

Letter to Editor

A brief evaluation of the concepts of omics, genomics, proteomics and metabolomics in terms of sperm cell

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Abstract

The ability to live things to transfer their genetic heritage to future generations in a healthy way forms the basis of the science of reproduction. In this sense, understanding the structure and functions of the sperm cell, which is one of the sexual cells, is one of the important issues that should be emphasized. Methods such as omics, genomics, proteomics, and metabolomics, which have been found in research in recent years, are also used to evaluate the functions of the sperm cell.

Introduction

Omics aims to perform structural and functional analyses on the sperm cell model as a biological component, including molecular gene level (genomics), transcript level (transcriptomics), protein level (proteomics), and metabolite level (metabolomics) [1].

Omics studies have many application areas and potentials today and since more than one molecule can be studied at the same time, it paves the way for the discovery of new biomarkers [2].

Genomics enables the identification of all functional genomes and genes present in all living organisms, the interaction of genes with each other and with the environment, as well as the determination of their activation in time, place and amount [3].

Genomics allows comparing the genetic information of different organisms or evaluating the genes of a cell or tissue. Genomic studies are divided into two different groups, structural and functional genomics, according to their fields. Structural genomics includes the study of genome mapping and DNA sequencing by showing the locations of genes on chromosomes. Apart from understanding the functions of genes, functional genomics is concerned with the study of gene expression, the study of genes at the genome level, and helping to make sense of the organism [4].

More Information

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The proteome is all protein encoded by the genome that is present or expressed in a living thing [5]. Proteomics examines the amount of proteome, its functions, and the mechanism of interaction with other proteins and macromolecules. Together, the genome and proteome allow us to obtain a complementary information set [3].

Using transcriptomic analyses, researchers can characterize transcriptional activity (coding and noncoding), focus on a subset of target genes and their associated transcripts, or profile thousands of genes simultaneously to build an overall picture of cell function. The purpose of the transcriptomic analysis is to gain insight into gene expression that influences certain phenotypic characteristics of an individual. Sperm transcriptional activity occurs in the phase of spermiogenesis until round spermatozoa are formed. The gene expression process begins with the transcription of the genetic information stored in DNA molecules and then produces three types of RNA molecules: messenger RNA (mRNA), transfer RNA (tRNA), and ribosomal RNA (rRNA) [6].

Whole transcriptome analyses have determined that a large portion of the living genome also transcribes non-protein-coding transcripts, including lncRNAs (long non-coding RNAs), miRNAs (microRNAs) and circRNAs (circular RNAs) [7].

In contrast to the use of transcriptomics, the preference



for proteomics in spermatozoon biology plays a unique and arguably very important role not found in any other cell type. Therefore, the sperm cell is an excellent material for proteomic analysis [8].

Metabolomics is the determination of low molecular weight metabolites from metabolism products (in physiological fluids; carbohydrates, vitamins, hormones, etc.). Metabolic evaluation of body fluids is important and has a wide range of applications [9].

Single-cell multi-omics studies

Advances in experimental technologies and data methods related to single-cell multi-omics analysis reveal that molecules that play a role in the pathogenesis of diseases are of critical importance. The dynamic process of pathogenesis is associated with molecular mechanisms at the single-cell level, as well as multiple collective omics data. These molecular mechanisms may have potential strategies for the diagnosis and treatment of diseases [10-14].

Biomarkers

Biomarkers are used to have an idea about the healthy or diseased cells, tissues, or general state of the organism. Today, biomarkers are mostly genes, proteins, metabolites, glycans and other molecular factors that can be used for disease diagnosis, prognosis, prediction of therapeutic responses, and therapeutic development [15-18].

Sperm omics

Biochemical studies called the omics revolution have also included spermatology. Omics studies include studies such as genomics, proteomics, and metabolomics, and also help to determine the effects of the presence of other metabolites and changes among themselves on the cell. Studies such as molecular and cell biology, proteomics, and genomics are beneficial in protecting and controlling the reproduction of animals and endangered creatures [1].

With the initiation of omics studies, genomics, transcriptomics, proteomics, and metabolomics play an important role in the recognition and identification of the causes involved in the pathogenesis of male infertility [1].

