EXAMINATION SECTION
ALL INDIA INSTITUTE OF MEDICAL SCIENCES
ANSARI NAGAR, NEW DELHI – 110 608

Addendum No.14/2017

No.F.AIIMS/Exam.Sec./(Ph.D.-JULY-2017) Dated: 05.08.2017

Change of Seat position in the Department of Lab Oncology for Ph.D. Courses, July 2017 session

With reference to the letter received Depatment of Lab Oncology, Dr.BRA IRCH duly forwarded by Registrar, Academic Section, AIIMS, New Delhi the following changes have been carried-out in respect of number of seats and Project in Ph.D. at AIIMS for July, 2017 session. The details are as under:

Code No.	Seat/Eligibility of Department (Earlier)			Seat/Eligibility of Department (Revised)	
	No. of Seats	Project Code		No. of Seats	Project Code
133	02	133 (a)	**133**	**Project 1 = 01** **Project 2 = 01** **----** **02** **-----**	**133 (a)** **133 (b)**
133	**Fellowship required**	133 (a)	**133**	**Fellowship not required (Both Projects are funded)**	

Project Code	Summary of Project (Earlier)	Summary of Project (Revised)
133 (a)	*A prospective study to evaluate WT1 gene expression as predictive molecular marker of disease progression in de novo cases of Acute myeloid Leukemia"* Acute myeloid leukemia (AML) is group of hematological malignancy. Treatment protocols for AML cases are available. However, for the successful implementation of treatment protocols close laboratory follow up for the disease progression is required. Minimal residual disease (MRD) is an important aspect to evaluate the quality of response and predicting relapse rate in AML patients. Several studies have shown the usefulness of various modality such as multiparametric flow cytometry, polymerase chain reaction and fluorescence in situ hybridization for detection of MRD in AML patients. PCR-based quantification of MRD has a high sensitivity but its applicability is restricted to subgroups of AML with leukemia specific molecular targets. Wilm's tumor gene 1 (WT1) expression can be found in 70 % to 90 % of patients with acute leukemia (AL). However, there is paucity of data regarding the normal expression level of WT1 in Indian population and it effect on treatment response. In this study, we will be evaluating the expression of WT1 with help reverse quantitative polymerase chain reaction (RQPCR) in all de novo cases of AML. WT1 expression values will be compared with progression of disease to validate *WT1* as possible molecular marker in AML.	**Project Code 133 (a):** *"A prospective study to evaluate WT1 gene expression as predictive molecular marker of disease progression in de novo cases of Acute myeloid Leukemia"* Acute myeloid leukemia (AML) is group of hematological malignancy. Treatment protocols for AML cases are available. However, for the successful implementation of treatment protocols close laboratory follow up for the disease progression is required. Minimal residual disease (MRD) is an important aspect to evaluate the quality of response and predicting relapse rate in AML patients. Several studies have shown the usefulness of various modality such as multiparametric flow cytometry, polymerase chain reaction and fluorescence in situ hybridization for detection of MRD in AML patients. PCR-based quantification of MRD has a high sensitivity but its applicability is restricted to subgroups of AML with leukemia specific molecular targets. Wilm's tumor gene 1 (WT1) expression can be found in 70 % to 90 % of patients with acute leukemia (AL). However, there is paucity of data regarding the normal expression level of WT1 in Indian population and it effect on treatment response. In this study, we will be evaluating the expression of WT1 with help reverse quantitative polymerase chain reaction (RQPCR) in all de novo cases of AML. WT1 expression values will be compared with progression of disease to validate *WT1* as possible molecular marker in AML. **Project Code 133 (b):** *"Comparative study of Genetic, Clinical and Epidemiological risk factors of breast cancer in Indian*

		population" Western populations across the world shows mutations in BRCA1/2 genes in breast and ovarian cancer. There is marker paucity of data for this gene in Indian population; however, few of the studies indicate the prevalence between 2.5-28%. This indicates that apart from BRCA1/2 mutation, other genetic risk factors are contributing to breast cancer in Indian subcontinent. Hence, it is important to look up for more reliable markers for diagnosing and prognosticating breast and ovarian cancer. The present study will attempt to discover novel mutations in the through exome sequencing. Additionally, transcriptome analysis will also be studied to identify novel genes expression and / aberrant pathways in with objective to identify breast cancer pathobiology and biomarker discovery.

All other contents available in the Prospectus will remain unchanged.

Important: For Prospectus, detailed information etc. please visit the website www.aiimsexams.org. All applicants are required to visit the website regularly since all subsequent Corrigendum/'Updates will only be uploaded on the website.

Sd/-
Asstt. Controller (Exams)