal development. In this talk, I will discuss the role of Drosophila genetics in the elucidation of these processes. In addition, since cells are the architects, builders and bricks of any multicellular animal, I will look at the way the form and behaviour of single cells is regulated and coordinated to give rise to processes at the tissue scale.

2. **Dr. Johnny Stiban,** Department of Biology & Biochemistry, Birzeit University, Palestine.

"Initiation of apoptosis in cancer cells by post-translational modifications of ceramide producing enzymes"

Ceramide is a bioactive sphingolipid involved in cellular signaling and apoptosis. The pathways by which ceramides are produce depend on a group of six ceramide synthases (CerS) homologs in mammals. Since ceramide is at a steady state level in cells under normal conditions, we investigated the mechanisms by which CerS enzymes are activated. All six CerS homolgs are activated by phosphorylation and their activity is lowered considerably by dephosphorylation. *In vivo* studies show that treating cells with PKC activator PMA activates CerS whereas BIM (an inhibitor of PKC) significantly reduces

ceramide production. The generation of ceramide can be correlated with the permeabilization of the mitochondrial outer membrane by the formation of ceramide channels, hence initiating intrinsic caspase-mediated apoptosis. In all we provide evidence that CerS enzymes are phosphorylated and dephosphorylated and this is important for the regulation of ceramide synthesis and therefore control of apoptosis.

3. **Dr. Elena Levashina,** Cell and Molecular Biology Institute, Strasbourg. France

"Molecular approaches to Malaria"

Malaria is one of the most prominent infectious diseases, which is transmitted exclusively by mosquitoes of the *Anopheles* genus. Current strategies aimed at tackling malaria rely extensively on the control of vector populations in the field, chiefly through the use of insecticides and insecticide-impregnated bed nets. However unstable socio-economic environments, insurgence of insecticide resistance in mosquitoes and of parasite resistance to current anti-malarials, increase dramatically the number of malaria cases every year in the majority of disease endemic countries. To efficiently and timely identify and address global health issues, including emerging epidemics, novel alternative strategies are urgently needed to monitor risks and to roll back the disease.

Malaria involves an intricate interplay between 3 organisms - the human, the Plasmodium parasite and the mosquito. A series of biological features renders a limited number of *Anopheles* species very efficient vectors for the transmission of *Plasmodium* parasites, the causative agents of malaria. These include a genetically determined preference for blood meals on a human host for egg development, a high reproductive rate and a long life span, combined with the

ability to support parasite development. On the other hand, malaria parasites have developed sophisticated strategies to establish infection while evading the host immune system, to cope with a changing host environment and to increase the duration of infection in both human host and the mosquito vector. In this lecture, we will summarize our molecular understanding of the malaria parasite life cycle with the two hosts with a particular attention to the mosquito stages of development.

4. **Dr. Sabri M. Naser,** Department of Biology & Biotechnology, An-Najah National University, Palestine.

"Molecular identification of lactic acid bacteria *Enterococcus*, *Lactobacillus*, and *Streptococcus* based on pheS, rpoA and atpA multilocus sequence analysis (MLSA)"

Lactic acid bacteria (LAB) belonging to the *Enterococcus*, *Lactobacillus* and *Streptococcus* comprise a heterogeneous group. LAB have been widely used in food fermentations and as probiotics in health-promoting food products. In addition to their beneficial actions, some particular LAB are pathogenic. Hence, the accurate species identification of lactic acid bacteria (LAB) remains of crucial importance in clinical and food microbiology.

The main goal of this study is to evaluate the contribution of the multilocus sequence analysis (MLSA) of three housekeeping genes to the species identification and delineation in LAB, particularly the genera *Enterococcus*, *Lactobacillus* and *Streptococcus*.

A total of 195 species of *Enterococcus*, *Lactobacillus* and *Streptococcus* were included in this study. The partial sequences of phenylalanyl-tRNA synthase alpha subunit (*pheS*) (382-455nt), the RNA polymerase alpha subunit

(*rpoA*) (402-694 nt) and the ATP synthase alpha subunit (*atpA*) (611-1102nt) genes were determined for 494 strains representing the three genera. All *Enterococcus*, *Lactobacillus* (*rpoA* and *atpA*) and *Streptococcus* species were clearly differentiated on the basis of *pheS*, *rpoA* and *atpA* sequences.