Certain biomarkers that have historically been used to determine the etiology of the causes of male infertility have led to the discovery of markers that are easy to use, cost-effective, and can determine fertility outcomes. Following the mapping of the human genome, studies in the field of genetic medicine have increased with treatment modalities tailored to the specific genetic makeup of a patient. Genomic studies such as epigenetics, metabolomics, and proteomics offer hope for the intended diagnosis of male infertility [19].

Sperm genomics and proteomics

Genomic studies and mapping methods are useful methods

for finding diseases or disorders transmitted by genes. It has an important place in the regulation of the cloned parts by enabling the determination of the genes that make up the DNA [3].

Identification of biomarkers of semen and various biological fluids with proteomic and genomic studies is important for fertility prediction. Studies on these biomarkers in terms of fertility are expressed to be effective in increasing the insemination ability of male animals, pregnancy rates of female animals, and offspring intake [20].

Spermatozoa can be analyzed by evaluating processes such as epididymal maturation, capacitation, acrosome reaction, and fertilization. Proteomic studies are emerging methods to determine male fertility and semen defect rates [21].

In one study, the concentration of major seminal plasma proteins, which function as surface proteins in spermatozoa, was determined in adult bull semen. In addition, increased proteins in young bull spermatozoa are considered to be associated with cell development [22].

Sperm metabolomics

It has been shown that sperm metabolites can directly or indirectly control signaling pathways such as signaling related to sperm motility, hyperactivation, and energy acquisition [23].

In recent years, spermatozoa and seminal plasma metabolomics have been used to identify biomarkers, mostly in humans [3] and also in bulls [20].

While studies of proteomic and metabolomic markers of sperm and semen remain a minimally invasive marker for diagnosing infertility phenotypes, the application of these studies in the field is limited due to the wide range of proteins and peptides, and because they are metabolites found in semen that can be affected by various environmental factors that may occur due to individual diversity. Much more work needs to be done before these markers can be applied [19].

Conclusion

Proteomic information has an important place in genetic, genomic, transcriptomic and metabolomic databases and there is still a long way to go in proteomic sperm cell studies.

Applied to semen cell research, proteomics has led to the creation of variants of thousands of proteins so far found in the testicles and testicles [24]. In addition, as a result of extensive research, the epigenetic material in the male gamete was better understood when genomic and proteomic analyzes of sperm chromatin were performed [25].

Omics-based applications combined with computational and bioinformatic methods play an important role in terms of biomarkers and are widely used to facilitate diagnostic



and therapeutic developments in many diseases, especially cancers [18].

- On the other hand, in recent years, an approach has been developed regarding omics data by making use of artificial intelligence, which is a current field; AI-based models, methods, and software for processing, analysis, visualization, and interpretation of Omics data;
- AI-based algorithms for analysis of clinical and health data;
- AI-based platforms to improve disease diagnosis and patient care;
- AI-based approaches for protein structure prediction, gene function prediction, and drug discovery [26].

The determination of unwanted genetic defects or various biomarkers by proteomic and genomic studies after the examinations to be made with the samples taken will constitute an important place for fertility prediction.

As a result, we can provide the opportunity to obtain the desired fertility much better by avoiding the directions from the past.

