

Most of you know the famous statement by the Russian-born US evolutionary biologist Theodosius Dobzhansky, one of the central figures in shaping the unifying modern evolutionary synthesis during the 1940s. You don't? Okay, here we go: in a 1964 article in *American Zoologist* he wrote the sentence "Nothing in biology makes sense except in the light of evolution."

The reason that Dobzhansky's statement became so famous is that apparently many agree with it. That in turn means that evolutionary biology is regarded as a kind of umbrella discipline for most, if not all, of the subfields of biology. The reason is simple: every biological mechanism and every biological molecule discovered are the results of a long evolutionary history of adaptation.

Of course, this is a fact that could easily hamper a fair comparison of performance in evolutionary biology research because it is difficult to draw clear boundaries. On the one hand, what is research that has pure evolutionary biology as its main focus? On the other hand, how can it be separated from research that primarily aims at solving problems from, for example, biochemistry or developmental biology, but in addition carries with it some evolutionary aspects? Or similarly, how to judge research that uses insights from evolutionary biology to tackle problems from other subfields? Like, for example, assigning functions to unknown protein coding sequences by comparative genomics, or optimising the characteristics of certain molecules by so-called directed *in vitro* evolution.

Really evolution in focus?

Thus, the only way to conduct a fair analysis of publication performance in evolutionary biology research is to set tough standards. Accordingly, we excluded research that studied or used evolutionary aspects only as part of a different field and accepted only publications which clearly aimed at solving questions from evolutionary biology.

In principle, this requirement should be met *a priori* when restricted to specialist journals in evolutionary biology. On the other hand, most of the top papers of the field are traditionally pub-

lished in multidisciplinary journals like *Nature*, *Science* or *PNAS*. Since, however, the *Web of Science* publication database from Thomson Scientific which was used for this analysis doesn't provide tools to extract "real" evolutionary biology articles with sufficient reliability, we had to omit them anyway, at least from the analysis of individual countries' performance during the period 1996 to 2006 (see tables p. 39).

Of course, this way some of the most prominent papers in the field did not go into this part of the analysis. Despite this limitation, however, we believe that a survey of expert journals alone nevertheless provides sufficiently valid indicators for countries' overall productivity in evolutionary biology research. In contrast, for the rankings of the most-cited researchers and papers (see tables p. 40); publications in all journals were included.

Applying this approach to European countries and Israel, England published the most articles in the evolutionary biology expert journals over the period 1996 to 2006 (4,619). Already far out of sight, Germany and France followed closely together in the next places (3,498 and 3,377, respectively).

Best average rates for Sweden and Scotland

Behind these two, another wide gap opened up before Spain came in at fourth place with 1,856 articles. Going further down the ladder, only five more countries achieved more than 1,000 articles between 1996 and 2006: Sweden (1,493), Russia (1,394), Italy (1,309), Scotland (1,101) and Switzerland (1,047).

When, however, it comes to how frequently the articles of individual nations have been cited to-date, this order got mixed up again. France, for example, left Germany behind to make it to a clear second place. Similarly, Sweden outran Spain, which thus came in fifth by number of citations. Furthermore, Italy and Russia dropped to 9th and 14th place, respectively.

The reason for these shifts, of course, is different rates of citations per article. Accordingly, Sweden achieved the highest rate with each of its articles from between 1996 and 2006 cited exactly 20 times on average to-date. Very close behind, however, followed Scotland with 19.9 citations per article, thereby gaining a bit more distance until the Netherlands came in third (17.8).

Two surprises were Israel and the Czech Republic – the former for performing weakly in the comparison with other biomedical fields, the latter for achieving a comparatively strong performance.

Altogether, European authors signed slightly more articles in evolutionary biology journals over the period 1996 to 2006 than their US colleagues. Due to a higher citation-per-article rate, however, the papers co-authored by US researchers have been cited more frequently to-date.

When comparing the number of overall citations, Canada even outran Germany whereas Australia came in clearly better than Europe's fourth, Sweden. Japan this time performed more weakly than these two.

Let's switch to articles and authors (see tables p. 40). The five most-cited articles from 1996-2006 with a corresponding address in Europe or Israel demonstrate one thing at first sight: questions from evolutionary biology are particularly suited to the application of methods from computational biology. In particular, the establishment of phylogenetic trees by comparing ever growing amounts of sequence data has become a real playground for the application of stochastic maximum likelihood approaches.

Europe...

