

1. Genomic variants of Human Papillomavirus in HIV-positive and HIV-negative women from Pune, India.	
Principal Investigator	Dr. Arati Mane
Co-Principal Investigator(s)	Nil
Other Investigator(s)	Dr. Arun Risbud
Category / Nature	STI and OI category
Collaboration / Participating Centers	Nil
Funding Agency(ies) / Sponsors	NARI-Intramural
Budget	Rs. 7,00,000/-
Study Period	Jan 2013 - Dec 2014
Objectives	<ul style="list-style-type: none"> • To determine the genomic variants of HPV types 16 and 18 in E6, E7 oncogenes and L1 capsid protein regions in HIV positive and HIV negative women. • To study the phylogeny of these variants.
Brief description (one paragraph)	Infection with carcinogenic HPV types is established as the primary cause of cervical intraepithelial neoplastic lesions and invasive cervical cancer. HPV type is defined by nucleotide sequence variation of more than 10% in the L1 open reading frames compared with other known HPV types. HPV intratype variants are those that vary up to 2% in L1 coding region. Study of intratype variants will help in the identification of more persistent/ oncogenic variants which could constitute as markers of cervical cancer progression and be important for improved HPV diagnostic tests.
Current status	Analysis of genomic variants from HIV-positive women and recruitment of HIV-negative group is ongoing.
Publications	Nil
Presentations	Nil

2.Genetic basis of Fluconazole resistance in clinical <i>Candida albicans</i> isolates	
Principal Investigator	Dr. Arati Mane
Co-Principal Investigator(s)	Nil
Other Investigator(s)	Dr. Arun Risbud
Category / Nature	STI and OI category
Collaboration / Participating Centers	Nil
Funding Agency(ies) / Sponsors	NARI-Intramural
Budget	Rs. 7,75,000/-
Study Period	Jan 2013 – Dec 2014
Objectives	<ul style="list-style-type: none"> • To study the mutations drug targets (Erg11 and Erg 3 gene) in <i>Candida albicans</i> isolates. • To study the efflux pump mechanisms in <i>Candida albicans</i> isolates.
Brief description (one paragraph)	<p>Candidiasis is one of the commonest opportunistic fungal infections. The azoles, particularly Fluconazole, remain among the most common antifungal drugs, but their intensive clinical use for both therapy and prophylaxis has favored the emergence of resistant strains. Increasing resistance to Fluconazole over the past decade from 0 % to upto 20% has been reported by various researchers from India. The present study is undertaken to analyze the genetic basis of Fluconazole resistance in clinical <i>Candida albicans</i> isolates. Specific mutations in the drug targets, especially in resistant and intermediate resistant isolates, if identified can help in design of drug derivatives whose binding is not affected by the resistance mutations.</p>
Current status	We completed the collection of the proposed isolates and analysis of mutations in the Erg11 gene. Determination of Erg 3 gene mutations and efflux pump mechanisms is ongoing.
Publications	Nil
Presentations	Nil

Intra-mural projects of Ph D Students:

3. Role of HSV-2 in HIV-1/ HSV-2 Co-infection.	
Principal Investigator	Guide Dr. Smita Kulkarni, Scientist E, National AIDS Research Institute, Pune Ph.D. Student : Mr. Dipen Vijay Desai
Co-Principal Investigator(s)	Nil
Other Investigator(s)	Nil
Category / Nature	Opportunistic Infection and STI's
Collaboration / Participating Centers	Nil
Funding	NARI Intramural
Budget	Rs. 15, 00,000/-
Study period	Three Years (2012 to 2015)
Description	Herpes Simplex Virus Type-2 is one of the sexually transmitted pathogens that cause genital ulcerative diseases. It has been identified as an important co-infecting pathogen that increases the risk of HIV-1 acquisition. Literature also shows that HIV-1 viral loads are higher amongst HIV-1 and HSV-2 co-infected individuals. Therefore, there is a need to investigate the interplay between the two viruses to understand the influence of HSV-2 on HIV-1 replication.
Objectives	1) Development of an <i>in vitro</i> T-cell line model to study HIV-1/HSV-2 co-infection. 2) Determining the influence of HSV-2 on host gene expression. 3) Analyzing the effects of perturbations of HSV-2 mediated host gene expression on HIV-1 replication.
Current status	Nil
Publications	Nil
Presentations	Nil

4. Impact of HTLV-II on HIV-1 replication	
Principal Investigator	Guide: Dr. Smita Kulkarni, Scientist E, National AIDS Research Institute Ph.D. Student: Mr. Rajkumar Bibhishan Londhe
Co-Principal Investigator(s)	Co-Guide: Dr. Vidhya Arankalle, Ex-Scientist G, National Institute of Virology, Pune.
Other Investigator(s)	Nil
Category / Nature	Opportunistic Infection and STI's
Collaboration / Participating Centers	Nil
Funding:	NARI Intramural
Budget:	Rs. 16, 28,000/-
Study period:	Three Years (2013 to 2016)
Description:	Viral co infections associated with HIV-1 influence its replication and alter disease progression. Although both, HIV and HTLV belong to the same family ' <i>Retroviridae</i> ', their pathogenesis and immune escape mechanisms differ. Previous studies report that HTLV-I accelerates HIV-1 disease progression whereas HTLV-II deaccelerates HIV-1 disease progression in HTLV/HIV-1 co infected individuals. Therefore, it is important to understand the molecular interactions responsible for causing the differential effects of HTLV-II on HIV-1 replication.
Objectives:	1) Assessing the impact of HTLV-II on HIV-1 replication using an <i>in vitro</i> model. 2) Determining the role of APH-2 (Antisense Protein HTLV-II) on HIV-1 transcription.
Current status	Nil
Publications	Nil
Presentations	Nil