

# The Australian Society for Microbiology



bringing Microbiologists together

NSW-ACT Branch

## Syntrophy

Volume 22 Issue 1 2021

### From the editor

By Jim Manos

Dear Members

Greetings from the Chair. We hope you will enjoy this first issue for 2021!

Our branch will be starting the year with the Nancy Millis Award Night on March 24, with abstracts due by March 15. More information is provided below. This event will be held via Zoom, but we hope that as the year progresses, we will have more face-to-face meetings, where members can not only hear the speaker, but socialize and discuss microbiology before or after the event.

Today's issue also contains an article by Lijuan Luo from Ruiting Lan's lab at UNSW on the epidemiology of *Salmonella enteritidis* elucidated by multilevel genome typing, demonstrating the versatility and utility of this typing method for surveillance of *S. enteritidis* outbreaks.

Also see below information on our partner organization JAMS who will be having their regular monthly seminar on the last Tuesday of March. These well attended seminars are always interesting!

Last but not least, the ASM education special interest group Edsig has launched their website. See below how to visit the site to join in the events planned and enjoy!

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Syntrophy is distributed via email to ASM members located in NSW and the ACT using details included on the ASM National Office Database.

Not yet a member? Join today!  
[www.theasm.org.au/membership](http://www.theasm.org.au/membership)

Submissions and enquiries can be directed to the Syntrophy Coordinator via the ASM NSW-ACT Branch Secretary.

Organisations with research opportunities, or companies seeking to fill positions are welcome to place an advertisement in an upcoming issue of Syntrophy. Please contact the Syntrophy Coordinator with your details for inclusion.

## Focus Article

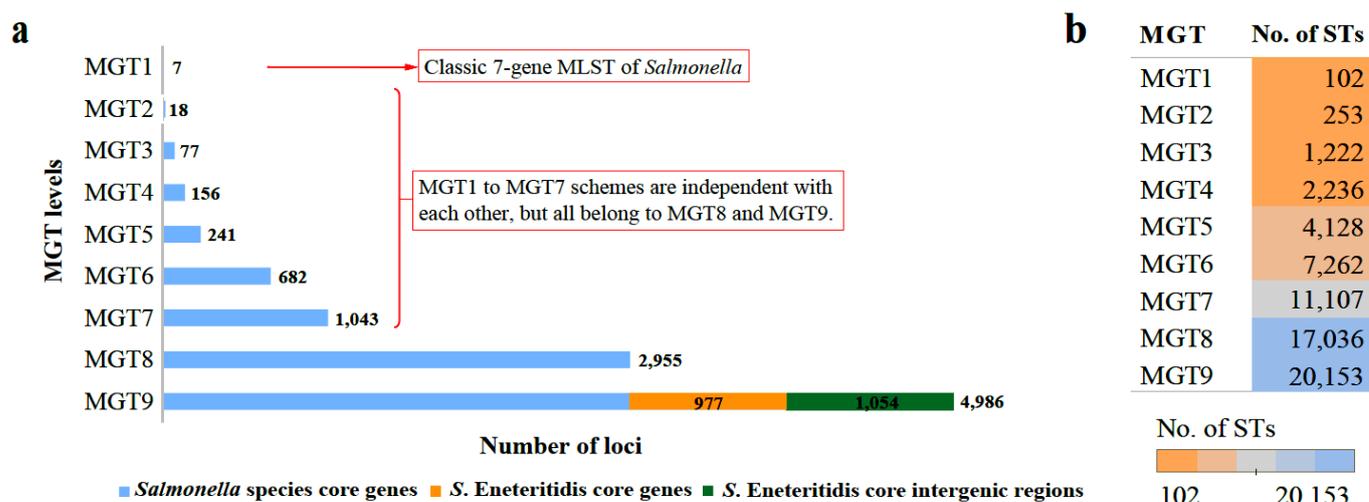
# Elucidation of global and local epidemiology of *Salmonella* Enteritidis through multilevel genome typing

Lijuan Luo

School of Biotechnology and Biomolecular Sciences, University of New South Wales.

Whole genome sequencing (WGS) has been adopted by public health laboratories for surveillance of many pathogens and offers the ultimate resolution for strain typing [1]. *Salmonella* enterica serovar Enteritidis is a major foodborne pathogen in many parts of the world. Some high-risk subtypes cause large scale outbreaks and invasive infections, making surveillance vitally important [2]. However, the use of WGS data for *S. Enteritidis* surveillance is not yet standardised and there is a lack of a stable and uniform nomenclature system to track these high-risk subtypes. My PhD project has developed a novel genome typing system, Multilevel Genome Typing (MGT) for *S. Enteritidis*; we have used this to elucidate the global epidemiological characteristics of *S. Enteritidis* in unprecedented detail [3, 4].

