Lecture 1. Postgenomic Technologies: Subject, Goals, Objectives, and Role in Modern Biology

Aim of the lecture

To introduce students to the concept of postgenomic technologies, explain their emergence following the development of genome sequencing, and demonstrate their role in studying the structure, function, regulation, and interactions of genes, proteins, metabolites, and other molecular components of biological systems.

DNA → RNA → Protein → Metabolites → Cellular processes → Phenotype

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Genomics → Transcriptomics → Proteomics → Metabolomics → Phenomics

Expected Learning Outcomes

1. Define postgenomic technologies and explain their significance in modern biology.
2. Describe the main objectives and research directions of postgenomic studies.
3. Distinguish between genomics, transcriptomics, proteomics, metabolomics, and phenomics.
4. Explain the relationships between genomic information, gene expression, molecular functions, and phenotype.
5. Identify major analytical and computational technologies used in postgenomic

1. The concept of the postgenomic era

The postgenomic era represents a new stage in biological research that emerged following major advances in whole-genome sequencing, particularly the completion of the Human Genome Project in 2003.

It marks the transition from determining genome sequences to understanding gene functions, molecular interactions, and the mechanisms underlying biological processes.

Key characteristics:

1. Transition from genome sequencing to functional genome analysis.
2. Development of high-throughput omics technologies.
3. Investigation of gene expression, protein functions, and metabolic pathways.
4. Integration of molecular data using bioinformatics and systems biology.
5. Understanding genotype–phenotype relationships.
6. Application of molecular knowledge in biotechnology, medicine, and agriculture.

Key concept: The postgenomic era focuses not only on what information is encoded in the genome, but also on how this information is expressed, regulated, and translated into biological functions and phenotypes.

From genome sequence to biological function and phenotype

Genomic Era

Genome sequencing and gene identification

Postgenomic Era

Gene functions, molecular networks, and biological systems

2. Subject and concept of “Postgenomic Technologies”

- Definition of postgenomic technologies.
- What is studied at the postgenomic level?
- Functional analysis of genes and genomes.
- From individual genes to biological systems.

3. Goals and objectives of postgenomic technologies

1. **Identification of gene functions.**
2. **Analysis of gene expression.**
3. **Characterization of proteins and their interactions.**
4. **Investigation of metabolites and metabolic pathways.**
5. **Study of regulatory networks.**
6. **Integration of molecular data to explain phenotype.**

4. Major areas of postgenomic research

- **Functional genomics**
- **Transcriptomics**
- **Proteomics**
- **Metabolomics**
- **Epigenomics**
- **Phenomics**
- **Interactomics**
- **Single-cell omics**

5. From “omics” to multi-omics

- A very important conceptual progression for the students would be:
- **Genome → Epigenome → Transcriptome → Proteome → Metabolome → Phenome**
- and then:
- **Genomics + Transcriptomics + Proteomics + Metabolomics + Phenomics → Multi-omics → Systems biology**

6. Main technological platforms

1. Next-generation sequencing (NGS)
2. RNA sequencing (RNA-seq)
3. Mass spectrometry
4. Chromatin and epigenetic profiling
5. Single-cell technologies
6. High-throughput phenotyping
7. Bioinformatics and computational biology
8. Artificial intelligence and machine learning

7. Applications of postgenomic technologies

1. **Human and personalized medicine**
2. **Molecular diagnostics**
3. **Drug discovery**
4. **Industrial biotechnology**
5. **Agricultural biotechnology**
6. **Plant stress biology**
7. **Crop improvement and molecular breeding**
8. **Gene editing and precision breeding**

1. From the genomic to the postgenomic era

What is a genome?

The genome is the complete set of genetic information of an organism, including protein-coding genes, non-coding sequences, regulatory regions, repetitive DNA, and other genomic elements.

The development of DNA sequencing technologies made it possible to determine complete genome sequences for thousands of organisms.

- Major milestones include:
- 1977 → development of Sanger DNA sequencing
- 1990 → launch of the Human Genome Project
- 2000–2001 → first plant genome (Arabidopsis thaliana) and first draft human genome
- 2005 onward → rapid development of next-generation sequencing
- 2010s → expansion of transcriptomics, proteomics, metabolomics and epigenomics
- 2020s → single-cell omics, spatial omics, multi-omics and AI-assisted biological analysis

1. From the genomic to the postgenomic era

Genome sequencing was not the endpoint

Genome sequencing answered an important question:

What genetic information is present?

