signios bio
powered by MEDGENOME

Accelerating plant and animal research with cutting-edge genomic solutions

Enabling breakthroughs in agriculture and biodiversity through multi-omics technologies and expert bioinformatics.

Your partner in genomics-driven innovation

Signios Bio combines advanced multi-omics platforms and bioinformatics expertise to deliver high-quality genomic solutions for plant and animal sciences. Our end-to-end services empower researchers to address critical challenges in agriculture, biodiversity conservation, and evolutionary biology.

Key benefits

- **End-to-end support:** Comprehensive services from sample preparation to advanced data analysis.
- **State-of-the-art technologies:** Access to Illumina short-read, PacBio long-read, single-cell sequencing, and spatial transcriptomics platforms.
- **Expert Bioinformatics:** Specialized pipelines for:
  - **Genome assembly and annotation:** High-quality assemblies and functional insights into genes and pathways.
  - **Population genetics:** Analyze genetic diversity, detect inbreeding, and study evolutionary dynamics.
  - **Variant analysis:** Accurate detection of SNPs, CNVs, and structural variants.
  - **Transcriptomics and expression analysis:** Comprehensive gene expression profiling, including single-cell and spatial resolution.
- **Customized Solutions:** Tailored workflows for a wide range of plant and animal species.
- **Proven Impact:** A track record of delivering high-quality genomic data for impactful discoveries in agriculture and biodiversity research.
- **Global Expertise:** A team of skilled scientists and bioinformaticians with experience across diverse plant and animal systems.

Our solutions for plant and animal genomics

WGS for crop improvement, trait mapping, evolutionary genomics, and species characterization.

- **PacBio Long-Read Sequencing:** Resolving complex genomes, structural variants, and repeat-rich
- regions.

  Illumina Short-Read Sequencing: Accurate variant detection and high coverage at scale.

Genetic diversity studies, marker-assisted selection, and evolutionary analysis.

- SNP detection, CNV analysis, and GWAS for plants and animals.

Gene expression analysis, identification of stress-response pathways, and biomarker discovery.

- **Bulk RNA-Seq:** Quantify gene expression under different conditions.
- **Single-Cell Sequencing:** Unravel cellular heterogeneity and function at single-cell resolution.

Spatially resolved gene expression to study tissue-specific responses, developmental processes, and disease.

- Map gene expression in plant tissues (e.g., roots, leaves, seeds) to uncover stress responses and growth patterns.
- Analyze animal tissues for disease pathways, immune response, or organ development.

Technology. Expertise. Impact.

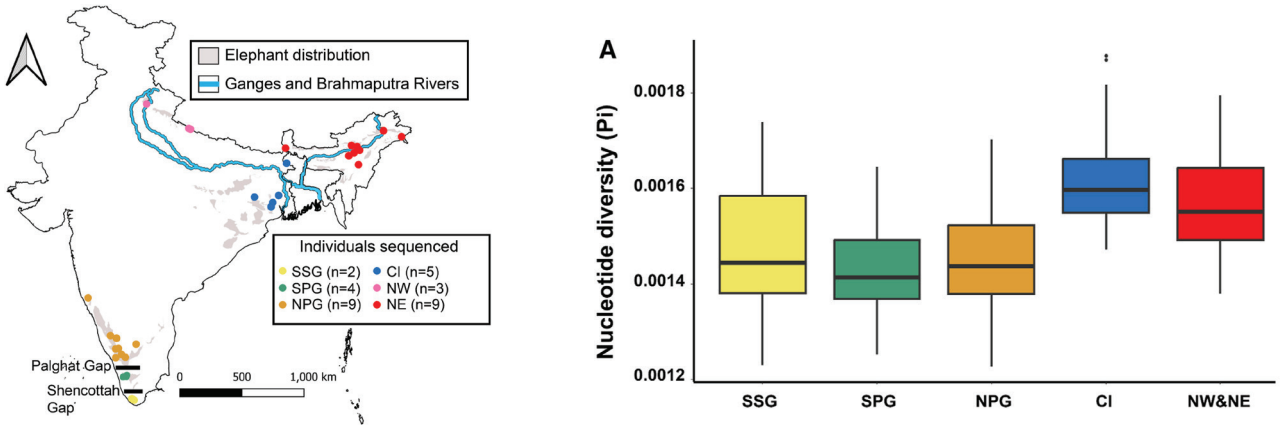
- **Leading Technologies:** Access to Illumina, PacBio, single-cell sequencing, and spatial transcriptomics platforms.
- **Expert Bioinformatics:** Robust pipelines for genome assembly, transcriptomics, variant analysis, and functional annotation.
- **Customized Research Support:** Solutions tailored for plants and animals, from crop genomics to wildlife conservation.
- **Proven Impact:** Successfully enabled genomics projects for agriculture, biodiversity, and evolutionary biology research.

Explore this table showcasing a small selection of plant and animal genomes we've successfully sequenced and assembled

Plants					
Species	Genome Size (Mb)	Assembly Size (Mb)	Contig N50 (Mb)	Scaffold N50 (Mb)	Busco score (%)
Curry Leaf	~315	331	29.1	38.2	99.3
Cardamom	~1060-1400	1245	0.133	49	94.2
Caucasian Wingnut	(Chinese wingnut ~550)	619	17.8	-	-
Avocado	920	902	18.8	-	-
Animals					
Bengal tiger (Mammal)	2400	2410	4.4	145.47	95.1
Indian cobra (Snake)	1800	1790	0.3	233.3	94
Russels Viper (Snake)	1800	1860	1.64	133.1	94
Centipede	1036	1040	0.13	76.72	96.7
Jellyfish C. Arborifera	~770-1250	817	44.15	-	84.7

Mapping conservation units through genomic analysis of asian elephants

In support of leading researchers, Signios Bio applied advanced genomic techniques to sequence and analyze the genomes of 34 Asian elephants across diverse regions of India[1]. The study utilized short-read whole genome sequencing for variant detection, long-read sequencing for genome assembly, and sophisticated bioinformatics pipelines to uncover population structure, genetic diversity, and inbreeding levels. High-resolution data analysis identified five distinct conservation units shaped by geographic barriers and serial colonization.



Sampling locations and potential geographic barriers to elephant dispersal and boxplots of pairwise nucleotide differences per site (pi) in the populations from Khan, Anubhab *et al.* (2024).

Reference

1. Khan, Anubhab *et al.* Divergence and serial colonization shape genetic variation and define conservation units in Asian elephants, *Current Biology*, Volume 34, Issue 20, 2024, https://doi.org/10.1016/j.cub.2024.08.062

Partner with Signios Bio for your next project in plant and animal sciences

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