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Non-coding RNAs: A tale of junk turning into treasure

Editorial perspective

Biochemists and molecular biologists, who have been in the field for a couple of decades, would probably remember the time when it was a norm to term all RNA ‘junk’ if it did not translate into a protein product. Gone are those days. The erstwhile ‘junk’ RNA is now a much pursued and sought entity. The RNA molecules that do not code for any proteins; the ‘non-coding RNAs’, are now a hot topic in modern day research. Many non-coding RNAs are very much functional in biological systems, and compensate for their inability to be translated into proteins through alternate mechanisms.

As it turns out, the non-coding RNAs are quite abundant [1]. The sequencing of human genome at the turn of century, followed by recent advancements in the technical capabilities have resulted in a much better understanding of transcriptional landscape i.e. the fate of a majority of RNAs that are transcribed from human genome [2]. It is believed that three quarters of human genome is capable of being transcribed, which, simply speaking, is a lot of RNA. Only a tiny fraction (3%) of the genome consists of protein-coding genes [3] which means that a vast majority of genome gets transcribed into non-coding RNAs. While our knowledge on the subject is far from complete, by all estimates it can be concluded that the number of non-coding RNAs is much more than the ‘coding RNAs’ that get translated into proteins [3,4]. This immediately raises a red flag – after all, why these seemingly useless genome portions, that produce numerous non-coding RNA transcripts, have not been lost during the course of evolution. A logical explanation would be that these RNA transcripts are not useless after all. They have definite functionality. It can even be envisioned that the complexity of life, and the intricate regulation of cellular processes, better correlates with the repertoire and diversity of non-coding RNAs, as opposed to the coding-RNAs [4,5].

Research efforts over last several years have established an ever-increasing importance of non-coding RNAs in many human health conditions [6,7]. Not all non-coding RNAs are alike. There are several different subtypes - microRNAs (miRNAs), small interfering RNAs (siRNAs), small nucleolar RNAs (snoRNAs), U-RNAs/small nuclear RNAs (snRNAs), exosomal/extracellular RNAs (exRNAs), Piwi-interacting RNAs (piRNAs) and long non-coding RNAs. Of course, a few have been investigated more than the others. miRNAs have attracted enormous interest in recent years, so much so that it is hard to consider them as a subtype of non-coding RNAs. The published work on miRNAs is many folds higher than all the other non-coding RNAs combined [8]. The other non-coding RNA that has been investigated in sufficient detail is the long non-coding RNA [1,4,8]. The importance of non-coding RNAs is also not limited to just one human condition/disease. Accumulating literature suggests that these RNAs are relevant to aging [9], cancer [10–12], cardiovascular diseases [12], diabetes and related complications [13–15], endocrine system [16], immune system [17], kidney diseases [18], obesity [19], neurodevelopment [20,21] – pretty much everything. Non-coding RNAs are a subject of research investigations into origin of individual diseases, with differential expression of select non-coding RNAs being tied to disease onset [6,22]. They are also being evaluated for their putative role in disease diagnosis as a biomarker [23,24] as well as in prognosis and predictor of response to therapy [24,25]. It is not surprising, therefore, that many non-coding RNAs are being tested for their possible use in therapy of individual diseases [8,26–28].

With such a high level of interest in the role of non-coding RNAs in human health and diseases, it is about time that a platform dedicated to the comprehensive exchange of information on non-coding RNAs is established. The journal “Non-coding RNA Research” is an effort in this direction. The primary aim of this interdisciplinary journal is to disseminate cutting edge research focused on non-coding RNAs in modern day research and medicine. Without setting any boundaries, with regards to specific diseases or the precise nature of non-coding RNA-mediated regulation, this journal will welcome all rigorously performed primary research and clinical studies as well as timely reviews focusing on virtually all aspects of non-coding RNAs – their biogenesis, inter-regulation(s) and functional role in human diseases.