The interspecies variation between individual species and the nearest neighbour based on a specific locus is variable among the different genera. The investigated housekeeping genes show variation in their discriminatory power for the differentiation of species. The *pheS* gene provides the highest interspecies variation, followed by *atpA* and *rpoA* genes, respectively. The three loci have a high degree of homogeneity among strains of the same species.

In comparison to the 16S rRNA gene sequence data, the MLSA data indicate that *pheS*, *rpoA* and *atpA* genes provide higher resolution for differentiating *Enterococcus*, *Lactobacillus* and *Streptococcus* species and very useful in the differentiation of the closely related species with almost identical 16S rRNA gene sequences.

The use of MLSA for identification of the genus *Enterococcus*, *Lactobacillus*, and *Streptococcus* was evaluated. For *Enterococcus*, The *pheS* and *atpA* gene sequence analyses provide interspecies gaps, which mostly exceed 13% and 7% divergence, respectively. The *rpoA* gene sequences revealed a lower resolution with an interspecies gap of 3%. For *Lactobacillus*, The *pheS* gene sequence analysis provides an interspecies gap, which exceeds 10% divergence. The *rpoA* gene sequences revealed a somewhat lower resolution with an interspecies gap exceeding 5%. For *Streptococcus*, The *pheS* and *atpA* gene sequence analyses provide interspecies gaps, which mostly exceed 6% and 5% divergence, respectively. The *rpoA* gene sequences revealed a lower resolution with an interspecies gap mostly exceeding 3%.

MLSA provide a new dimension into the elucidation of genomic relatedness at the inter- and intraspecies levels by sequence analyses of *pheS*, *rpoA* and *atpA* housekeeping genes. The MLSA provides to *Enterococcus*, *Lactobacillus* and *Streptococcus* electronically portable, highly reproducible data with lower costs for their accurate identification. MLSA also provide genomic markers that serve as valuable alternatives to 16S rRNA gene sequencing for species identification.

5. **Dr. Buzz Baum,** Department of Cell and Developmental Biology, University College, London

"Preparing for division - in normal and cancer cells"

Animal cells undergo a complex sequence of morphological changes as they pass through mitosis. This begins at the onset of mitosis with retraction of the cell margin and cell rounding, and is followed after the onset of anaphase by axial cell elongation and cytokinesis. I will describe our efforts to explore the role of cytoskeletal regulators in mitotic cell rounding and the molecular mechanisms that couple mitotic actin re-organisation to the cell cycle clock using Drosophila and human cells in culture as model systems. Our analysis revealed that Moesin is activated at the onset of mitosis, and is required for the increase in cortical rigidity that accompanies entry into mitosis and for mitotic cell rounding. Strikingly, soft cells that lack Moesin also exhibit profound defects in spindle morphogenesis and chromosome alignment, which can be rescued by re-establishing cortical tension from the outside the cell. These data reveal the importance of cortical stiffening and cell rounding as a prelude to chromosome segregation in animal cells, and in doing so help to explain the universality of this process. These data also suggest that mitotic cell mechanics may play a critical

process in tumour development, making it a potential target for anti-cancer therapies.

6. **Dr. Elena Levashina,** Cell and Molecular Biology Institute, Strasbourg

"Mosquito complement-like system and its role in mosquito immune responses"

7. **Dr. Yacoub Ashhab and Mahmoud Al-Saheb,** Palestine Polytechnic University, Hebron, Palestine.

"Transcriptional profiling of segmental genomic duplication".

Gene duplication has been considered as the leading mechanism for the evolution of new genes. A characteristic of eukaryotic genomes is that a large number of protein-coding genes belong to multigene families.

With the availability of information about the entire genome of an increasing number of organisms, it has become possible to investigate and characterize various kinds of DNA sequence repeats including segmental genomic duplications. However little is known about the transcriptomic maps and profiles of recently duplicated genomic segments and their impact on the evolution of novel genes.