Country	Citations	Articles	Cit./Art.
1. England	79,852	4,619	17.3
2. France	55,130	3,377	16.3
3. Germany	47,343	3,498	13.5
4. Sweden	29,825	1,493	20.0
5. Spain	22,424	1,856	12.1
6. Scotland	21,855	1,101	19.9
7. Switzerland	18,094	1,047	17.3
8. Netherlands	17,486	984	17.8
9. Italy	13,976	1,309	10.7
10. Belgium	10,423	751	13.9
11. Denmark	9,628	613	15.7
12. Finland	9,040	608	14.9
13. Austria	8,933	678	13.2
14. Russia	7,891	1,394	5.7
15. Norway	6,869	391	17.6
16. Israel	4,786	428	11.2
17. Czech Rep.	3,301	333	9.9
18. Wales	3,142	245	12.8
19. Portugal	3,100	313	9.9
20. Ireland	2,979	195	15.3

Articles appeared between 1996 and 2006 in evolutionary biology journals as listed by Thomson Scientific. Their citation numbers were recorded up until March 2008. A country's figures are derived from articles where at least one author working in the respective European nation is included in the author's list. Israel is included because it is a member of many European research organisations (EMBO, FEBS etc.), as well as participating in the EU Research Framework Programmes.

... and the world

	Citations	Articles	Cit./Art.
Europe	291,615	20,767	14.0
USA	320,554	20,243	15.8
Canada	48,586	2,795	17.4
Australia	39,785	2,668	14.9
Japan	29,952	2,305	13.0
China	8,664	1,414	6.1

All five top evolutionary biology papers belong in this category, each presenting a specific software tool for evolutionary tree construction. Interestingly, by far the most-cited article is a two page application note written by Glasgow's Roderic Page as a single author.

When looking at the thirty most-cited authors the strong performance of some microbiologists is immediately striking. Among them are some of the pioneers of applying specific DNA probes to elucidate by sequence comparison bacterial diversity as well as their molecular taxonomy, systematics, phylogeny and evolution. These are, for example, Rudolf Amann (1st), Erko Stackebrandt (8th), Michael Wagner (12th) and Wolfgang Ludwig (13th) who all at different times went through the lab of Karl Heinz Schleifer (7th) at the Technical University of Munich.

A pariah, but nothing proven

In second place came a man who has recently evoked a lot of controversy: Anders Pape Møller, Danish bird expert from the University of Paris. With his findings in the early 1990s that barn swallow females preferred the most symmetrical males Møller was the central figure in postulating the theory that bilateral symmetry is an indicator of "good genes" and therefore a key parameter in sexual selection. At the end of the 1990s, however, he was accused of fabricating data in a specific paper. The Danish Committee on Scientific Dishonesty as well as his home institution, the National Centre for Scientific research (CNRS) in Paris, investigated the case but couldn't find Møller guilty of intentional fraud. However, they also stated that the material evidence necessary to establish innocence was lacking. Møller has since fallen "from superstar evolutionary biologist to pariah" (*The Scientist*) but continues to publish at a normal pace.

In third place was the most-cited of the subgroup of mathematical and computational evolutionary biologists: London's Ziheng Yang. Completely different fields are represented by the following two researchers: Svante Pääbo (4th) focusses on human evolution whilst Mark Chase (5th) is a specialist in plant systematics and phylogeny. Then, of course, there are more examples that demonstrate the real diversity of evolutionary biology research: Axel Meyer (14th) is an expert in fish speciation; Eddie Holmes (15th) investigates virus evolution; William Martin (17th) studies the evolution of the first eukaryotic cells and Andrei Lupas (26th) is head of a department for protein evolution.

Well, on the other hand, such diversity is exactly what you'd expect from an "umbrella discipline" like evolutionary biology.

RALF NEUMANN



Publication Analysis 1996-2006 – Evolutionary Biology

Most Cited Authors...