But knowing a DNA sequence does not automatically tell us:

- when a gene is active;
- where it is expressed;
- how strongly it is expressed;
- what protein it produces;
- how the protein is modified;
- which molecules it interacts with;
- how metabolism changes;
- how environmental conditions affect gene activity;
- how all these processes produce a phenotype.

This led to the emergence of postgenomic biology.

2. What is the postgenomic era?

The postgenomic era is the stage of biological research in which genome sequence information is combined with large-scale functional analyses to understand how genomes operate within cells, tissues, organisms, and populations.

- A simple distinction is:
- Genomic era:
- What is the sequence?
- Postgenomic era:
- What does the sequence do, how is it regulated, and how does it contribute to phenotype?

Thus, modern biology has moved from primarily descriptive sequencing toward functional and systems-level understanding.

3. What are postgenomic technologies?

Postgenomic technologies comprise high-throughput experimental and computational approaches used to investigate the functional activity of genomes and their molecular products at different levels of biological organization.

They include:

- **Genomics → Epigenomics → Transcriptomics → Proteomics → Metabolomics → Phenomics** as well as:

1. *interactomics;*
2. *single-cell omics;*
3. *spatial omics;*
4. *functional genomics;*
5. *systems biology;*
6. *multi-omics;*
7. *computational biology and bioinformatics.*

3. What are postgenomic technologies?

Central concept. A scheme idea is:

- **Genome**
  ↓
  Epigenome
  ↓
  Transcriptome
  ↓
  Proteome
  ↓
  Metabolome
  ↓
  Cellular/physiological processes
  ↓
  Phenome

However, it is necessary to understand that biological information is not simply a one-directional chain.

Regulatory networks, feedback mechanisms, protein interactions, metabolites, and environmental signals influence multiple levels simultaneously.

4. Subject of postgenomic technologies

The subject of postgenomic technologies is the comprehensive study of genome function and its molecular manifestations using high-throughput approaches.

Postgenomic research investigates:

1. ***genome organization and variation;***
2. ***gene expression;***
3. ***transcriptional regulation;***
4. ***epigenetic modifications;***
5. ***proteins and protein modifications;***
6. ***protein–protein interactions;***
7. ***metabolites and metabolic pathways;***
8. ***regulatory networks;***
9. ***genotype–environment interactions;***
10. ***molecular mechanisms underlying phenotype.***

Therefore, the main transition is:

- **Single gene → thousands of genes → molecular networks → biological system**

Main goal of postgenomic technologies

The overall goal is: To understand how genomic information is converted into biological function and phenotype.

This involves establishing relationships between:

Genotype × Regulation × Environment → Molecular phenotype → Organismal phenotype. For example, in a plant exposed to drought:

Drought signal

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Changes in chromatin and gene regulation

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Changes in gene expression

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Changes in protein abundance/activity

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Changes in metabolites

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Physiological responses

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Drought-tolerant or drought-sensitive phenotype

- **This is a very good example for biotechnology because it shows why analyzing only DNA is insufficient.**

6. Major objectives of postgenomic research

Postgenomic technologies aim to:

1. **Identify gene functions.**
2. **Determine gene-expression patterns under different conditions.**
3. **Identify regulatory regions and epigenetic mechanisms.**
4. **Characterize the complete set of proteins produced by cells and tissues.**
5. **Determine post-translational modifications of proteins.**
6. **Identify protein–protein and other molecular interactions.**
7. **Characterize metabolites and metabolic pathways.**
8. **Discover molecular markers and biomarkers.**
9. **Establish relationships between molecular variation and phenotype.**
10. **Integrate multiple molecular datasets into biological networks.**
11. **Predict biological responses using computational approaches.**
12. **Functionally validate candidate genes and molecular pathways.**

7. Major “omics” technologies

Omics field	Object studied	Main question
Genomics	**DNA/genome**	**What genetic information is present?**
Epigenomics	**DNA/chromatin modifications**	**How is genome activity regulated?**
Transcriptomics	**RNA**	**Which genes are expressed?**
Proteomics	**Proteins**	**Which proteins are present and active?**
Metabolomics	**Metabolites**	**What metabolic processes are occurring?**
Interactomics	**Molecular interactions**	**How do biological molecules interact?**
Phenomics	**Phenotypic traits**	**How is genotype expressed as phenotype?**
Single-cell omics	**Individual cells**	**How do individual cells differ?**
Spatial omics	**Molecules within tissues**	**Where are molecular processes occurring?**

8. Functional genomics

Functional genomics investigates the functions and interactions of genes at a genome-wide level. Its objectives include:

1. identification of gene functions;
2. analysis of gene-expression patterns;
3. identification of regulatory elements;
4. investigation of gene interactions;
5. association of genes with phenotypic traits.

