Murdoch University | Harry Butler Institute

New APL funded project
Understanding the national status of swine dysentery & related diseases associated with other *Brachyspira* spp.

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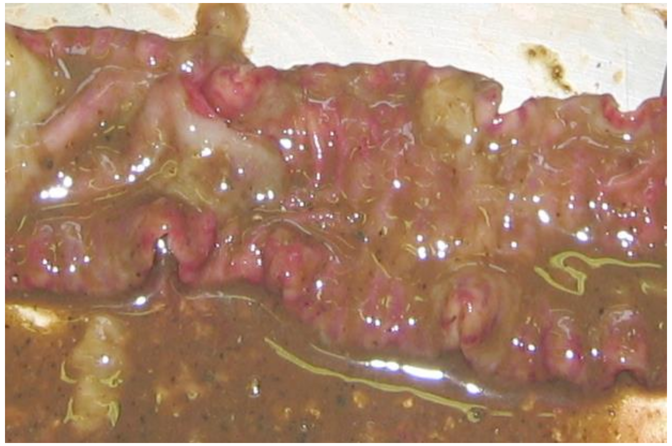
SWINE DYSENTERY (SD)

Classically = a severe mucohaemorrhagic colitis caused by infection with the intestinal spirochaete *Brachyspira hyodysenteriae*

- Mainly seen in growers and finishers

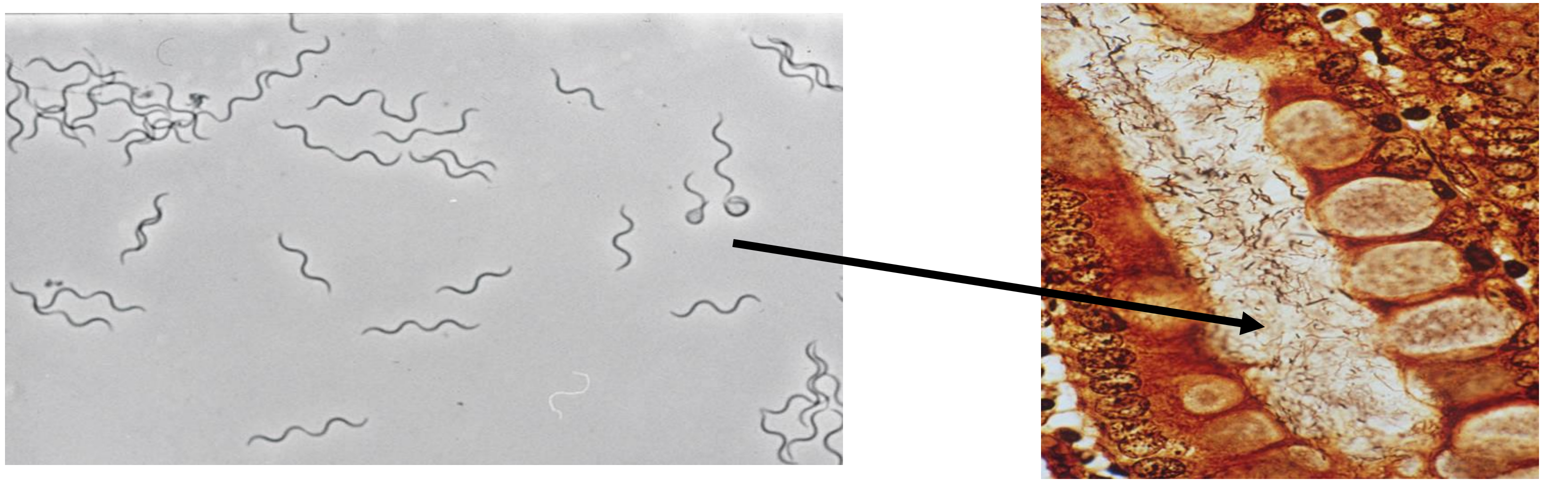


BUT
It is increasingly recognized that *B. hyodysenteriae* may be isolated from pigs in “healthy” herds