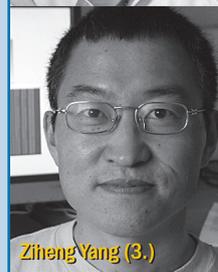
	Cit-ations	Art-icles
1. Rudolf Amann , Max Planck-Inst. f. Marine Microbiol. Bremen	10,003	176
2. Anders Pape Møller , Lab Parasitol. Evol., CNRS, Univ. Paris	8,708	305
3. Ziheng Yang , Genet. Environm. & Evol. Univ. Coll. London	7,844	73
4. Svante Pääbo , Max Planck-Inst. Evol. Anthropol. Leipzig	7,429	142
5. Marc W. Chase , Jodrell Lab Royal Bot. Gardens Kew Richmond	7,271	183
6. Peter Vandamme , Microbiol. Lab Univ. Ghent	6,655	235
7. Karl Heinz Schleifer , Microbiol. Tech. Univ. Munich	6,048	98
8. Erko Stackebrandt , Ger. Collect. Microorg. & Cell Cult. Braunschweig	5,858	261
9. Godfrey M. Hewitt , Ctr. Ecol. Evol. & Conserv. Univ. E. Anglia, Norwich	5,560	92
10. Roderic D.M. Page , Environm. & Evolutionary Biol. Univ. Glasgow	5,506	40
11. Hans Ellegren , Evol. Biol. Centre Univ. Uppsala	5,488	133
12. Michael Wagner , Microbiol. Univ. Vienna	5,441	111
13. Wolfgang Ludwig , Microbiol. Tech. Univ. Munich	5,033	106
14. Axel Meyer , Evol. Biol. Univ. Konstanz	4,966	165
15. Eddie C. Holmes , Evol. Biol. Dep. Zool. Univ. Oxford	4,480	171
16. Arndt von Haeseler , Ctr. Integrative Bioinform. Univ. Vienna	4,444	53
17. William Martin , Bot. Univ. Düsseldorf	4,438	105
18. Hans Jürgen Bandelt , Mathematics Univ. Hamburg	4,154	75
19. Vincent Savolainen , Jodrell Lab Royal Bot Gardens Kew Richmond	4,017	73
20. Manolo Gouy , Lab Biometrie & Biol. Evolut., CNRS, UMR, Univ. Lyon	3,943	33
21. Linda Partridge , Dep. Biol. Univ. Coll. London	3,927	111
22. Eviatar Nevo , Inst. Evol. Univ. Haifa	3,885	292
23. Josephine M. Pemberton , Evol. Biol. Univ. Edinburgh	3,796	74
24. Mark Stoneking , Max Planck-Inst. Evol. Anthropol. Leipzig	3,763	121
25. Brian Charlesworth , Evol. Biol. Univ. Edinburgh	3,732	122
26. Yves van de Peer , Plant Syst. Biol. Univ. Ghent	3,678	88
27. Andrei Lupas , Protein Evol. Max Planck-Inst. Dev. Biol. Tübingen	3,656	76
28. Laurence D. Hurst , Evol. Genet. Univ. Bath	3,643	118
29. Ben C. Sheldon , Zool. Univ. Oxford	3,613	74
30. Pierre Taberlet , Lab. d'Ecologie Alpine, CNRS, Univ. Grenoble	3,588	87



Rudolf Amann (1.)



Anders P. Møller (2.)



Ziheng Yang (3.)



Svante Pääbo (4.)



Roderic Page (10.)



Hans Ellegren (11.)



Linda Partridge (21.)



Eviatar Nevo (22.)

Citations of articles published between 1996 and 2006 were recorded until March 2008 using the database *Web of Science* from Thomson Scientific. The "most cited papers" had correspondence addresses in Europe or Israel.

... and Papers

	Citations
1. Page, RDM TreeView: An application to display phylogenetic trees on personal computers. <i>COMPUTER APPLICATIONS IN THE BIOSCIENCES</i> , 12 (4): 357-358 AUG 1996	4,512
2. Strimmer, K; von Haeseler, A Quartet puzzling: A quartet maximum-likelihood method for reconstructing tree topologies. <i>MOLECULAR BIOLOGY AND EVOLUTION</i> , 13 (7): 964-969 SEP 1996	1,788
3. Ronquist, F; Huelsenbeck, JP MrBayes 3: Bayesian phylogenetic inference under mixed models. <i>BIOINFORMATICS</i> , 19 (12): 1572-1574 AUG 12 2003	1,729
4. Yang, ZH PAML: a program package for phylogenetic analysis by maximum likelihood. <i>COMPUTER APPLICATIONS IN THE BIOSCIENCES</i> , 13 (5): 555-556 OCT 1997	1,654
5. Guindon, S; Gascuel, O A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood. <i>SYSTEMATIC BIOLOGY</i> , 52 (5): 696-704 OCT 2003	1,118

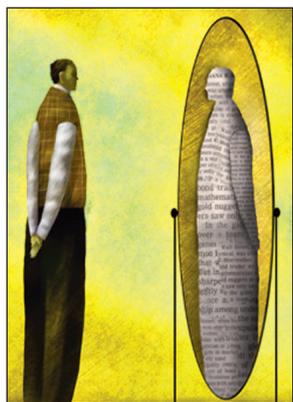
Don't be misled by citation figures! (11)

Cling Together, Swing Together

Tunicates were the passion of zoologist Raúl Guti. Animals like salps, sea squirts or Appendicularia such as *Oikopleura dioica* belong to this group. Also known as urochordates they represent – beside vertebrates and cephalochordates – the third subphylum of the chordates.