Modern functional genomics combines:

Genome sequencing + RNA-seq + gene perturbation + CRISPR/Cas + phenotyping + bioinformatics

- This represents an important bridge between genome information and biological function.

Transcriptomics

The transcriptome is the complete set of RNA molecules expressed in a cell, tissue, or organism under particular conditions.

Unlike the genome, the transcriptome is highly dynamic.

It changes according to:

1. **developmental stage;**
2. **tissue;**
3. **environmental conditions;**
4. **stress;**
5. **nutrition;**
6. **disease;**
7. **genotype.**

9. Transcriptomics. RNA sequencing

- RNA-seq is now one of the major technologies for transcriptome analysis.
- Typical workflow:
- RNA isolation → library preparation → sequencing → read processing/mapping → quantification → differential expression → pathway analysis
- For example:Control wheat vs drought-stressed whe
- at
- ↓
- RNA-seq
- ↓
- Identification of differentially expressed genes (DEGs)
- ↓
- Identification of drought-responsive pathways.

Proteomics: Analysis of Proteins and Their Functions

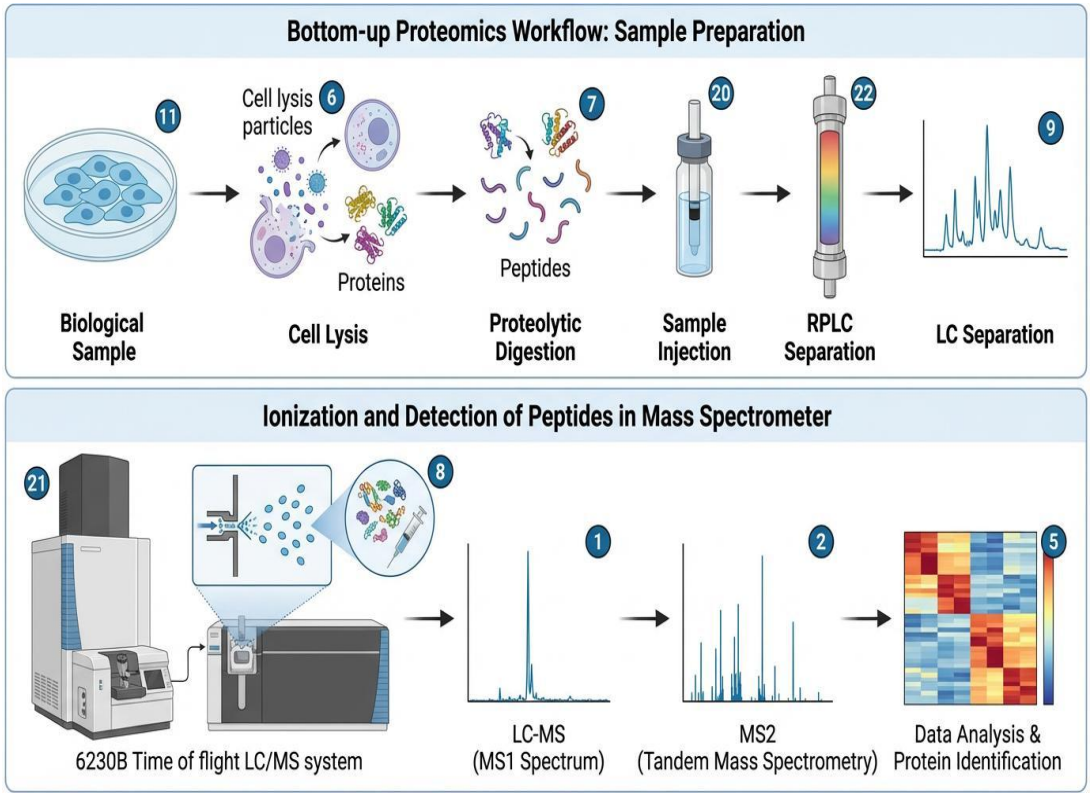
Proteomics is the large-scale study of proteins, including their abundance, structure, functions, modifications, and interactions.