AND
two other *Brachyspira* spp. can cause SD

Brachyspira hyodysenteriae



An anaerobic intestinal spirochaete that colonises the large intestine of pigs, and occasionally other species

- Grows slowly (3+ days for growth to appear on plates)
- Requires selective agar to suppress other microorganisms
- Characteristically produces strong beta-haemolysis on blood agar

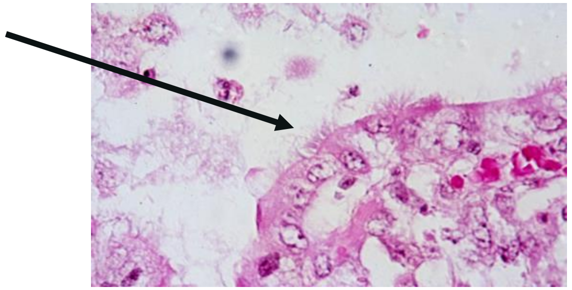
Haemolysis on blood agar

Strong haemolysis

Weak haemolysis

Brachyspira species

	β-haemolysis	Disease
B. hyodysenteriae	Strong	SD in Pigs; chickens
B. hampsonii	Strong	SD in Pigs
B. suanatina	Strong	SD in Pigs; mallards
B. pilosicoli	Weak	Intestinal spirochaetosis in Pigs, chickens, humans etc
B. murdochii	Weak	Pigs?
B. innocens	Weak	-
"*B. pulli*"	Weak	-
"*B. canis*"	Weak	-
B. alvinipulli	Weak	Chickens
B. aalborgi	Weak	Humans



The current study builds on our 2014-2016 Australian survey, funded by the Pork CRC

La T, Phillips ND and Hampson DJ (2016). An investigation into the etiological agents of swine dysentery in Australian pig herds. *PLoS ONE* 11(12): e0167424.

97 Australian herds of different <u>reported</u> health status sampled between June 2014 – June 2016

Samples (n=1103) mainly from healthy pigs obtained at the abattoir

- *B. hyodysenteriae* isolated from samples from 34 of the 97 herds (**35.1%**)

    - 25 herds reported as having a history of SD; 12 were culture positive (**48%**)

    - 48 herds reported as of uncertain health status; 8 were culture positive (**16.7%**)

    - 24 herds reported to be SD-free; 14 were culture positive (**58.3%**)

Findings from our 2014-2016 Australian survey: *B. hyodysenteriae* isolates

96 *B. hyodysenteriae* isolates recovered from the 34 infected herds (30 sequence types)