This first issue very well represents the non-coding RNAs' diverse functional role, with articles on very distinct topics. Even with all the published literature on non-coding RNAs, it is safe to conclude that this research area is still in its infancy and we have barely scratched the surface. The ‘seemingly’ inconsequential non-coding RNA molecules definitely hold a lot of promise, and it will be this journal's endeavor to publish articles that showcase the ever-evolving importance of non-coding RNAs.

References

[1] J.T. Kung, D. Colognori, J.T. Lee, Long noncoding RNAs: past, present, and future, Genetics 193 (2013) 651–669.

[2] S. Djebali, C.A. Davis, A. Merkel, A. Dobin, T. Lassmann, A. Mortazavi, A. Tanzer, J. Lagarde, W. Lin, F. Schlesinger, C. Xue, G.K. Marinov, J. Khatun, B.A. Williams, C. Zaleski, J. Rozowsky, M. Roder, F. Kokocinski, R.F. Abdelhamid, T. Alioto, I. Antoshechkin, M.T. Baer, N.S. Bar, P. Batut, K. Bell, I. Bell, S. Chakrabortty, X. Chen, J. Chrast, J. Curado, T. Derrien, J. Drenkow, E. Dumais, J. Dumais, R. Duttagupta, E. Falconnet, M. Fastuca, K. Fejes-Toth, P. Ferreira, S. Foissac, M.J. Fullwood, H. Gao, D. Gonzalez, A. Gordon, H. Gunawardena, C. Howald, S. Jha, R. Johnson, P. Kapranov, B. King, C. Kingswood, O.J. Luo, E. Park, K. Persaud, J.B. Preall, P. Ribeca, B. Risk, D. Robyr, M. Sammeth, L. Schaffer, L.H. See, A. Shahab, J. Skancke, A.M. Suzuki, H. Takahashi, H. Tilgner, D. Trout,

http://dx.doi.org/10.1016/j.ncrna.2016.12.001

N. Walters, H. Wang, J. Wrobel, Y. Yu, X. Ruan, Y. Hayashizaki, J. Harrow, M. Gerstein, T. Hubbard, A. Reymond, S.E. Antonarakis, G. Hannon, M.C. Giddings, Y. Ruan, B. Wold, P. Carninci, R. Guigo, T.R. Gingeras, Landscape of transcription in human cells, Nature 489 (2012) 101–108.

[3] H. Ling, K. Vincent, M. Pichler, R. Fodde, I. Berindan-Neagoe, F.J. Slack, G.A. Calin, Junk DNA and the long non-coding RNA twist in cancer genetics, Oncogene 34 (2015) 5003–5011.

[4] J.J. Quinn, H.Y. Chang, Unique features of long non-coding RNA biogenesis and function, Nat. Rev. Genet. 17 (2016) 47–62.

[5] J.S. Mattick, R.J. Taft, G.J. Faulkner, A global view of genomic information–moving beyond the gene and the master regulator, Trends Genet. 26 (2010) 21–28.

[6] M. Esteller, Non-coding RNAs in human disease, Nat. Rev. Genet. 12 (2011) 861–874.

[7] R.J. Taft, K.C. Pang, T.R. Mercer, M. Dinger, J.S. Mattick, Non-coding RNAs: regulators of disease, J. Pathol. 220 (2010) 126–139.

[8] H. Ling, M. Fabbri, G.A. Calin, MicroRNAs and other non-coding RNAs as targets for anticancer drug development, Nat. Rev. Drug Discov. 12 (2013) 847–865.

[9] K.J. Abraham, L.A. Ostrowski, K. Mekhail, Non-coding RNA molecules connect calorie restriction and lifespan, J. Mol. Biol. (2016).

[10] A.M. Schmitt, H.Y. Chang, Long noncoding RNAs in cancer pathways, Cancer Cell 29 (2016) 452–463.

