

Virulence potential of dairy cow isolates of *Listeria monocytogenes*

Aaron R. Gall¹, TuAnh N. Huynh¹

¹Department of Food Science, UW-Madison



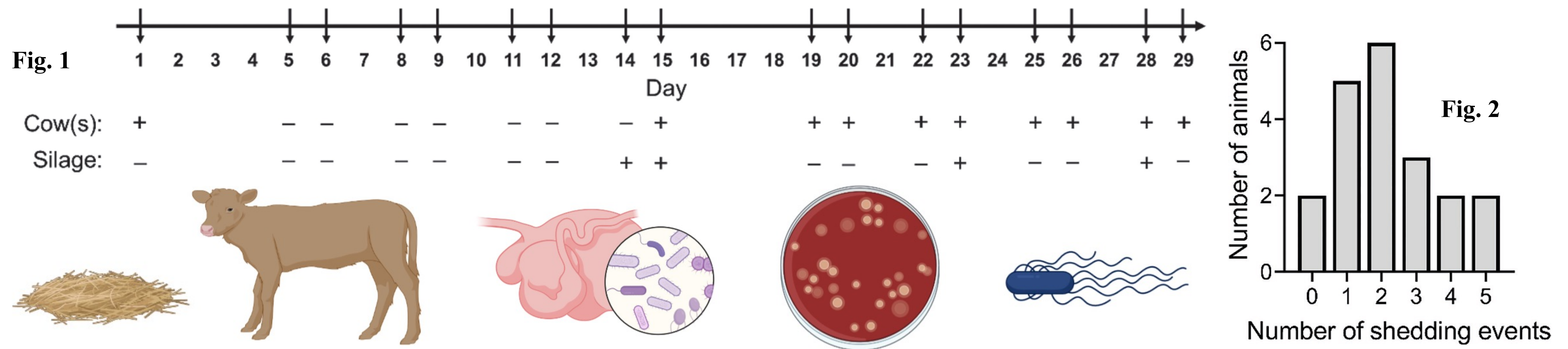
Listeria monocytogenes

A wide-spread intracellular bacterial parasite of animals and humans, *Listeria monocytogenes* spreads primarily through fecal shedding and ingestion of contaminated food products, such as raw and pasteurized milks and cheeses, and ready-to-eat (RTE) deli meats [1].

In a typical infection cycle, *L. monocytogenes* survives gut defenses, crosses the small intestine into the blood stream, colonizes the liver and spleen, and traverses the blood-brain or placental barrier, causing listeriosis in those susceptible (e.g. immunocompromised and the aged) or fetal abortions in those pregnant [2].

Dairy Cow Fecal Shedding of Listeria monocytogenes

In 2019, our lab identified more than 50 isolates of *L. monocytogenes* from a commercial dairy cow farm in Wisconsin over a 29-day period (**Figure 1**) [3]. Shedding of *L. monocytogenes* was prevalent, in which individual cows shed multiple times, with each shedding event lasting consecutive days (**Figure 2**).



Genetic Diversity and Antimicrobial Resistance of Fecal Isolates

Our dairy cow isolates of *L. monocytogenes* exhibited genetic diversity, with representatives of the more frequent food-borne serotype 1/2a and human epidemic serotype 4b (**Figure 3**), and increased resistance against veterinary and clinically used antibiotics for the treatment of listeriosis (**Figure 4**).