The MGT system was designed based on multi-locus sequence typing (MLST), a gene by gene comparison approach of strain typing, through comparison of allelic differences between isolates [3]. When one or more allelic differences are identified, a new sequence type (ST) is assigned. The more alleles compared, the higher the resolution of the MLST scheme. The MGT for *S. Enteritidis* includes multiple MLST schemes referred to as levels, with increasing resolution from MGT1 to MGT9. MGT1 is the classic 7 housekeeping gene MLST for *Salmonella* [5], while MGT9 includes 4986 loci belonging to the core genome of *S. Enteritidis* (Figure 1a). A total of 26,670 publicly available *S. Enteritidis* isolates from 86 countries over 101 years were analysed. For every isolate, sequence types (STs) were assigned at each MGT level. As the resolution of typing increased from MGT1 to MGT9, an increasing number of STs were assigned from MGT1 to MGT9. For example, at MGT2, the 26,670 isolates were subtyped into 252 STs, in contrast, MGT9 divided the isolates into 20,153 different STs (Figure 1b). The MGT scheme of *S. Enteritidis* is available through an online database that is publicly available for submission and analysis (<https://mgtdb.unsw.edu.au/enteritidis/>).



**Figure 1.** Makeup and assignments of each *S. enteritidis* MGT level. **a.** Number of loci included. The first eight levels are composed of *Salmonella* core genes, orthologous to those of the *S. Typhimurium* MGT scheme [3], except for one gene at MGT8 which was excluded due to duplication in *S. enteritidis*. The MGT9 scheme includes core genes of *S. Enteritidis* (those not belonging to *Salmonella* core in yellow) and core intergenic regions (green). The number behind or within each bar refers to the number of loci included. **b.** The number of sequence types (ST) assigned at each MGT level among the 26,670 genomes analysed. As MGT9 included 4986 loci with highest subtyping resolution, the 26,670 isolates were subtyped into 20,153 different ST types.

Different MGT levels were found to have different applications in long-term and short-term surveillance of *S. Enteritidis* [4]. A total of 10 main lineages were defined in the globally distributed *S. Enteritidis*, which can be represented by STs from MGT1 to MGT4. For example, MGT3-ST10 and MGT3-ST15 represent more than 90% of the two African lineages that cause invasive infections. At the MGT4 level, globally prevalent and regionally restricted STs were identified. For example, MGT4-ST99, ST136, ST135, ST171 and ST163 were the most prevalent STs in North America, while in Europe, MGT4-ST25, ST13, ST100 and ST31 were common. We also analysed drug resistance genes and resistance mutations. The overall antibiotic resistance rate was 9.4% and the multidrug resistance (MDR, defined as predicted resistance to 3 or more drug classes) rate was 3.8%. Eleven MDR associated STs defined at MGT3 to MGT6 levels were identified, revealing emergence and spread of MDR clones which can now be readily monitored using MGT. MGT9 offers the highest resolution and can be used for outbreak detection. We found STs that are associated with large scale outbreaks were more common in poultry associated lineage of *S. Enteritidis*. In summary, MGT provides a flexible, high resolution and stable genome typing tool for long term and short long surveillance and epidemiology of *S. Enteritidis* infections [4].

## References

1. Robilotti E, Kamboj M: Integration of whole-genome sequencing into infection control practices: the potential and the hurdles. *Journal of clinical microbiology*. 2015;53(4):1054-1055.
2. Feasey NA, Hadfield J, Keddy KH, Dallman TJ, Jacobs J, Deng X, Wigley P, Barquist L, Langridge GC, Feltwell T et al: Distinct *Salmonella* Enteritidis lineages associated with enterocolitis in high-income settings and invasive disease in low-income settings. *Nat Genet*. 2016;48(10):1211-1217.
3. Payne M, Kaur S, Wang Q, Hennessy D, Luo L, Octavia S, Tanaka MM, Sintchenko V, Lan R: Multilevel genome typing: genomics-guided scalable resolution typing of microbial pathogens. *Euro Surveill*. 2020;25(20):1900519.
4. Luo L, Payne M, Kaur S, Hu D, Cheney L, Octavia S, Wang Q, Tanaka MM, Sintchenko V, Lan R: Elucidation of global and local epidemiology of *Salmonella* Enteritidis through multilevel genome typing. *bioRxiv*. 2020:2020.2006.2030.169953.
5. Achtman M, Wain J, Weill FX, Nair S, Zhou Z, Sangal V, Krauland MG, Hale JL, Harbottle H, Uesbeck A et al: Multilocus sequence typing as a replacement for serotyping in *Salmonella enterica*. *PLoS Pathog*. 2012;8(6):e1002776.

