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9th World Congress on

Immunology and Cancer

December 09-10, 2019 | Barcelona, Spain

Scientific Tracks & Abstracts

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Intelligent design, synthesis and validation of drug delivery systems targeted against breast cancer stem cells

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Tumor recurrence, metastatic spread and progressive gain of chemo-resistance of advanced cancers are sustained by the presence of Cancer Stem Cells (CSCs) within the tumor. Targeted therapies with the aim to eradicate these cells are thus highly regarded. However, often the use of new anti-cancer therapies is hampered by pharmacokinetic demands. Drug delivery through nanoparticles has great potential to increase efficacy and reduce toxicity and adverse effects. However, its production has to be based on intelligent design. Likewise, we developed polymeric nanoparticles loaded with Zileuton™, a potent inhibitor of Cancer Stem Cells (CSCs), which was chosen based on high throughput screening. Its great potential for CSCs treatment was subsequently demonstrated in *in vitro* and in *in vivo* CSC fluorescent models. Encapsulated Zileuton™ reduce amount of CSCs within the tumor and effectively block the Circulating Tumor Cells (CTCs) in the blood stream and metastatic spread.

Biography

Petra Gener is currently a research scientist in Hospital Universitari Vall d'HebronVall d'Hebron Institut de Recerca, Spain. Her research interest includes drug delivery and targeting against cancer.

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Lyme neuroborreliosis in children: Etiology and comparison of clinical findings of lyme neuroborreliosis caused by *B. garinii and B. afzelii*

Mojca Rožič
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Statement of the problem: Information on the etiology of Lyme Neuroborreliosis (LNB) in children in Europe and the influence of *B. burgdorferi* sensu lato species isolated from Cerebrospinal Fluid (CSF) on clinical presentation of LNB in children are limited.

Methodology: The study was monocentric. During its 17-year period, children younger than 15 years with presentation suggestive of LNB or confirmed Lyme borreliosis that had B. burgdorferi sensu lato isolated from CSF and had species of B. burgdorferi sensu lato identified by pulsed-field gel electrophoresis were included. Demographic and medical data were compared for children infected with *B. garinii* to those infected with *B. afzelii*.

Findings: 153 children had Borrelia burgdorferi sensu lato isolated from CSF. In 71/113 (62.8%) *B. garinii* and in 42/113 (37.2%) *B. afzelii* were identified. Patients infected with *B. garinii* did not report symptoms suggestive of CNS involvement or any other symptoms more often than patients infected with *B. afzelii*. Compared with children infected with *B. afzelii*, children infected with *B. garinii* had erythema migrans less often (18.3% vs. 45.2%), but had positive meningeal signs (69.0% vs. 38.1%), CSF lymphocytic predominance (97.1% vs. 75.0%), and elevated albumin CSF/serum quotient (80.6% vs. 50.0%) more often.

Conclusion & Significance: In Slovenia, LNB in children is more often caused by *B. garinii*, followed by *B. afzelii*. The clinical picture of LNB in children caused by *B. garinii* is not more often suggestive of CNS involvement, but CNS inflammation is more pronounced in children infected with *B. garinii*, compared with children infected with *B. afzelii*.

Biography

Mojca Rožič, M.D., is Assistant of Infectious Diseases at Department of Infectious Diseases and Epidemiology, Faculty of Medicine, University of Ljubljana and Consultant of Pediatrics at Department of Infectious Diseases, University Medical Centre Ljubljana, Slovenia. She has great interest in pediatric infectious diseases and clinical research. Since the beginning of her clinical work she has been involved in research of Lyme borreliosis in children. Currently she is PhD candidate working on her dissertation on Lyme neuroborreliosis in children.