Main research directions:

- Protein identification and quantification.
- Analysis of protein structure and function.
- Investigation of post-translational modifications.
- Identification of protein–protein interactions.

Major technologies: LC-MS/MS, gel electrophoresis, quantitative proteomics.

Significance: Proteomics connects gene expression with cellular functions and physiological processes.



Metabolomics: Analysis of Cellular Metabolism

Metabolomics is the comprehensive study of small molecules (metabolites) present in cells, tissues, and organisms under specific physiological and environmental conditions.

Major groups of metabolites:

1. Primary metabolites: sugars, amino acids, organic acids, and nucleotides.
2. Specialized metabolites: phenolic compounds, flavonoids, alkaloids, and terpenoids.
3. Regulatory metabolites: plant hormones and signaling molecules.

Main analytical technologies:

GC-MS: analysis of volatile compounds and derivatized primary metabolites.

LC-MS/MS: identification and quantification of a broad range of metabolites.

NMR spectroscopy: structural characterization and quantitative metabolic profiling.

Key concept: Metabolomics provides a biochemical snapshot of cellular activity and helps connect molecular regulation with physiological responses and phenotype.

Plant cells and tissues

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Metabolite extraction

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GC-MS | LC-MS/MS | NMR

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Metabolite identification and quantification

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Metabolic pathways and physiological responses

Applications in biotechnology:

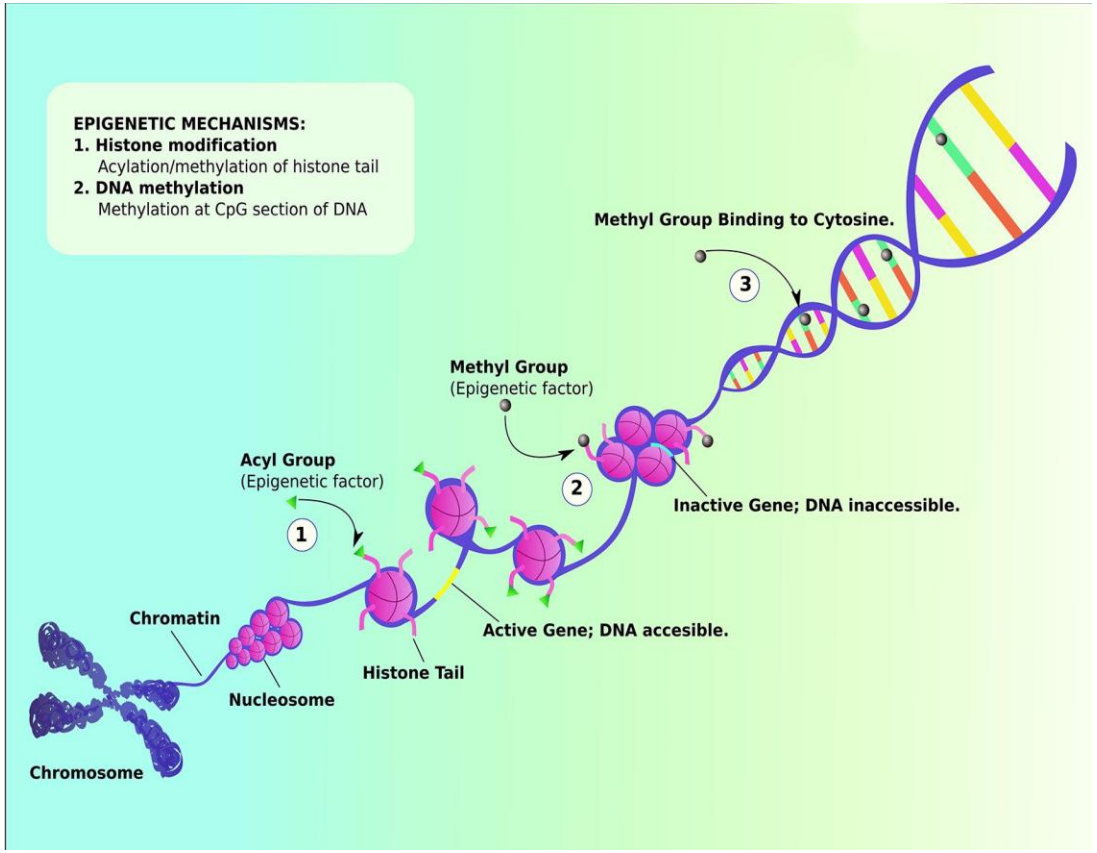
1. Investigation of metabolic pathways and cellular regulation.
2. Identification of biochemical biomarkers.
3. Analysis of plant responses to drought, salinity, and pathogens.
4. Evaluation of crop nutritional quality and metabolic diversity.