Guti knew all of them. Taking into account even the most recent morphological and physiological insights, he was able to allocate each of them its exact position in the tunicates' phylogenetic tree without any difficulty. He was already a real expert at this, despite still being “only” a postdoc.

At that time, however, dark clouds were gradually accumulating over the idyllic world of systematics. The first complete genomes had already been sequenced, so it was clear that more and more sequences would soon be flooding the banks at an ever-increasing rate. Of course, at the same time, the completely new opportunity would open up to compare organisms on the level of their genomes. The buzzword “comparative genomics” had already been flying around for a while and it was clear what this would finally mean to taxonomy and systematics. Some were openly talking of a forthcoming revolution.



There was no doubt. If Guti didn't want to be flushed away by this revolution-to-be he would have to learn these new methods of genomics and bioinformatics. Therefore, it was a blessing in disguise that for exactly this purpose a certain European foundation granted him half a year's fellowship at the Joint Genome Institute (JGI) of the US Department of Energy, one of the worldwide “powerhouses” of genome sequencing and annotation.

When Guti finally arrived, the whole JGI was in a great state of excitement. For more than a year a vast portion of the institute's staff had been working on the dolphin genome. And just at the point when the successful conclusion of their ambitious project was already in sight, a rumour was leaked that the Chinese Beijing Genome Centre (BGC) was also working on a “Flipper project”, as it was called by the JGI people. Nobody knew exactly how much progress the Chinese had already made, but the JGI had already witnessed their competitive style on another genome project, a bad experience they would prefer to forget. In any case, the Chinese were fast and good.

Naturally, the people at the JGI were annoyed about the senselessness of sequencing the same thing twice. However, if it was already fact, they at least wanted to be first. Subsequently, everybody was summoned to join the “Flipper project”, even those who were actually working on other organisms. The JGI bosses calculated that this way they could be “through” within the next four months.

Raúl Guti was also unable to escape this “privilege”. After a quick crash course he was, along with everybody else, feeding the sequencing robots with dolphin DNA, applying the JGI software to the resulting sequences and passing the data on for further analysis.

In the end, Guti spent five of his six months at the JGI on the dolphin genome. This didn't actually bother him as, ironically, he learned exactly the methods that he had wanted to learn.

Inevitably, the JGI published the dolphin genome first, which wasn't any wonder. It turned out that the Chinese “Flipper project” was exactly what it had started as – a rumour. Instead, the BGC had the mink whale genome in the pipeline.

Guti, to his great pleasure, was indeed included on the JGI's dolphin paper as author no. 123 of 278. Two years later, this paper had boosted his “citation account” by more than 500 citations.

Back at his home institute, Guti had immediately busied himself with work on the phylogeny of tunicates again. By applying his newly acquired expertise in genomics he was able to produce a handful of papers in rather a short time, although, none of them received more than ten citations.

RALF NEUMANN

2 Dream Teams



with PBS

with CrossDown Buffer

Problems with cross-reactivity and high background?

The newly developed CrossDown Buffer minimizes cross reactivities, unspecific binding and matrix effects in immunoassays like ELISA, EIA, Western blotting, immuno-PCR, protein arrays, multianalyte immunoassays and immunohistochemistry.

Premium

Blocking Buffer I

- THE blocking reagent of highest quality
- based on low-molecular weight casein
- most effective blocking; used as an alternative if standard blocking procedures do not work
- applications in ELISA, RIA, EIA, Western blotting, protein arrays and Immuno-PCR

Cost-effective

Blocking Buffer II EGrade

- THE economical alternative to Blocking Buffer I
- serum-free, BSA-free, phosphate-free
- peptide-based
- effective blocking
- applications in ELISA, RIA, EIA, Western blotting, protein arrays and Immuno-PCR

AppliChem

There is another top address in Darmstadt:
AppliChem GmbH Ottoweg 4 64291 Darmstadt
Phone 0049 6151/93 57-0 Fax 0049 6151/93 57-11
service@appliChem.de www.appliChem.com