## About the author

Lijuan Luo is a PhD candidate under the supervision of Professor Ruiting Lan and Doctor Michael Payne in School of Biotechnology and Biomolecular Sciences, University of New South Wales, Sydney, Australia. Her research focuses on establishment of genomic typing system and genomic epidemiological analysis of *Salmonella* Enteritidis.

## ASM NSW-ACT Branch Nancy Millis Student Award

**THE AWARD:** This award provides the opportunity for one student member from each ASM State Branch to attend and give an oral presentation at the 2021 ASM Annual Scientific Meeting (to be held in May 31-Jun 3 in Melbourne). All postgraduate microbiology students who have submitted or are intending to submit an abstract for the ASM Annual Scientific Meeting are invited to apply. **ALL finalists will receive a \$250 prize.**

### Each Award consists of:

- a return economy airfare
- full conference registration
- an allowance for accommodation (currently \$500)

### ELIGIBILITY:

Applicants must:

- be student members of the ASM or, if not currently a student member, applicants must be eligible for membership and must pay for such at the time of application for the Award.
- not have previously received an ASM Student Award

**APPLICATION:** Finalists for the Award will be selected on the basis of their abstract /presentation summary submitted for consideration to their ASM State Branch. Please submit an abstract by **COB March 15, 2021** (.doc or .docx file; 500 words) to:

Mohammad Hamidian [mohammad.hamidian@uts.edu.au](mailto:mohammad.hamidian@uts.edu.au)

All applications will be reviewed and applicants selected as finalists will be invited to present their work at the ASM Nancy Millis Student Award evening:

**When:** 6pm start; **Wednesday March 24, 2021**

**Where:** **ZOOM (TBA)**

The recipient of the Award will be selected on the basis of an oral presentation - 12 minutes plus 3 minutes question time, to be given at the ASM Student Award Evening of each ASM State Branch. The recipient of the Award will be selected and announced at the Award evening.

### CONDITIONS:

Within 5 days of receiving the Award from their State Branch the recipient must email their presentation abstract to the National Office for publication in the Program & Abstract Book. The recipient of the Award will be required to present their paper at the special ASM Student Award Session at the ASM Annual Scientific Meeting.

<https://www.theasm.org.au/asm-nancy-millis-student-award>

All Finalists will be required to write a brief 1-page report on their project (approx. 600 words) as requested for publication in the ASM NSW-ACT Branch newsletter 'Syntrophy'. Syntrophy reports to be submitted with supervisor's approval.



**JAMS seminars: last Tuesday of each month**  
**For details, join our mailing list:**

<http://jams.org.au/index.php/jams-sydney/>

**Or follow us on Twitter:**

<https://twitter.com/jamsorgau>



# \*\* ANNOUNCEMENT \*\*

## THE EDSIG WEBSITE IS LIVE

[www.theasm-edsig.org.au](http://www.theasm-edsig.org.au)

Check it out!!

ASM Education Special Interest Group

[About EdSIG](#) [Upcoming events](#)

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Contact Us

### Our Mission

The Education SIG is focused on advancing microbiology educators and fostering networks, collaborations and professional development opportunities for educators in microbiology and the related sciences

## \*\*\* Launched \*\*\*

### ASM Online community

This is an online space for members to interact with each other. Please start discussions and let's make this a wonderful collaborative experience.

Details on how to log in:

<https://www.theasm.org.au/news/2021/2/17/you-asm-online-community>

1/2/17/you-asm-online-community  
You can find your SIG by clicking on the 'Communities' button and selecting 'All Communities'. Scroll down to Education and click on Join.

## CONGRATULATIONS DR JACK WANG

Named University Teacher of the Year by Universities Australia.



## COMING SOON

### VIRTUAL EDUCON 2021



Contact

[megan.lloyd@uwa.edu.au](mailto:megan.lloyd@uwa.edu.au)  
with speaker ideas

## Key dates

Nancy Millis Award – application deadline: March 15

Nancy Millis Award – talks evening: March 24