Multiple isolates recovered from 20 of the 34 herds

Nine of these 20 herds had between 2-4 different sequence types (STs) identified

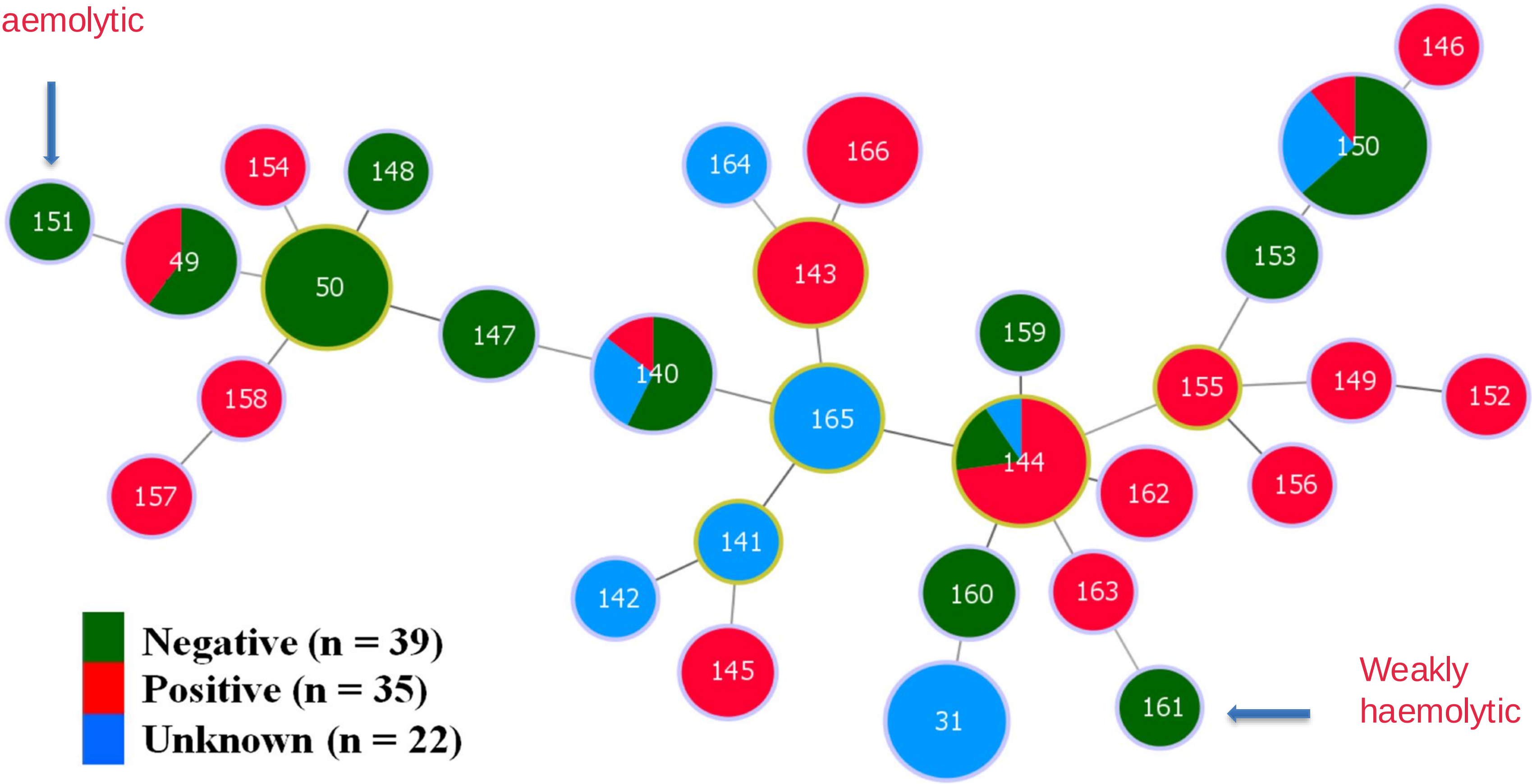
- ie multiple different strains present in these nine herd (including in four herds thought to be free of SD)

Four STs were shared by herds with different reported disease statuses

Two weakly haemolytic strains of *B. hyodysenteriae* identified

Minimum spanning tree (MST)

