conferenceseries.com

International Conference and Exhibition on

Pediatric Oncology and Clinical Pediatrics

August 11-13, 2016 Toronto, Canada

Familiar functionality with adolescent children with lymphoma no Hodgkin of the Hermanos Cruz Policlinic in Pinar del Río

Yanet Corvea Trujillo Havana University, Cuba

In the vital cycle of the family, one of the most stressed events, constituted the diagnoses of an oncology disease of a child, since it produces a significant socio-emotional impact in the entire family. This exploratory-descriptive investigation uses the qualitative method of multiple cases study and it has general objective to evaluate the function of the family with adolescent children with lymphoma no Hodgkin of the Hermanos Cruz policlinic in Pinar del Río. To fulfill the objective some techniques were used: Semi-structured interview, familiar of satisfaction scale, life's contour and familiar working test. The participating observation was present during the whole process of the investigation. Among the principal results were found that the structure of the studied families was characterized by the presence of parental roles and psycho-emotional dysfunctional, hierarchy and rigid limits, the presence of emotional unique leadership, over protectors and permissive. The familiar dynamic presented a dysfunctional quality characterized by the presence of harmful familiar relationship, like mixed, attachment relationship; the presence of an emotional system with a predominance of negative emotions like; fear, anxiety and uncertainty, the presence of unidirectional communicative styles, besides a low adaptability forward the presence of a child with an oncology disease in the familiar system. The presence of dysfunctional elements, in the subjacent structure of these families favored the dysfunction of its dynamic and in its functionality in general.

tenay@princesa.pri.sld.cu

Future paradigms for precision oncology

Giannoula Lakka Klement, Ali Hashemi, Christos Klement, Dalibor Valik, Paolo Carmassi, Edward Rietman, Ondrej Slaby, Tina Roffidal, Pavel Mazanek, Peter Mudry, Gabor Kovacs, Csongor Kiss, Koen Norga, Dobrin Kostadinov, Nicolas André, Irene Slavc, Henk van Den Berg, Alexandra Kolenova and Jaroslav Sterba

Floating Hospital for Children, USA

Research has exposed cancer to be a very heterogeneous disease with a high degree of intertumoral and intra-tumoral variability. Each individual harbors a unique tumor profile, and this cancer molecular signature makes the use of histology-based treatments problematic. These diagnostic categories, while necessary for care, thwart the use of molecular information for treatment as many molecular characteristics cross tissue type. This difficulty is compounded by the struggle to keep abreast the scientific advances made in all fields of science and by the enormous challenge to organize, cross-reference and apply molecular data for patient benefit. In order to supplement the site-specific, histology-driven diagnosis with genomic, proteomic and metabolomics information, a paradigm shift in diagnosis and treatment of patients is required. Most physicians are open and keen to use the emerging data for therapy. But even those physicians versed in molecular therapeutics are overwhelmed with the amount of available data, and the lack of tools to integrate it. It is not surprising that even though The Human Genome Project was completed thirteen years ago, our patients have not benefited from the information. Physicians cannot, and should not be asked to process the gigabytes of genomic and proteomic information on their own in order to provide patients with safe therapies. The following consensus summary identifies the needed for practice changes, proposes potential solutions to the present crisis of informational overload, suggests ways of providing physicians with the tools necessary for interpreting patient specific molecular profiles and facilitates the implementation of quantitative precision medicine.

glakkaklement@tuftsmedicalcenter.org