

MEDIA RELEASE

Scientists perform 'tricky' operation

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A team of international scientists has decoded the genome of the parasite behind trichomoniasis, a sexually transmitted infection (STI) that each year affects about 170 million people worldwide.

Trichomonas vaginalis colonises the urogenital tract and causes the infection also known as "trick", the most common non-viral STI.

University of Queensland PhD scholar Rebecca Dunne was one of a team of 65 scientists that worked on the project to sequence the genome, which could offer clues to better treatments for both men and women.

Ms Dunne said the results would allow researchers to hone in on genes and gene families of interest, particularly those involved in drug resistance.

"The completion of the genome sequence by The Institute for Genomic Research (TIGR) and subsequent annotation of the genome database has opened many avenues of research by providing a searchable data set," Ms Dunne said.

"Drug resistance in many human pathogens is increasing. *T. vaginalis* is among these, with no alternative drugs approved to treat resistant infections.

"This is particularly an issue in developing countries, where the number of infected individuals is high and the access to public health services is low.

"Now that researchers have access to a complete genome dataset the search for alternative drug targets can really take-off."

Amazingly, the pesky parasite was found to have an exceptionally large collection of DNA, with the possibility of having more genes than humans.

But Ms Dunne said while the sequencing of the genome project has largely elevated awareness of *T. vaginalis* among researchers, public awareness remains low, especially in developing countries where it has the most impact.

"This is a problem as infection with *T. vaginalis* increases the transmission and acquisition of many other serious STIs, including HIV.

"Furthermore, prolonged infection with *T. vaginalis* associates with pre-term birth, low infant birth weight and some cervical cancers.

"Alarmingly, trichomoniasis is not considered a notifiable disease."

Routine gynaecological check-ups do not test for this particular STI and the infection does not require public health notification.

Because of this, and also due to the broad and non-specific nature of symptoms, which can range from severe to negligible depending on the individual, some people pass it on without knowing.

"Furthermore, the non-specific nature (or in some cases, absence) of trichomoniasis

symptoms often confuses it with other STIs, making the process of diagnosis itself, difficult," Ms Dunne said.

"Many infections remain undiagnosed as a result."

It is hoped that the results of the project will help research and improve treatments, in turn sponsoring awareness.

Ms Dunne's contribution to the project involved the identification and annotation of several large families of genes related to those involved in various mechanisms of antimicrobial resistance.

As a result of the genome being sequenced, she has since been able to localise specific genes of interest to the whole chromosome and begin the mapping process.

"Mapping the genome is the next step in the genome sequencing of *T. vaginalis* and will create a visual blueprint of the parasite, allowing researchers to see where their genes fit in to the big picture."

The results of the collaborative project have been published in the prestigious international journal SCIENCE.

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