30 STs containing 96 *B. hyodysenteriae* isolates from 2014/16, from 34 herds with different reported health statuses

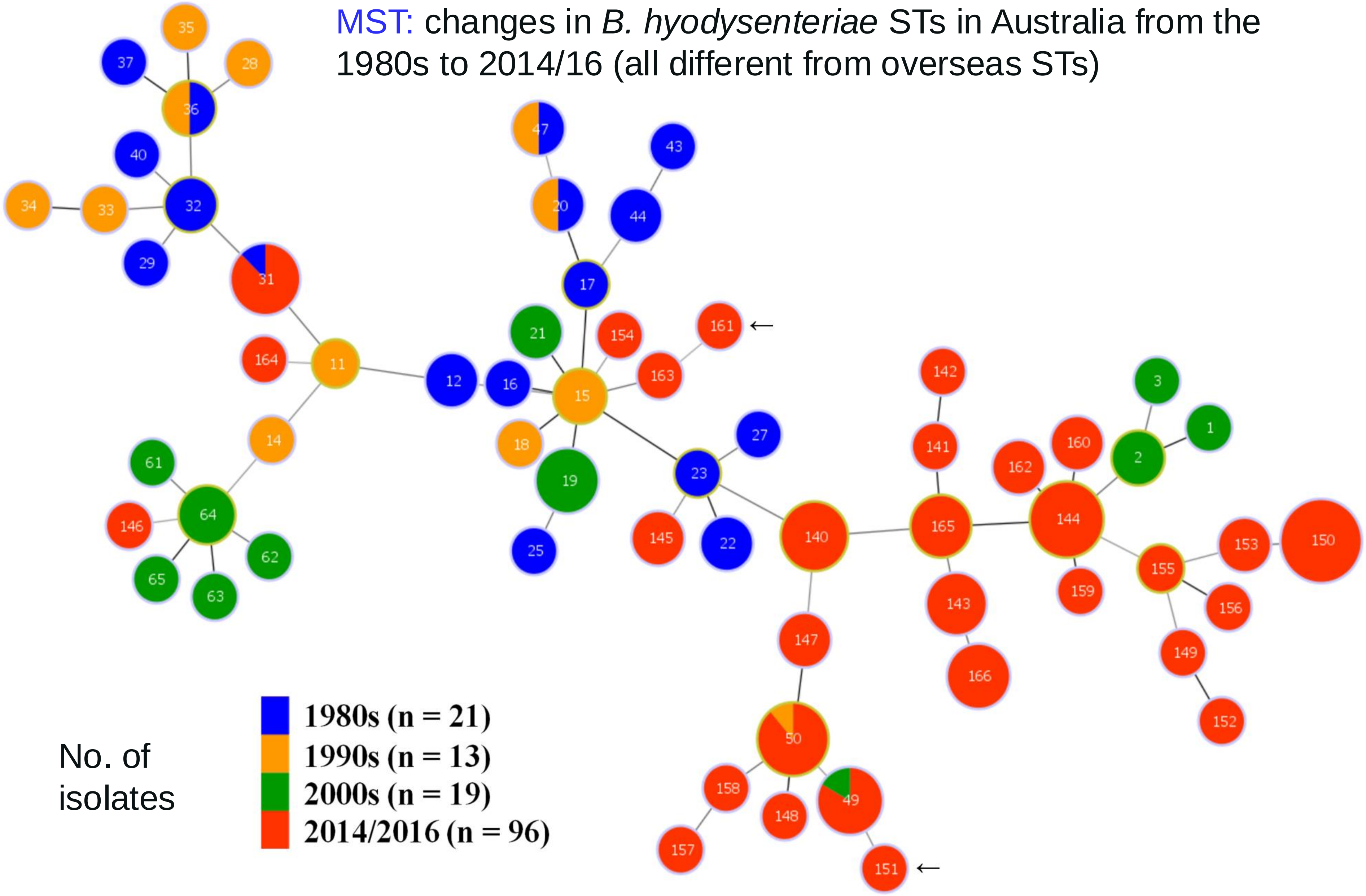


Weakly haemolytic

Weakly haemolytic

