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A human cytomegalovirus (HCMV) model to study the functions of HCMV encoded proteins in cancer progression

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Cancer is the leading cause of death worldwide. The Human Cytomegalovirus (HCMV) plays an important role in several malignancies, including breast cancer, colorectal cancer and brain tumor. Breast cancer is considered as the leading cause of death among women. Previous reports have demonstrated that the HCMV genome contains oncogenic genes and has potential to cause the different types of cancers. The HCMV is a herpes virus and its primary infection leads to the lifelong latent or persistent infection. Although, the primary HCMV infection is asymptomatic, but it can cause the severe health issues in immunocompromised population, especially in organ transplant patients, AIDS or cancer patients. Furthermore, the congenital HCMV infection causes the fetus malformation and is the leading cause of birth defects. Studies have found HCMV DNA in the numerous forms of tumors and concurrent HCMV specific antibodies in cancer patients. Taken together, these findings suggested a connection between HCMV and cancer progression. In the proposed research, we aimed to identify and study the essential oncogenic factors encoded by HCMV, which are responsible for the breast and brain cancer development. In order to understand the HCMV pathology and its role in cancers, we will use a robust, tightly controlled, reversible and highly sensitive inducible system. We believe that this system will serve as a springboard to identify and understand the role of unknown onco-protein in various cancers.

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