References

1. Omolaoye TS, Omolaoye VA, Kandasamy RK, Hachim MY, Du Plessis SS. Omics and Male Infertility: Highlighting the Application of Transcriptomic Data. *Life (Basel)*. 2022 Feb 14;12(2):280. doi: 10.3390/life12020280. PMID: 35207567; PMCID: PMC8875138.
2. Dai X, Shen L, Lu P. Advances and trends in omics technology development. *Frontiers in Medicine*. 2022; 1546.
3. Başaran E, Sümer ARAS, Cansaran-Duman, D. General Outlook and Applications of Genomics, Proteomics and Metabolomics. *Türk Hijyen ve Deneysel Biyoloji Dergisi*. 2010; 67(2):85-96.
4. Şahin-Çevik M. Microarray Technology and Applications in Plants. *Journal of Suleyman Demirel University Institute of Science and Technology*. 2005; 9(3).
5. Wilkins MR, Pasquali C, Appel RD, Ou K, Golaz O, Sanchez JC, Yan JX, Gooley AA, Hughes G, Humphery-Smith I, Williams KL, Hochstrasser DF. From proteins to proteomes: large scale protein identification by two-dimensional electrophoresis and amino acid analysis. *Biotechnology (N Y)*. 1996 Jan;14(1):61-5. doi: 10.1038/nbt0196-61. PMID: 9636313.
6. Indriastuti R, Pardede BP, Gunawan A, Ulum MF, Arifiantini RI, Purwantara B. Sperm Transcriptome Analysis Accurately Reveals Male Fertility Potential in Livestock. *Animals (Basel)*. 2022 Oct 27;12(21):2955. doi: 10.3390/ani12212955. PMID: 36359078; PMCID: PMC9657999.
7. Xu F, Jiang L, Zhao Q, Zhang Z, Liu Y, Yang S, Yu M, Chen H, Zhang J, Zhang J. Whole-transcriptome and proteome analyses identify key differentially expressed mRNAs, miRNAs, lncRNAs and circRNAs associated with HCC. *Oncogene*. 2021 Jul;40(29):4820-4831. doi: 10.1038/s41388-021-01908-0. Epub 2021 Jun 21. PMID: 34155346.
8. Baker MA. The 'omics revolution and our understanding of sperm cell biology. *Asian J Androl*. 2011 Jan;13(1):6-10. doi: 10.1038/aja.2010.62. Epub 2010 Oct 25. PMID: 20972449; PMCID: PMC3739389.
9. Kovac JR, Pastuszak AW, Lamb DJ. The use of genomics, proteomics, and metabolomics in identifying biomarkers of male infertility. *Fertil Steril*. 2013 Mar 15;99(4):998-1007. doi: 10.1016/j.fertnstert.2013.01.111. Epub 2013 Feb 15. PMID: 23415969; PMCID: PMC3652543.
10. Zhang B, Wang J, Wang X, Zhu J, Liu Q, Shi Z, Chambers MC, Zimmerman LJ, Shaddox KF, Kim S, Davies SR, Wang S, Wang P, Kinsinger CR, Rivers RC, Rodriguez H, Townsend RR, Ellis MJ, Carr SA, Tabb DL, Coffey RJ, Slebos RJ, Liebler DC; NCI CPTAC. Proteogenomic characterization of human colon and rectal cancer. *Nature*. 2014 Sep 18;513(7518):382-7. doi: 10.1038/nature13438. Epub 2014 Jul 20. PMID: 25043054; PMCID: PMC4249766.
11. Zhang H, Liu T, Zhang Z, Payne SH, Zhang B, McDermott JE, Zhou JY, Petyuk VA, Chen L, Ray D, Sun S, Yang F, Chen L, Wang J, Shah P, Cha SW, Aiyetan P, Woo S, Tian Y, Gritsenko MA, Clauss TR, Choi C, Monroe ME, Thomas S, Nie S, Wu C, Moore RJ, Yu KH, Tabb DL, Fenyö D, Bafna V, Wang Y, Rodriguez H, Boja ES, Hiltke T, Rivers RC, Sokoll L, Zhu H, Shih IM, Cope L, Pandey A, Zhang B, Snyder MP, Levine DA, Smith RD, Chan DW, Rodland KD; CPTAC Investigators. Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. *Cell*. 2016 Jul 28;166(3):755-765. doi: 10.1016/j.cell.2016.05.069. Epub 2016 Jun 29. PMID: 27372738; PMCID: PMC4967013.
12. Vasaikar S, Huang C, Wang X, Petyuk VA, Savage SR, Wen B, Dou Y, Zhang Y, Shi Z, Arshad OA, Gritsenko MA, Zimmerman LJ, McDermott JE, Clauss TR, Moore RJ, Zhao R, Monroe ME, Wang YT, Chambers MC, Slebos RJ, Lau KS, Mo Q, Ding L, Ellis M, Thiagarajan M, Kinsinger CR, Rodriguez H, Smith RD, Rodland KD, Liebler DC, Liu T, Zhang B; Clinical Proteomic Tumor Analysis Consortium. Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. *Cell*. 2019 May 2;177(4):1035-1049.e19. doi: 10.1016/j.cell.2019.03.030. Epub 2019 Apr 25. PMID: 31031003; PMCID: PMC6768830.
13. Mun DG, Bhin J, Kim S, Kim H, Jung JH, Jung Y, Jang YE, Park JM, Kim H, Jung Y, Lee H, Bae J, Back S, Kim SJ, Kim J, Park H, Li H, Hwang KB, Park YS, Yook JH, Kim BS, Kwon SY, Ryu SW, Park DY, Jeon TY, Kim DH, Lee JH, Han SU, Song KS, Park D, Park JW, Rodriguez H, Kim J, Lee H, Kim KP, Yang EG, Kim HK, Paek E, Lee S, Lee SW, Hwang D. Proteogenomic Characterization of Human Early-Onset Gastric Cancer. *Cancer Cell*. 2019 Jan 14;35(1):111-124.e10. doi: 10.1016/j.ccell.2018.12.003. PMID: 30645970.
14. Lee J, Hyeon DY, Hwang D. Single-cell multiomics: technologies and data analysis methods. *Exp Mol Med*. 2020 Sep;52(9):1428-1442. doi: 10.1038/s12276-020-0420-2. Epub 2020 Sep 15. PMID: 32929225; PMCID: PMC8080692.
15. Ransohoff DF. Cancer. Developing molecular biomarkers for cancer. *Science*. 2003 Mar 14;299(5613):1679-80. doi: 10.1126/science.1083158. PMID: 12637728.
16. Riesterer O, Milas L, Ang KK. Use of molecular biomarkers for predicting the response to radiotherapy with or without chemotherapy. *J Clin Oncol*. 2007 Sep 10;25(26):4075-83. doi: 10.1200/JCO.2007.11.8497. PMID: 17827456.
17. Kim YS, Maruvada P, Milner JA. Metabolomics in biomarker discovery: future uses for cancer prevention. *Future Oncol*. 2008 Feb;4(1):93-102. doi: 10.2217/14796694.4.1.93. PMID: 18241004.
18. Hu ZZ, Huang H, Wu CH, Jung M, Dritschilo A, Riegel AT, Wellstein A. Omics-based molecular target and biomarker identification. *Methods Mol Biol*. 2011;719:547-71. doi: 10.1007/978-1-61779-027-0_26. PMID: 21370102; PMCID: PMC3742302.
19. Krzastek SC, Smith RP, Kovac JR. Future diagnostics in male infertility: genomics, epigenetics, metabolomics and proteomics. *Transl Androl Urol*. 2020 Mar;9(Suppl 2):S195-S205. doi: 10.21037/tau.2019.10.20. PMID: 32257860; PMCID: PMC7108983.
20. Choudhary KK, Kavva KM, Jerome A, Sharma RK. Advances in reproductive biotechnologies. *Vet World*. 2016 Apr;9(4):388-95. doi: 10.14202/vetworld.2016.388-395. Epub 2016 Apr 18. PMID: 27182135; PMCID: PMC4864481.
21. Park YJ, Kwon WS, Oh SA, Pang MG. Fertility-related proteomic



