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Editorial Note on Clinical chemistry eponyms

Srihari Nichen

Centurion University of Technology and Management, Bhubaneswar,India

Editorial Note

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***For Correspondence**

Nichen S, Department chemistry. Centurion University of Technology and Management, Bhubaneswar,India.

E-mail: nichen4455@gmail.com

Tel: 9032531962

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EDITORIAL NOTE

While eponyms are widely used in medicine, there have been no research on their use in clinical chemistry. From 1847 to 2020, clinical chemistry eponyms were manually compiled from books, review papers, and journal articles. The use of eponyms was investigated by searching PubMed for titles and abstracts. Custom Python scripts were used to permute eponyms into different forms before using Biopython to scan PubMed. Two clinical chemistry papers, Clinica Chimica Acta [CCA] and Clinical Chemistry [CCJ], were used to narrow down the eponyms found in PubMed. In clinical chemistry, the manual set yielded over 300 eponyms. In 33,232 posts, a Biopython search of PubMed found a subset of 97 distinct eponyms. In 130 CCA posts, PubMed found 26 eponyms, while a full-text search found 1187 articles. In addition, a PubMed search found 36 eponyms in 158 CCJ posts, while a full-text CCJ search found 708. The journals CCA and CCJ had a peak number of eponym citations in 1977, followed by a gradual decline, according to PubMed. In clinical chemistry, eponyms are widely used, with 97 eponyms contained in PubMed. Overall, clinical chemistry eponyms tend to be on the decline.In molecular biology, a Southern blot is a technique for detecting a particular DNA sequence in DNA samples. Southern blotting is a technique that involves moving electrophoresis-separated DNA fragments to a filter membrane and then using probe hybridization to detect the fragments. Sanger sequencing is a DNA sequencing process that relies on DNA polymerase's selective incorporation of chain-terminating dideoxynucleotides during in vitro DNA replication. It was invented by Frederick Sanger and colleagues in 1977, and for the next 40 years, it was the most commonly used sequencing tool. Applied Biosystems was the first to commercialise it in 1986. Sanger sequencing has been largely replaced by "Next-Gen" sequencing methods in recent years, especially for large-scale, automated genome analyses. The Sanger process, on the other hand, is still widely used for smaller-scale projects and for confirming Next-Gen findings. It also has an advantage over short-read sequencing technologies (such as Illumina) in that it can generate DNA sequence reads of up to tens of thousands of bases. An international group of developers developed the Biopython project, which is an open-source series of non-commercial Python resources for computational biology and bioinformatics.It has classes for describing biological sequences and annotations, as well as the ability to read and write a number of file formats. It also enables programmatic access to online biological databases, such as those at the National Center for Biotechnology Knowledge (NCBI).

• This is the first study to look at how eponyms are used in medicinal chemistry.

•There are 97 clinical chemistry eponyms in use in the scientific literature.

•In clinical chemistry journals, eponyms associated with molecular diagnostics are widely used.

•The use of eponyms in medicinal chemistry has declined over time.