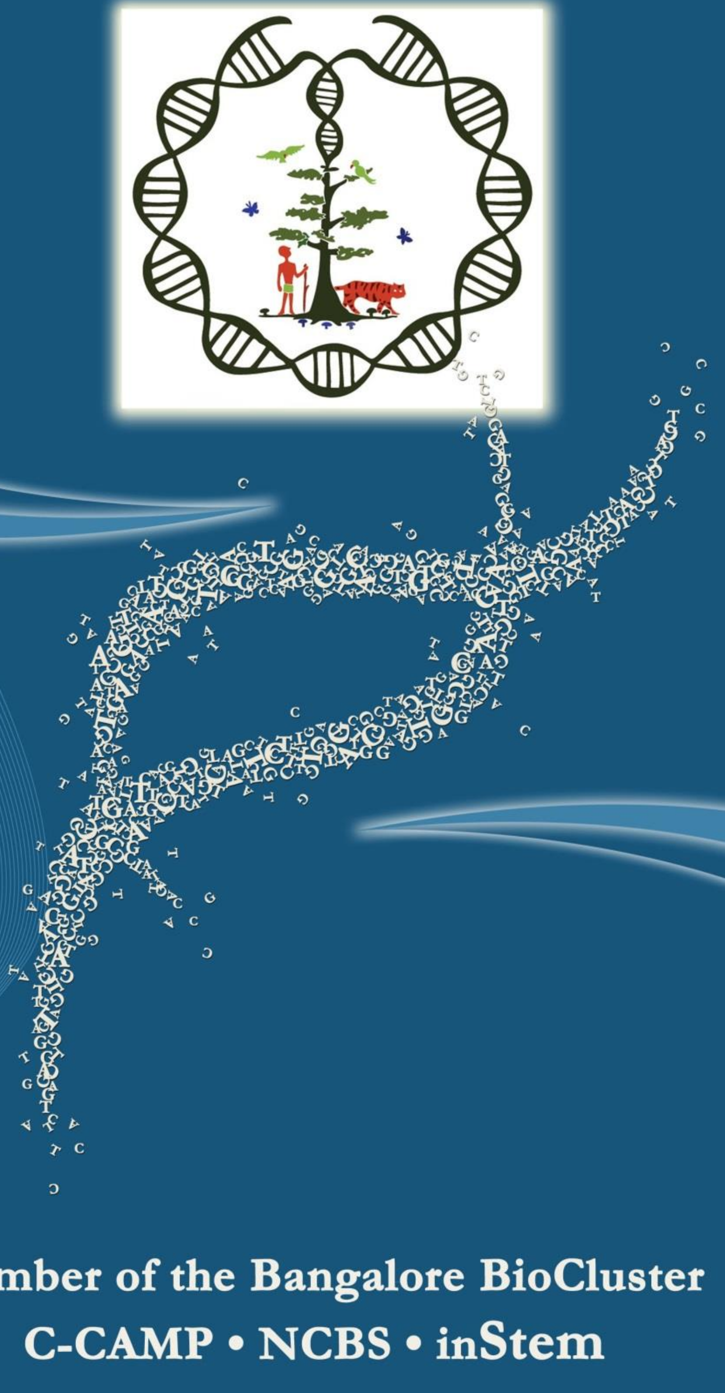
Centre for Cellular and Molecular Platforms

A Dept. of Biotechnology (DBT, Govt. of India) Initiative

Next Generation Genomics Facility (NGGF)

"Catalyzing Life Science Research in India"



Member of the Bangalore BioCluster

C-CAMP • NCBS • inStem

C-CAMP

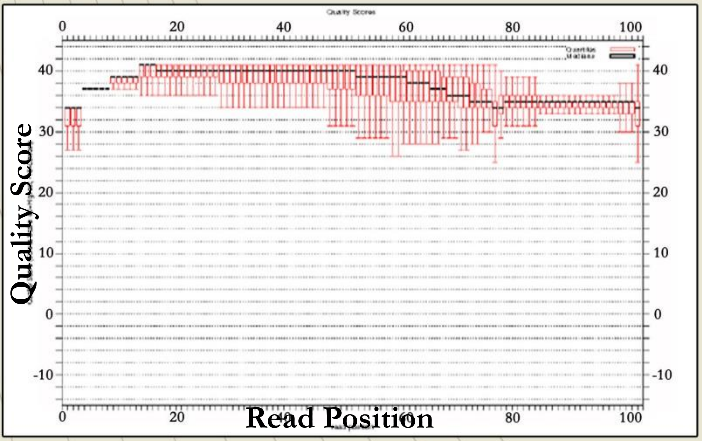
Centre for Cellular and Molecular Platforms