We have developed several bioinformatics approaches to study the phenomenon of recent segmental duplication and its association with the genes of innate immune system that are known to encode for pathogen recognizing receptors.

Our results showed that, in contrast to the relatively low frequency of segmental

duplications in housekeeping genes, the genes of innate immune system have a significantly higher rate of segmental duplication that are transcriptionally active.

Understanding the role of recent segmental duplication in the evolution of new genes of our immune system can provide deep insights into the mechanisms of host-pathogen evolution and the interethnic differences in the susceptibility and immune reactivity to infectious diseases.

8. **Dr. Wa'el Qara'een,** Department of Physics, Birzeit University, Palestine.

"Investigating the Dynamic Transition in proteins using recurrence quantification Interval analysis"

The Recurrence Quantification Interval (RQI) analysis technique is used to study the dynamic transition in the Olea Europaea (Ole6) allergen protein. Total energy time series for the protein at 100K, 150K, 200K, and 300K, obtained from 5ns molecular dynamics simulations, are analyzed. Preliminary results point to an increase of slow recurrences with increasing temperatures.

9. **Dr. Henry Jaqaman,** Department of Physics, Birzeit University, Palestine.

"A computer vision program for the detection of large numbers endocytosis pits in fluorescent microscopy"

Clathrin-mediated endocytosis is a major endocytic pathway. The formation of the Clathrin-coated pits (CCPs) is the first step in this pathway. It is experimentally studied by tagging fluorescent proteins to the Clathrin molecule. The time development of the CCPs is recorded by Total Internal Reflection

Fluorescent Microscopy and the results stored as digital images. Each of these images typically contains hundreds of such pits of various sizes and shapes.

In the current work a computer vision program is developed for the detection and tracking of the CCPs from one image to the next with the aim of measuring the lifetimes of these pits and their dependence on various factors, such as cell type and the cargo, i.e. the molecules that enter the cell by this process. The "a trous" algorithm used for the treatment of images in astronomy is used for the analysis and elimination of noise in the current work

10.Dr. Karim Labib, Patterson Institute for Cancer Research, Manchester.

"How cells copy their chromosomes and avoid genetic diseases

All of life on earth begins as a single cell, and cell proliferation is fundamental to the proliferation of all living creatures. To survive the dangerous process of cell division, eukaryotic cells must do at least three key things: make a nearly perfect copy of the chromosomes, segregate the two copies to distinct parts of the cell, and then divide the cytoplasm specifically between the separated chromosomes. Chromosome replication is one of the oldest fields of molecular biology, and yet is still understood relatively poorly. One key reason for this is that chromosome replication is coupled to a variety of other interesting processes that allow cells to survive cell division. So, for example, complex epigenetic modifications along each chromosome must be copied at the same time as duplicating the DNA, in order to maintain patterns of gene expression from one generation to the next. Secondly, the sister chromatids produced by chromosome replication must be held together until mitosis by a mechanism called cohesion, which is established in a mysterious fashion during replication. Finally, the

process of chromosome replication must be monitored very carefully to detect problems when they occur and try to correct them, in order to preserve genome integrity and avoid mutations. For all these reasons, chromosome replication is a fascinating process that underlies the development and survival of all living creatures. Defects in chromosome replication can lead to genetic diseases, and there is now increasing evidence to indicate that the process of chromosome replication is defective in many human cancers.

11.Dr. Hani al Ahmad, Department of Biology and Biotechnology, Al-Najah National University, Palestine.

"Tandem Mitigation Technology for Reducing Risks of Transgene Flow from Genetically Modified Plants.

