

International Conference on

Antimicrobial Agents and Chemotherapy

August 04-06, 2015 Valencia, Spain

Expression of the Human Papilloma Virus (HPV): Comparative assessment in peripheral blood and retinoblastomas

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The Human Papilloma Virus (HPV) has been extensively studied due to its carcinogenic potential, related to the integration of viral DNA into the host genome. About 120 different types of HPV have already been described based on the heterogeneity of genome. Among the high-risk types, also called oncogenic, the most common is HPV-16, accounting for about 60-70% cases of cervical cancer associated with viruses. In addition to carcinoma of the cervix, HPV has been linked to several cancers, including retinoblastoma. This work aims to verify the activity of HPV by different approaches, as the clastogenic action and viral protein expression analysis on samples of children from the city of Recife, Pernambuco, Brazil, evaluating this activity by Immuno-histochemistry techniques and in situ hybridization. The biological material for analysis was peripheral blood and retinoblastoma tumor samples. Ten children with retinoblastoma were evaluated. Viral detection was performed by PCR with specific primers for the HPV types 16 and 18. HPV was in eight children with retinoblastoma, being HPV-16 the most frequent. By Immunohistochemistry was possible to evidence the presence of viral proteins E1^E4 (antibody anti-HPV-16), L1 (anti-HPVs antibody 1, 6, 11, 16, 18 and 31) and E6 (antibody anti-HPV-16 and HPV-18) in waxed tissue in various segments of the eye, confirming the viral activity in the sample. The data are discussing the presence and expression of oncogenic HPV in retinoblastoma and the evidences of damage in the DNA of the host as a consequence of the presence and viral activity.

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Emerging concepts in breast cancer neoadjuvant chemotherapy

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Necessity of the aggressive forms of breast cancer (BC), in order to reduce tumor burden and allow breast-preserving surgical treatment. After years of uniform administering the taxane/anthacycline-based regimens to all the BC patients indicated for a NACT, two major changes in BC NACT have taken place during last 10 years and have been rapidly developing: a) use of molecular methods in estimation of BC aggressiveness and b) use of agents which specifically target oncogenic driver-molecules. Those new approaches were made possible by important advances in cancer biopathology. Molecular classification of BC into luminal A, luminal B, HER2+ and triple-negative (TN) subgroup, associated to clinical parameters, provides a basis for the choice of NACT. That way luminal and TN BC are treated by "nonspecific" cytotoxics while the clinical course of HER2+BC has been markedly improved by agents specifically targeting HER2. In order to avoid overtreatment of luminal BC, there is an increasing use of multigenic tests to predict tumor recurrence risk. On the other side, the resistance to anti-HER2 agents, observed in approximately half of the HER2+BC, is being reduced by new targeted approaches: inhibition of several HER-family receptors or of the receptors and their downstream signal transducers. In TNBC, targeting EGFR and/or DNA damage response pathway are emerging neoadjuvant approaches. Further development of BC NACT depends on advances in prediction of response to a given treatment. In this light we will present some recent results our group has obtained in the biomarker research.

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