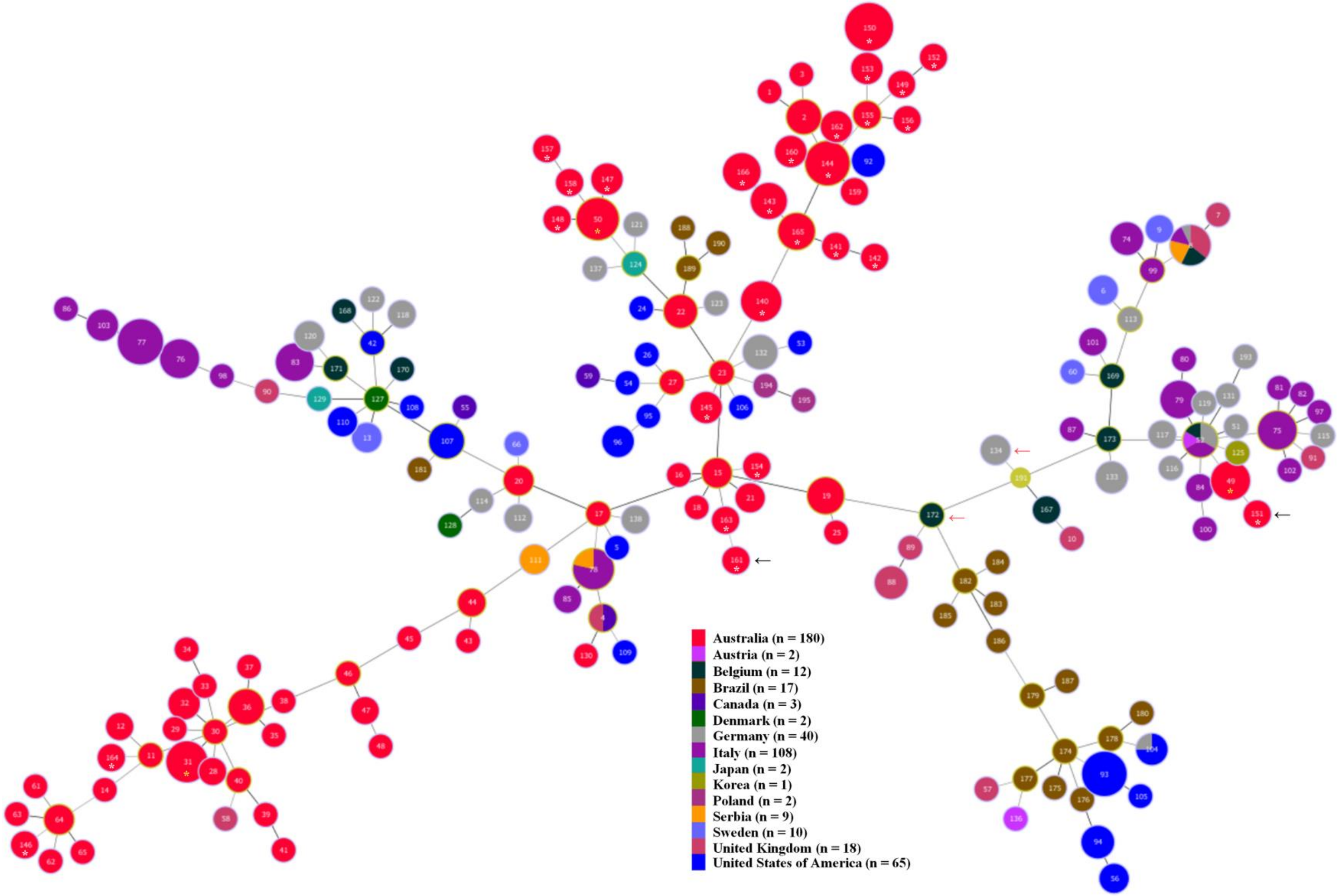
No. of isolates from herds of different status

MST: changes in *B. hyodysenteriae* STs in Australia from the 1980s to 2014/16 (all different from overseas STs)