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Eplet: A unique comrade with the finest expression in transplantation immunology

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Over the past two decades, organ transplantation procedures have become a potential milestone in the field of modern medicine. Even though physiological barriers and technical limitations exist in the process of organ transplantation, the therapeutic breakthroughs happened during the recent years has made this process a historic achievement. Human Leucocyte Antigen (HLA) has been known for its complexity as well as its identity in becoming a protein fingerprint. The lack of a healthy matching donor is one of the major problems faced during renal transplantation. Till this time, the question of what causes graft rejection still possesses a multifaceted answer which leaves the clinicians confused. In general, allo-graft transplantation causes strong immune reaction between a donor and the recipient as both the individuals possess sequentially different HLA. Identification of a single molecular target between such protein complexes like HLA and T Cell Receptor (TCR) could be a breakthrough in transplantation immunology. Use of high-throughput molecular simulation techniques or a highly established protein docking binary systems might be of great use for clinicians as this can lead to reduction in the use of administration of immunosuppressants. The traditional procedures incorporates direct complement depended cell cytotoxicity crossmatching (CDC-cxm) and HLA Typing which still possess its significance in transplantation medicine. Our aim relies on another perspective which targets Eplets. Eplets are those amino acid triplet confirmations which are spatially adjacent but linearly discontinuous. Epitope and Eplet matching has been a great part globally. The analysis of eplet matching after pinpointing the HLA ID of both donor and recipient are performed molecularly as well as computationally. Therefore targeting the identification and matching of each eplets between unrelated individuals may open new avenues in modern medicinal research. Analysis and calculation of antibody–verified eplets can be used to predict the outcome of less matched allo-graft transplants. The method of protein-protein docking can be also implemented to identify the hotspots in HLA which might cause such strong immune reactions.

Biography

Nidheesh Roy T. A, has earned appreciable skills in working with human cell lines, membrane protein isolation, CDC-CXM, HLA Typing, HLA Matchmaker and Protein docking. He has acquired good knowledge in computational biology; have used various protein docking softwares for studies related to the ongoing research work. Has a year of teaching experience for post graduate students, which include topics related to both biotechnology as well as general knowledge. Have earned laboratory skills from working in two research labs, microbiology and immunotechnology laboratory, as well as in a sophisticated transplantation immunology and molecular diagnostic facility. Have published two papers as a result of the contributions provided to the previous laboratory. Have a great passion for acquiring knowledge and new skills, effective time-management skills, flawless with computers, expert in Photoshop and Aftereffects, confident level of skills in using OnShape-CAD and high enthusiasm in photography.

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Personalized organ survival strategies based on cellular and molecular information about donor and recipient compatibility in transplantation

Elyas K K
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Human Leucocyte Antigen (HLA) or human Major Histocompatibility Complex (MHC) molecules are the most polymorphic gene clusters that are involved in immune recognition. Though polymorphic, these genes are inherited as a cluster without much recombination. With the advancement of molecular techniques like high resolution typing of HLA alleles using sequence- specific primer polymerase chain reaction, Flow cytometry, Luminex technology, next generation sequencing, etc., the allelic differences in a cluster of genes can be identified. This helps in getting the haplotype of an individual which in turn help in assessing the longevity of Solid Organ Transplants (SOT). Historically, Antibody-Mediated Reaction (AMR) and Cell- Mediated Reaction (CMR) implicated two discrete ways of immune responses in the individuals including transplant recipients. Conventionally, Complement depended cell cytotoxicity cross-matching, Elispot, Mixed Lymphocyte Culture, etc., are performed for CMR and AMR evaluation. The final rejection of the SOTs is a result of cellular damage. Control of these rejection responses is done by administration of pre- and post- transplantation immunosuppressive drugs that can target AMR as well as CMR. Categorizing the recipients' AMR and CMR is important in this context for assuring the survival of a graft. HLA 'Epitope Matching' is another concern in transplantation immunology which is generally addressed by tissue typing. Allelic difference, binding affinity and level of HLA expression vary from individual to individual which determines the rejection potential. The recent development in identifying the allelic epitope match has gained its momentum through the concept of 'Eplet Matching'. This relies on the presence of triplets of amino acid sequences, Eplets, and its count across a donor and a recipient. Immuno- informatics tools enable peptide interaction study, binding pocket identification, algorithms for eplet count, haplotype of an individual etc. Characterization of individual differences in each rejection episode using biochemical, molecular and cellular markers like creatinine, exosomes, Tregs, etc., is of the prime important observations in assessing the transplant rejection. Therefore, cellular and molecular interactions gathered by the above methods should be categorized for the recipients' thus preventing graft rejection. This information should be conveyed to the clinicians to take appropriate decisions in an organized manner.

