Exploring the Field of Genome Editing: A Bibliometric Look

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Unlike traditional genetic engineering technologies, which introduced changes in genome randomly, targeted genetic modification is a set of new methods, which allow scientists to insert new DNA sequences at precise locations, to remove unwanted sequences, or to introduce subtle modifications, such as single-base substitutions that alter the activity of individual genes.

Our paper analyzes recent publications in TagMo to map the development of research using or exploring the new genetic engineering methods and draws some conclusions relevant to governance based on the results of the analysis. Using a set of keywords identified with the help of experts in TagMo, we generated a bibliographic database containing 1,517 articles for the period from 2007 to 2012. We used the VantagePoint software to clean the data, to generate ranked lists, to create correlation matrices, and to draw social-network maps. As a result of the analysis, we identified the key actors in the field, including countries, organizations, individuals, and publication venues (journals). We also revealed most influential articles, authors, and contributing fields; and explored collaborative relations and citation patterns existing among the actors.

Our preliminary results indicate that while the number of TagMo publications is steadily increasing with the US, Japan, and China being the most notable contributors, the level of international collaboration is relatively low. We found that 616 different organizations are involved in the field. Although over half of all research is conducted by the U.S. academia with Harvard being the leader, the most productive and the most cited researchers in the field work at Sangamo, which publishes more papers than any university in the U.S.

Most leading government and public entities conducting research on TagMo are from France, China, and Japan. The U.S. occupies the fourth place in terms of activity of government agencies in research with the U.S. National Cancer Institute contributing most in terms of publications and the U.S. National Institutes of Health contributing most in terms of dollars.

Most cited journals in the field are Nucleic Acids Research, Procedures of the National Academy of Sciences U. S. A, and Public Library of Science ONE. Two of the top three journals do not specialize in genetics or biotechnology. The main fields contributing to TagMo research are Biochemistry-Molecular Biology, Biotechnology and Applied Microbiology, Genetics and Heredity, and Cell Biology. Among applied areas, most notable is participation of various medical fields, such as oncology, cardiology, immunology, hematology, endocrinology, and pathology.

One of our preliminary conclusion is that the U.S. NIH is currently most active in funding TagMo research, which results in disproportionate attention to health-related applications. Another conclusion is that private sector has assumed leadership in the early stage development of TagMo. Given the natural desire of the private sector to patent, this may have significant implications for the capacity of the public sector to equally participate in research and for certain topics in research not presenting immediate interest for business to be marginalized.