Transgenic plants can interbreed with related weeds and crop cultivars. Depending on the transgene, this may increase the fitness of the hybrid offspring. Two mechanisms have been suggested to control transgene escape and establishment: either containing the transgene(s) within the biotech crop, and/or by employing transgenic mitigation (TM) techniques to minimize the environmental effects of the primary transgenic trait (e.g. herbicide resistance, pharmaceutical trait, etc.) should it escape. In TM technology, mitigator genes that lower the competitive ability of transgenic hybrids are linked in tandem to the primary transgene. Such mitigator genes are neutral or positive to the biotech crop, conferring traits such as dwarfism, no secondary dormancy, non-shattering of seedpods, etc. The TM concept was tested in tobacco (*Nicotiana tabacum*), and oilseed rape (*Brassica napus*) that may remain in fields as volunteer weeds and the latter can interbreed with nearby weedy *B. rapa*. The two TM crops were

transformed with a tandem construct of *ahas*^{R} conferring herbicide-resistance in tandem with Δ*gai* for dwarfism. In both plant systems, the risk of transgene establishment in transgenic volunteer or intraspecific hybrids was effectively reduced at different levels of competition, at the close spacing typical of weed populations. The yield of transgenic monocultures was significantly higher than the corresponding wild type of both crop species due to the increased harvest index conferred by dwarfism. The yield of TM *B. napus* was double the wild type when growing by itself. In contrast, TM hybrids with wild type *B. napus* or with weedy *B. rapa* were unfit to reproduce well when grown interspersed with the non-transgenic cohorts, and when cocultivated in competition with wheat. Their reproductive fitness based on seed yield relative to the non-transgenic *Brassica* sibs was between zero and 11% depending on planting density, demonstrating the advantage of the TM technology to minimize the risk of transgene establishment and spread, while increasing crop yield.

12.Dr. Imad Matook, Department of Biology, Al-Quds University, Palestine.

"H19 RNA encounters oncogenic properties and may serve as anti-tumor target"

H19 is n imprinted gene that demonstrates maternal mono-allelic expression and does not code for a protein product. It is abundantly expressed during embryogenesis, but is normally shut off after birth in most tissues. However in more than 30 types of cancers, H19 gene is either highly expressed and/or shows aberrant allelic pattern of expression relative to normal tissues.

To explore the role of H19 RNA in cancer, we had applied the technology of RNA interference (RNAi). Our in vivo results show that H19 RNA is essential for tumor growth. Tumors induced from bladder, hepatocelluar and ovarian

carcinoma in which H19 gene is silenced, encountered a very significant reduction in both tumor volumes and weights.

H19 RNA level is induced by hypoxic stress in p53-dependent manner. HIF1-α is the critically involved in H19's induction. Our preliminary in vivo results show that H19 is involved in the survival of hypoxic cancer cells and also induces angiogenesis.

These results suggest that H19 RNA harbors oncogenic properties, enhancing the development of carcinogenesis. We propose that the oncogenic property of H19 is triggered by hypoxic stress associated with tumor growth. We further show that H19 RNA may be recognized as a new target for cancer therapy.

13. Dr. Petr Svoboda, Institute of Molecular Genetics, Prague.

"RNA silencing - small but mighty RNAs"

Almost all eukaryotic organisms produce in their cells small RNA molecules (20-30 nucleotides long), which function as sequence-specific guides for ribonucleoprotein complexes that regulate gene expression. A common term for mechanisms utilizing small RNAs is RNA silencing. It includes pathways causing diverse effects, such as sequence-specific mRNA cleavage, repression of mRNA translation, transcriptional silencing, or even DNA deletion. The talk will guide students through the history of discovering RNA silencing pathways and it will show that all RNA silencing pathways share the same principal components. The last part of the talk will focus on RNA interference, one of the RNA silencing pathways, which is nowadays used to experimentally block gene function.

14.**Dr. Karim Labib,** Patterson Institute for Cancer Research, Manchester.

"Genome instability and the eukaryotic replisome"

Chromosome replication is a highly complex process that is still understood relatively poorly in eukaryotic cells. Around 100 proteins act at DNA replication forks, and almost all of these have a single orthologue in all species, indicating that the mechanisms of chromosome replication are highly conserved throughout evolution. A subset of the proteins required for chromosome replication interact with each to make a large multi-protein machine called the replisome. Key components include the DNA helicase responsible for unwinding the parental DNA duplex at replication forks, and the DNA polymerases responsible for synthesizing the nascent DNA strands. The eukaryotic replisome is still poorly charaterised, and appears to contain many other regulatory proteins that help cells survive chromosome replication and preserve genome integrity from one generation to the next. In addition to controlling DNA synthesis at forks, these factors probably allow chromosome replication to be coupled to other interesting processes such as the duplication of epigenetic modifications along each chromosome, and the establishment of cohesion between the two sister chromatids that are produced by chromosome replication. These processes play a key role in preserving genome integrity from one generation of eukaryotic cells to the next.