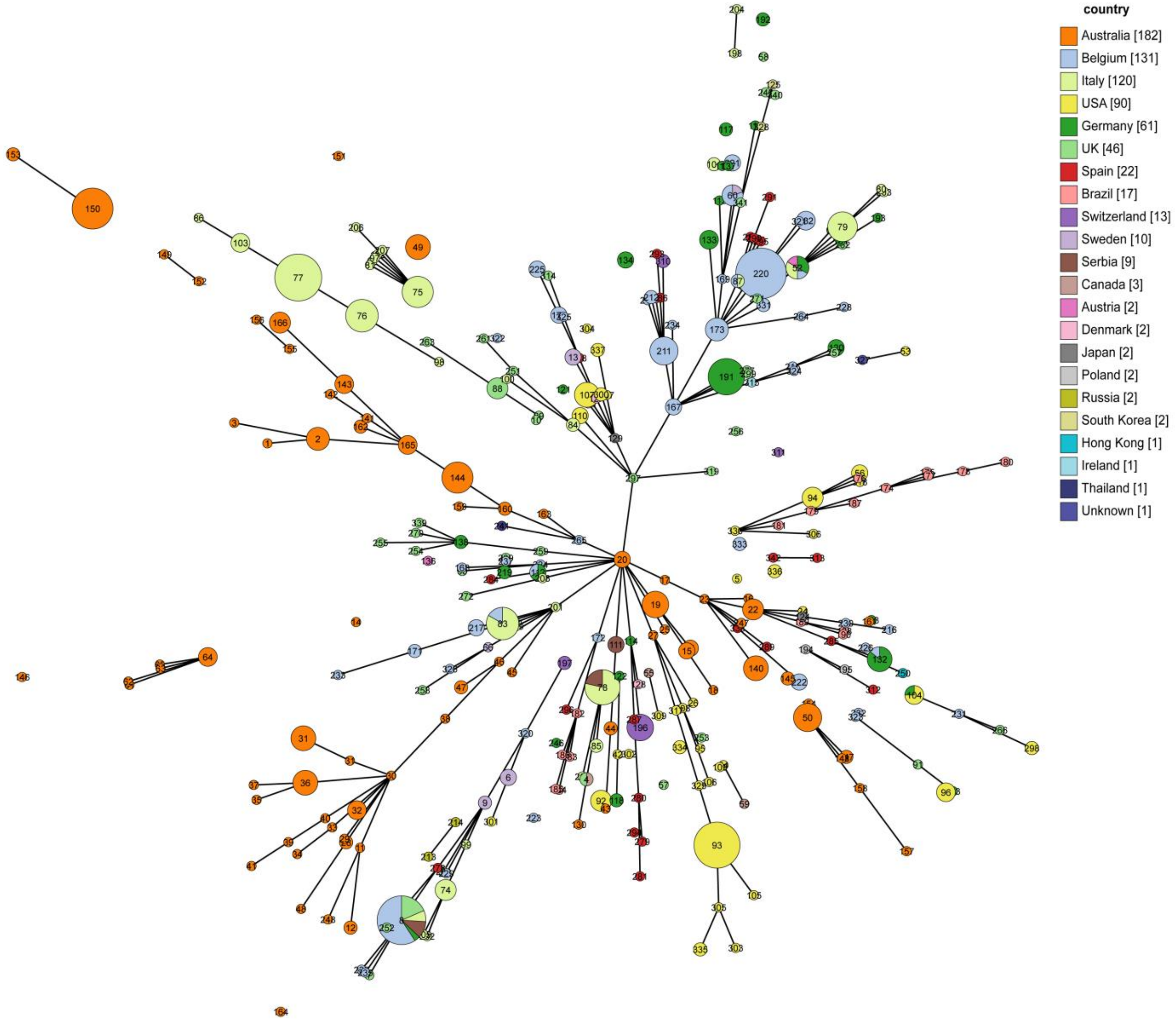


No. of isolates

MST: International STs of *B. hyodysenteriae* in 2016



MST: International STs of *B. hyodysenteriae* in 2024



The current study builds on our 2014-2016 Australian survey, with the following aims

- To determine the prevalence of Australian herds currently colonized with *B. hyodysenteriae* and other *Brachyspira* spp.
- To characterize the genetic and phenotypic makeup of current strains, including their distribution and susceptibility to antimicrobials and potential virulence factors (using whole genomic sequencing)
- To compare current strains with those from previous decades (giving insights into the spread and evolution of the pathogen) and from herds of different health statuses
- To assist individual herds to determine their current *Brachyspira* status, and to investigate whether strains in infected herds have changed since the last survey

The current study

- Aiming for 100 herds of different health status
- Ideally 30 faecal/colonic samples from unmedicated growers/finishers per herd (doesn’t need to be from diseased pigs but can accept samples from diseased pigs).
- *Brachyspira* spp. will be isolated, identified, and characterized by genomic sequencing and tested for antimicrobial susceptibility

Veterinarians and submitters – your participation is essential

- Please contact the lab before collecting/sending samples
- Record herd status (history of SD/uncertain/believed to be SD free)
- Answer survey questions about medication if possible
- The individual herd results will be returned to you (in confidence)
- An overview of results will be presented once the study is completed

Shipping

Dr Rebecca Abraham	**0413076742**
or Dr Kittitat Lugsomya ("Nick")	**0413347082**

- Ship samples at **4ºC overnight express** to:

  Attn: AMRID
  Loading Zone 5
  Murdoch University
  90 South Street
  Murdoch WA 6150

  Murdoch TNT account number 20118171