Next Generation Sequencing

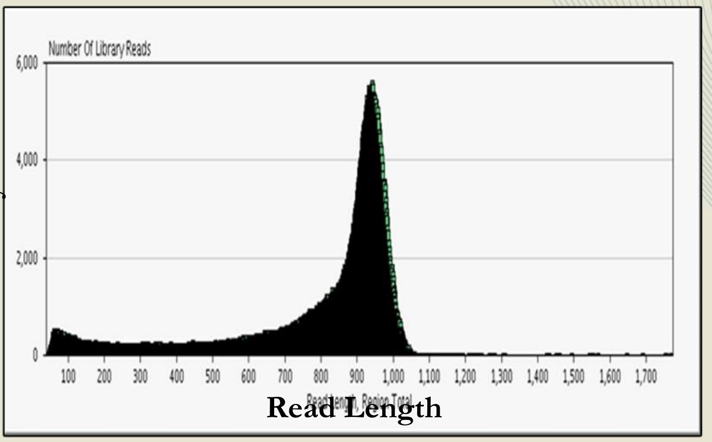
NGS technology has revolutionized Life Science research by dramatically reducing cost, time, and manpower needed for sequencing. Current NGS platforms enable researchers to dissect any type of genome/transcriptome/epigenome/metagenome.

Next-Generation Sequencing Platforms

Illumina HiSeq 1000
(Reads - 2x100 bases;
Data – upto 300Gb/run)



Roche 454
GS FLX Titanium/GS FLX+
(Reads - upto 1kb; Data - 1 Gb/run)



Features	HiSeq (Illumina)	GS FLX + (Roche/454)
Sequencing Method	Sequencing by Synthesis	Pyrosequencing
Read lengths (bases)	100 x 2	Upto 1Kb
Data per run	Upto 300 Gb	Upto 1Gb
Run time	10 days	24 hours
Multiplexing (barcoding)	192 samples – 24 adapters & 8 lanes	192 samples – 12 adapters & 16 regions
Applications (examples)	Sequencing of *de novo* /reference genomes, transcriptomes (mRNA/small RNA), DNA/Chromatin modifications, SNP Markers etc.	*De novo* Sequencing of genomes, transcriptomes and metagenomes, targeted sequencing, etc.

NGGF is a unique model that supports the growing needs of large-scale genomic projects in our country. NGGF has been accessed by over 45 organizations (institutes/ industries) both within and outside India. More than 75 species have been successfully sequenced, including more than 430 genomes and 730 transcriptomes, the data of which has been published in several peer-reviewed journals.
(http://www.ccamp.res.in/NGS-Genomics)

Workflow at NGGF

Source/ Library Type → Sequencing → Data Analysis

Library Type

DNA, RNA, RAD Seq, Small RNA, Mate-pair, Exomes, ChIP DNA, HLA typing, Amplicon Sequencing.

Source

Animals, Plants, Bacteria, Fungi, Insects, Viruses, Plasmids, Synthetic DNA and Metagenomes

NGS Platform

Illumina HiSeq 1000
Roche 454 GS FLX +

Sequencing Applications

DNA: Whole genome, Exome, ChIP-Seq, Mate-pair, HLA typing, Amplicons, Metagenomes
RNA: total RNA, RiboMinus RNA, small RNA

NGS Application

De novo / Reference Assembly, Reference Mapping, Genome and Transcriptome Assembly and Annotation, SNP analysis, Comparative Genome Analysis, Small RNA Analysis, ChIP-Seq Analysis, Restriction Site Mapping (RADseq), etc.

Bioinformatics and Data Analysis

Within NGGF, we have established a strong Bioinformatics team to help efficiently design data analysis pipelines and carry out complex NGS data analyses. Below we have listed our services and infrastructure

Data Analysis Services

- Genome Assembly and Annotation
- Gene Prediction (*de novo* / Reference)
- Differential Expression Analysis
- Small RNA analysis
- SNP Analysis
- ChIP – Seq analysis and other Protein – DNA/RNA interactions
- Metagenomics / Metatranscriptomics
- Genotyping by sequencing – RAD seq

Expertise & Infrastructure

- Team of Qualified Analysts offering Personalized Services and Training
- Expertise to understand and solve problems using a systems biology approach
- High Performance Servers
- High Capacity Redundant Storage System with Optional Data Security