- profiling bull spermatozoa separated by percoll. *J Proteome Res.* 2012 Aug 3;11(8):4162-8. doi: 10.1021/pr300248s. Epub 2012 Jul 23. PMID: 22794312.
22. Westfalewicz B, Słowińska M, Judycka S, Cierieszko A, Dietrich MA. Comparative Proteomic Analysis of Young and Adult Bull (*Bos taurus*) Cryopreserved Semen. *Animals (Basel).* 2021 Jul 5;11(7):2013. doi: 10.3390/ani11072013. PMID: 34359141; PMCID: PMC8300238.
23. Odet F, Gabel S, London RE, Goldberg E, Eddy EM. Glycolysis and mitochondrial respiration in mouse LDHC-null sperm. *Biol Reprod.* 2013 Apr 18;88(4):95. doi: 10.1095/biolreprod.113.108530. PMID: 23486916; PMCID: PMC4013879.
24. Oliva R, Castillo J. Proteomics and the genetics of sperm chromatin condensation. *Asian J Androl.* 2011 Jan;13(1):24-30. doi: 10.1038/aja.2010.65. Epub 2010 Nov 1. PMID: 21042303; PMCID: PMC3739392.
25. Castillo J, Amaral A, Azpiazu R, Vavouri T, Estanyol JM, Ballescà JL, Oliva R. Genomic and proteomic dissection and characterization of the human sperm chromatin. *Mol Hum Reprod.* 2014 Nov;20(11):1041-53. doi: 10.1093/molehr/gau079. Epub 2014 Sep 5. PMID: 25193639.
26. Gao F, Huang K, Xing Y. Artificial Intelligence in Omics. *Genomics, proteomics & bioinformatics.* S1672-0229.