Biography

K. K Elyas has earned his Doctorate in Immunology from Trissur Medical College, University of Calicut, Kerala, India, and has 20 years of teaching and research experience. He has 8 ongoing Ph.D research scholars and 7 Ph.D. degrees has been awarded under his supervision. He has almost 50 publications in well reputed journals and multiple book chapters and also a good number of GenBank accessions. He is a lifetime member of Society for Biotechnologists of India (SBTI), Association of Microbiologists of India, (AMI), Society of Clinical Chemists, Kerala and Society for Neurochemistry, India. He has completed 5 major projects during his research career. He has a well-established Transplantation Immunology and Molecular Diagnostic Laboratory at MIMS Hospital, Calicut, India which is a collaborative research center, working with Dr. Feroz Aziz, Consultant Nephrologist.

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Molecular dynamics simulations reveal a common conformation in the β chain constant region in T cell receptor activation

Josephine Alba
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The adaptive immune response is one of the most important systems of defense against pathogens. In this contest, the ability of the CD8+ Cytotoxic T Lymphocytes (CTLs) to recognize a wide number of foreign antigens represents a strong defense against diseases. The T cells response is regulated by T Cell Receptor (TCR) activation, which may occur following the epitope recognition (p), mediated by the Major Histocompatibility Complex (MHC). Experimental studies have suggested that conformational changes involving the constant region of the TCR α chain and of the CD3 complex are responsible for the TCR transduction signal across the plasma membrane, i.e. triggering. These conformational changes allow the phosphorylation of the CD3 complex ζ chain and the propagation of the signal downstream. By means of Molecular Dynamic simulations (MDs) we analyzed the conformational behavior of two TCRs (1G4 and ILAα1β1) interacting with the same MHC of class I (HLA-A2*01), in a lipid environment. When compared to experimental results, our data suggests a correlation between the conformations explored by the β-chain constant region and T cell activity. In particular, independently by the TCR type involved in the interaction, the TCR activation seems to be linked to a specific conformation affecting the β-chain constant region. Moreover, combining experimental and theoretical studies, we recently noted that the bound peptide can affect the conformation of the MHC of class I binding groove, suggesting a different presentation of the antigens possibly related to different CTLs responses. From Molecular Dynamics simulations of the whole pMHC/TCR complex we found that the interaction pMHC/TCR constraints the MHC binding groove in a more rigid conformation, contrary to our recent prediction where the MHC of class I (HLA -B27*) has been simulated alone.

Biography

Josephine Alba is a 2nd year-PhD student in Chemical Sciences at the University of Rome “Sapienza”, under the supervision of Prof. Marco D’Abramo. Her PhD project, titled “The effect of the conformational behavior of TCR related proteins on their function: a computational approach”, is focused on the structural-dynamical characterizations and the study of thermodynamic properties of the T-cell receptor related proteins (such as pMHC and Src family Kinase proteins) by means of theoretical-computational approaches. She was recently granted by EMBO short term fellowship to spent three months in the group of Prof. Miquel Pons, in Barcelona, for a project related to the structural characterization of the c-Src Kinase. The research group has active international collaborations with top-groups in the fields of molecular immunology (Prof. Oreste Acuto - University of Oxford and Prof. Wolfgang Schamel-University of Freiburg) and molecular biology (Dr. Maria Teresa Fiorillo - University of Rome “Sapienza”).

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