

*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 minke 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.

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