[11] R.A. Gupta, N. Shah, K.C. Wang, J. Kim, H.M. Horlings, D.J. Wong, M.C. Tsai, T. Hung, P. Argani, J.L. Rinn, Y. Wang, P. Brzoska, B. Kong, R. Li, R.B. West, M.J. van de Vijver, S. Sukumar, H.Y. Chang, Long non-coding RNA HOTAIR reprograms chromatin state to promote cancer metastasis, Nature 464 (2010) 1071–1076.

[12] J. Beermann, M.T. Piccoli, J. Viereck, T. Thum, Non-coding RNAs in development and disease: background, mechanisms, and therapeutic approaches, Physiol. Rev. 96 (2016) 1297–1325.

[13] M.L. Alvarez, J.K. Distefano, The role of non-coding RNAs in diabetic nephropathy: potential applications as biomarkers for disease development and progression, Diabetes Res. Clin. Pract. 99 (2013) 1–11.

[14] X. Sun, D. Wong, Long non-coding RNA-mediated regulation of glucose homeostasis and diabetes, Am. J. Cardiovasc Dis. 6 (2016) 17–25.

[15] N. Jae, S. Dimmeler, Long noncoding RNAs in diabetic retinopathy, Circ. Res. 116 (2015) 1104–1106.

[16] M. Knoll, H.F. Lodish, L. Sun, Long non-coding RNAs as regulators of the endocrine system, Nat. Rev. Endocrinol. 11 (2015) 151–160.

[17] M. Turner, A. Galloway, E. Vigorito, Noncoding RNA and its associated proteins as regulatory elements of the immune system, Nat. Immunol. 15 (2014) 484–491.

[18] J.M. Lorenzen, T. Thum, Long noncoding RNAs in kidney and cardiovascular diseases, Nat. Rev. Nephrol. 12 (2016) 360–373.

[19] P. Arner, A. Kulyte, MicroRNA regulatory networks in human adipose tissue and obesity, Nat. Rev. Endocrinol. 11 (2015) 276–288.

[20] I.A. Qureshi, M.F. Mehler, Emerging roles of non-coding RNAs in brain evolution, development, plasticity and disease, Nat. Rev. Neurosci. 13 (2012) 528–541.

[21] E. Salta, B. De Strooper, Non-coding RNAs with essential roles in neurodegenerative disorders, Lancet Neurol. 11 (2012) 189–200.

[22] P.P. Amaral, M.E. Dinger, J.S. Mattick, Non-coding RNAs in homeostasis, disease and stress responses: an evolutionary perspective, Brief. Funct. Genomics 12 (2013) 254–278.

[23] W.T. Wang, Y.M. Sun, W. Huang, B. He, Y.N. Zhao, Y.Q. Chen, Genome-wide long non-coding RNA analysis identified circulating LncRNAs as novel non-invasive diagnostic biomarkers for gynecological disease, Sci. Rep. 6 (2016) 23343.

[24] M. Weng, D. Wu, C. Yang, H. Peng, G. Wang, T. Wang, X. Li, Noncoding RNAs in the development, diagnosis, and prognosis of colorectal cancer, Transl. Res. (2016).

[25] S.O. Perakis, J.E. Thomas, M. Pichler, Non-coding RNAs enabling prognostic stratification and prediction of therapeutic response in colorectal cancer patients, Adv. Exp. Med. Biol. 937 (2016) 183–204.

[26] M.Y. Shah, A. Ferrajoli, A.K. Sood, G. Lopez-Berestein, G.A. Calin, microRNA therapeutics in cancer - an emerging concept, EBioMedicine 12 (2016) 34–42.

[27] T.C. Roberts, M.J. Wood, Therapeutic targeting of non-coding RNAs, Essays Biochem. 54 (2013) 127–145.

[28] M. Matsui, D.R. Corey, Non-coding RNAs as drug targets, Nat. Rev. Drug Discov. (2016).

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