15.**Dr. Nesrin Ozoren,** Department of Molecular Biology and Genetics, Boğaziçi University. Istanbul.

"The innate immune system: first line of defense"

Every multicellular organizm has to survive in the face of a constant challenge by different kinds of invading pathogens, viruses or damage from within. More

primitive organizms depend only on their innate immune system to provide this protection and they utilize a variety of mechanisms, including C-type lectins, complement activation and the TLR signaling pathways initiated at the cell membrane. Toll-like receptors recognize different pathogen associated molecular patterns and upon activation result in the activation of the NF-κB transcription factor, whose downstream targets include many pro-inflammatory cytokines. Cytoplasmic invasion is detected by the NLR and RLR family of receptors, which may lead to NF-κB activation, interferon production as well as caspase-1 activation. Caspase 1 activity results in the cleavage of the pro-form interleukins 1β and 18, which are secreted afterwards. IL-1β, together with IL-6 and TNFα is responsible for the induction of edema formation and establishment of systemic fever conditions

16.Dr. Petr Svoboda, Institute of Molecular Genetics, Prague.

"Rebooting the genome after fertilization"

Cells in our bodies contain the same genetic information but they use it differently as different genes are expressed in different cell types. Once in a lifecycle, the genetic information is used to build from a whole organism from a single fertilized egg. The unfertilized egg is using the genetic information to build and maintain properties of an egg. The talk will provide an insight into the complexity of the problem of reprogramming gene expression in the egg to produce an embryo, which can develop into a mouse.

17.Dr. Mahmoud A. Srour, Department of Medical Laboratory Science, Al-Quds University, Palestine.

Hepatitis B virus genotypes and pre-core/core-promoter mutations in Palestinian patients with chronic HBV infection

There are eight genotypes (A-H) of hepatitis B virus (HBV). The HBV genotypes show distinct geographic distribution and have been shown to influence the clinical course of infection. While genetic mutations in the Pre-core C (PC) and Basal Core Promoter (BCP) may predict the development of hepatocellular carcinoma. In this study, we have genotyped 150 HBV clinical isolates from West Bank region, Palestine. Patients were categorized into three groups, (i) chronic active hepatitis (n=118), (ii) liver cirrhosis (n=27) and (iii) hepatocellular carcinoma (HCC, n=5). Genotyping was performed using multiplex nested-PCR using specific primers complementary to pre-S1/S gene for A-F genotypes. While genotype G was genotyped by nested PCR using primers specific for a 36-bp insertion in the core gene. Genotyping was verified by DNA sequencing and phylogenetic analysis. RFLP analysis was used for investigation of PC / BCP mutations. The most prevalent genotypes were genotype D (25.3 %) and A (4.7 %) in the West Bank region/Palestine. However, a high prevalence of mixed infections was observed and was attributed mainly to D+A infections (35.3 %). The prevalence of negative HBeAg (68 %) was higher than positive HBeAg among our study population. However, mixed genotypes particularly A+D (71.1 %), tend to predominate among negative HBeAg patients compared to positive HBeAg patients. The correlation of PC/BCP mutations to liver cirrhosis and HCC are also discussed.

18.Dr. Nesrin Ozoren, Department of Molecular Biology and Genetics
Boğaziçi University. Istanbul.

"Inflammation and apoptosis

Inflammation is a local response mediated by several pro-inflammatory cytokines such as IL-1β, TNFα and IL-6. Inflammasomes are recently defined complexes whose main function is the regulation of caspase 1 or 5 activity upon the detection of danger signals. Inflammasomes are usually made of a NLR family member proteins such as Cryopyrin or Ipaf, the adapter ASC and procaspases 1 or 5. Certain pathogenic bacteria, including Salmonella and Shigella lead to excessive formation of inflammasomes and/or pyroptosomes (ASC and pro-caspase 1 complexes) and cause the death of the infected cell in a caspase 1 dependent manner.