Epigenomics: Regulation of Genome Activity

Epigenomics investigates genome-wide patterns of epigenetic regulation that influence gene activity without altering the underlying DNA sequence.

1. Major mechanisms:
2. DNA methylation.
3. Histone modifications.
4. Chromatin remodeling.
5. Regulatory interactions involving non-coding RNAs.

Significance: Epigenomic mechanisms contribute to development, cell differentiation, and environmental responses.



Phenomics: From Genotype to Phenotype

Phenomics is the comprehensive, quantitative analysis of observable and measurable biological traits.

Main approaches:

- High-throughput phenotyping.
- RGB and fluorescence imaging.
- Thermal and hyperspectral imaging.
- Sensor-based physiological measurements.
- AI-assisted trait analysis.

Significance: Phenomics helps connect genetic and molecular variation with growth, development, stress tolerance, and productivity.

Single-Cell and Spatial Omics Technologies

Single-cell omics investigates molecular characteristics of individual cells, revealing cellular heterogeneity.

Spatial omics analyzes molecular processes while preserving information about their location within tissues.

Major technologies:

1. Single-cell RNA sequencing (scRNA-seq).
2. Single-nucleus RNA sequencing (snRNA-seq).
3. Single-cell ATAC-seq.
4. Spatial transcriptomics.

Significance: These technologies reveal cell-specific gene regulation and tissue organization.

Multi-Omics Integration and Systems Biology

Multi-omics integration combines genomic, transcriptomic, proteomic, metabolomic, and phenotypic data to investigate biological systems.

Genomics → Transcriptomics → Proteomics → Metabolomics



Bioinformatics and integrated data analysis



Biological networks and regulatory pathways



Understanding biological functions and phenotypes

Significance: Systems biology provides an integrated understanding of molecular regulation and biological complexity.

Applications of Postgenomic Technologies in Biotechnology

Postgenomic technologies are widely applied in:

1. Medicine: biomarker discovery, molecular diagnostics, precision medicine.
2. Agriculture: crop improvement, stress tolerance, disease resistance.
3. Industrial biotechnology: metabolic engineering, enzyme discovery, bioprocess optimization.
4. Environmental biotechnology: microbial community analysis and environmental monitoring.

Example: Integration of genomics, transcriptomics, proteomics, and phenomics can help identify candidate mechanisms associated with drought tolerance in wheat.

Future Perspectives of Postgenomic Technologies

Major emerging directions:

1. Integration of multi-omics and high-throughput phenotyping.
2. Single-cell and spatial molecular analysis.
3. Artificial intelligence and machine learning.
4. Functional validation using genome editing.
5. Predictive modeling of biological systems.
6. Development of precision biotechnology approaches.

Key message: The future of postgenomic biology lies in integrating molecular information to understand, predict, and potentially modify biological functions.

Conclusion

1. Postgenomic technologies have transformed biological research from genome sequencing toward understanding gene functions, molecular regulation, and biological systems.
2. Genomics, transcriptomics, epigenomics, proteomics, metabolomics, and phenomics provide complementary information about biological organization and function.
3. High-throughput sequencing, mass spectrometry, advanced imaging, and bioinformatics enable comprehensive molecular investigations.
4. Multi-omics integration and systems biology help reveal molecular networks and relationships between genotype, environment, and phenotype.
5. Postgenomic technologies provide essential tools for modern biotechnology, precision medicine, sustainable agriculture, and crop improvement.

Key message: Postgenomic technologies connect molecular information with biological functions and phenotypic characteristics.

- **Recommended Literature**
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