Publications

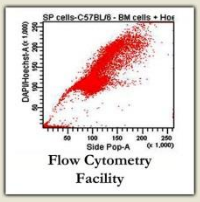
1. Singh et al. *Grimontia indica* AK16T, sp. nov., Isolated from a Seawater Sample Reports the Presence of Pathogenic Genes Similar to *Vibrio Genus*. *PLoS One* 2014, 9(1):e85590.
2. Sharma et al. Draft Genome Sequence of *Kocuria palustris* PEL. *Genome announcements* 2014, 2(1).
3. Khatri et al. Genome sequencing and annotation of *Amycolatopsis azurea* DSM 43854. *Genomics Data* 2014, 2:44-45.
4. Sasidharan et al. miRNAs in the planarian *Schmidtea mediterranea.* RNA. 2013 Aug 23.
5. Krishna et al. 2013. small RNA repertoire in *Hydra magnipapillata*. Nucleic Acids Res. 2013 Jan 7;41(1):599-616.
6. Prabhakara et al. 2013. Genome of *Staphylococcus aureus* ST772 from India. PLoS One. 2013; 8(3):e60013.
7. Bala et al. 2013. Genome of *Rhodococcus ruber* Strain BKS 20-38. Genome Announc. March/April 2013 vol. 1 no. 2 e00139-13.
8. Kaur et al. 2013. Genome of *Amycolatopsis decaplanina* Strain DSM 44594. Genome Announc. March/April 2013 vol. 1 no. 2 e00138-13.
9. Kumar et al. 2013. Genome of *Rhodococcus triatomae* Strain BKS 15-14. Genome Announc. March/April 2013 vol. 1 no. 2 e00129-13.
10. Kumar et al. 2013. Genome of *Streptomyces gancidicus* Strain BKS 13-15. Genome Announc. 2013 Apr 18;1(2):e0015013.
11. Singh et al. 2013. Genome of *Acinetobacter baumannii* Strain MSP4-16. Genome Announc. 2013 Apr 4;1(2):e0013713.
12. Srinivasan et al. 2013. Epistatic control of “expensive” genes in *Escherichia coli* K-12. Mol Biosyst. 2013 May 9.
13. Bala M. et al. 2013. Draft Genome of *Rhodococcus qingshengii* Strain BKS 20-40. Genome Announc. 2013 Mar 28;1(2):e0012813.
14. Prabhakara S. et al. 2012. Draft Genome of *Staphylococcus aureus* 118 (ST772), a major disease clone from India. J Bacteriol. 2012 Jul;194(14):3727-8.
15. Khedkar S. et al. 2012. Draft Genome of *Staphylococcus aureus* ST672, an emerging disease clone from India . J Bacteriol. 2012 Dec;194(24):6946-7.
16. Vikram S. et al. 2012. Draft Genome of Nitrophenol-Degrading Actinomycete *Rhodococcus imtechensis* RKJ300. J. Bacteriol. July 2012; 194(13): 3543.
17. Khatri I. et al. 2012. Draft Genome of *Rhodovulum sp.* Strain PH10 and *Alphaproteobacterium*. J. Bacteriol. November 2012; 194(22): 6363.
18. Kumar S. et al. 2012. Draft Genome of the marine bacterium *Marinilabilia salmonicolor* JCM 21150T. J. Bacteriol. 2012 Jul;194(14):3746.
19. Kumar S. et al. 2012. Draft Genome of f the Halotolerant Bacterium *Imtechella halotolerans* K1. J. Bacteriol. July 2012;194(14) 3731.

Many more ……

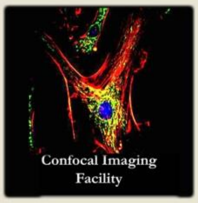
Users of NGGF

MKU
DRDE
Delhi University
IISc
JNCASR
TANUVAS
IIT Madras
ILS
UAS Bangalore
CMC Vellore
Dr. M.G.R Univ
CDFD
IBSD
IISER Bhopal
AMRF

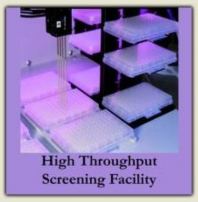
Our Other Technology Platforms



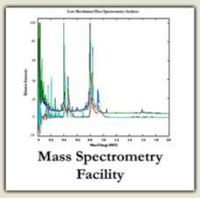
Flow Cytometry Facility



Confocal Imaging Facility



High Throughput Screening Facility



Mass Spectrometry Facility

Transgenic Fly Facility

Protein Technology Facility

Contact

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