Serotype	No.	%
1/2a, 1/2b, or 1/2c	16	36.3
4a	18	40.9
4b	5	11.4
4c	5	11.4

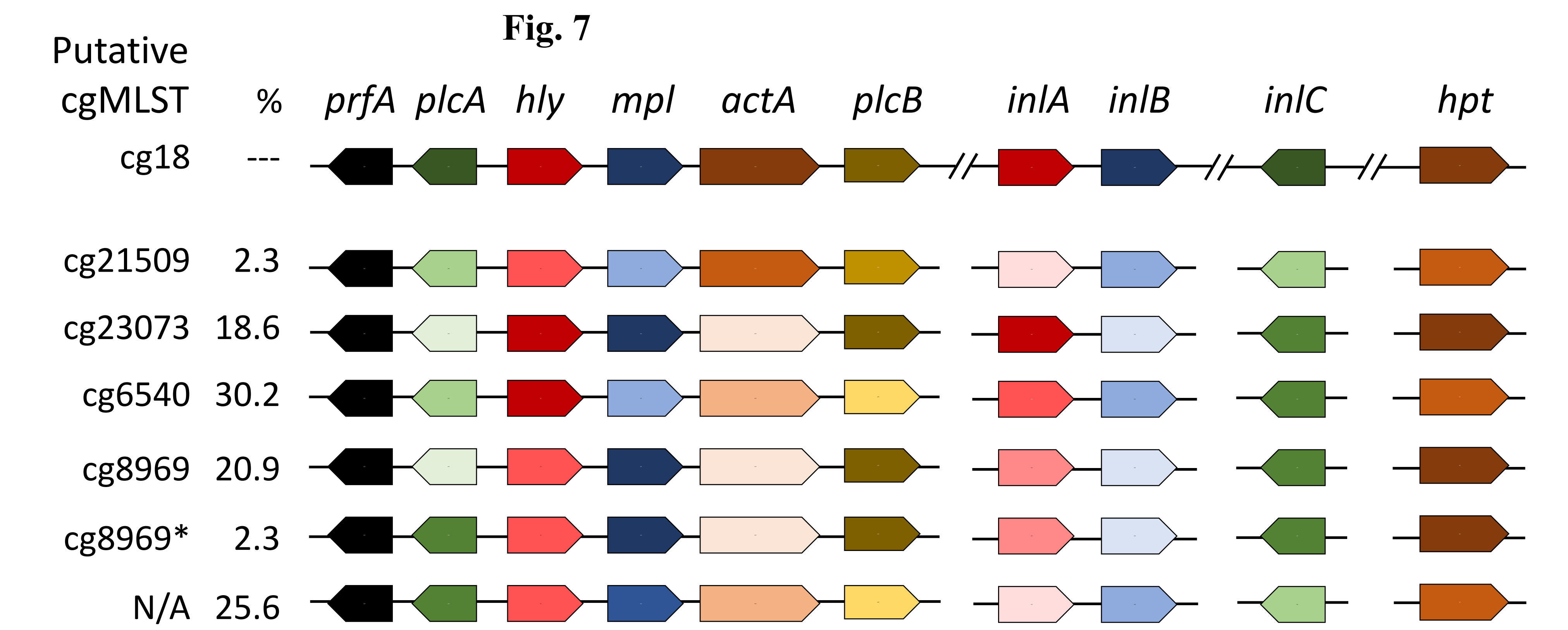
Fig. 3

Antibiotic	Clinical breakpoint (µg/mL)	Resistant isolates (no.)
Ampicillin	1	37
Gentamicin	1	9
TMP/SMZ (1:19)	0.06	2

Fig. 4

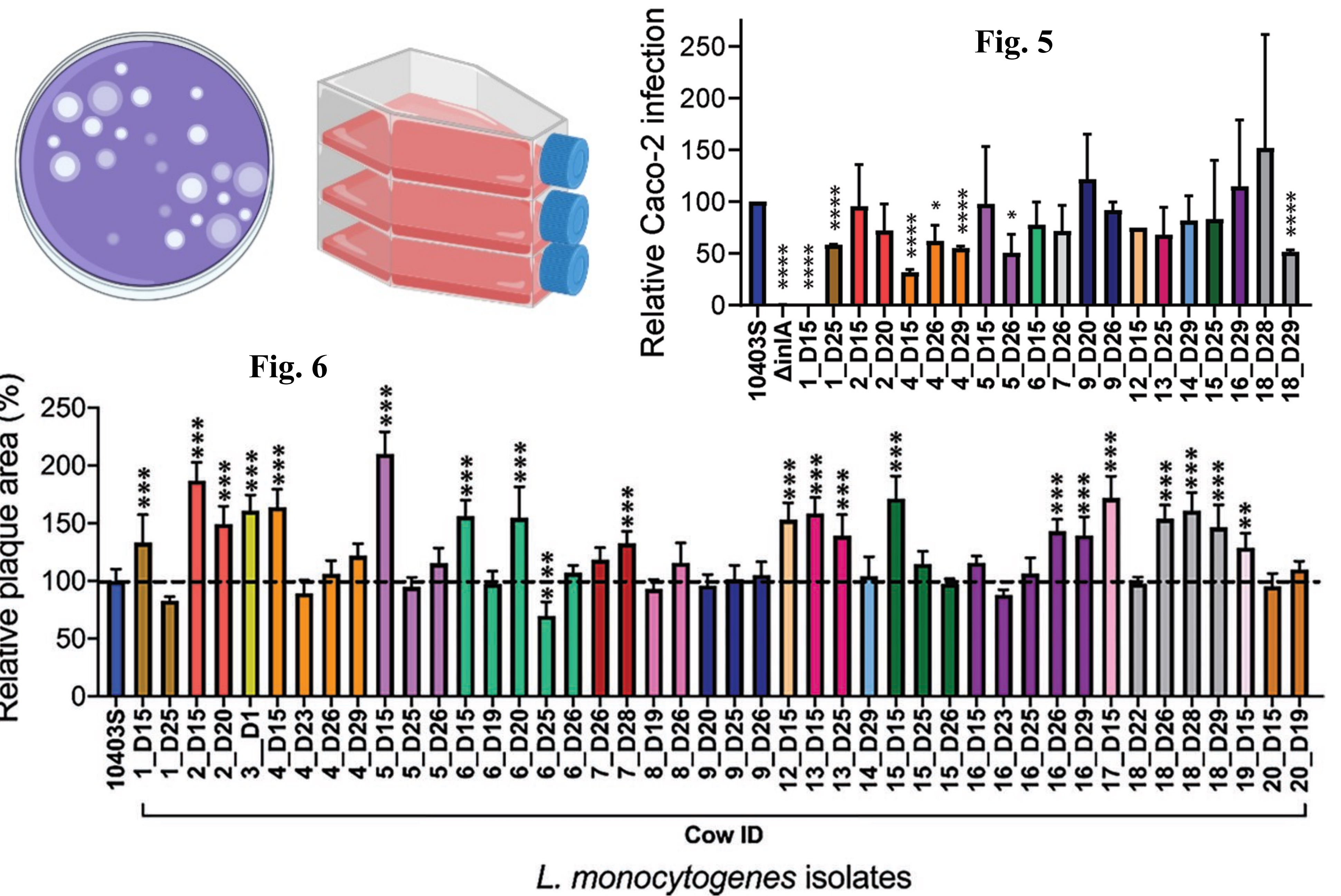
Virulence Factor Diversity of Fecal Isolates

We investigated the genetic determinants that might allow this zoonotic pathogen to colonize and disseminate from the cow GI tract to cause disease by analyzing whole genome sequence (WGS) data [5]. Putative core genome multi-locus sequence typing (cgMLST) of the *L. monocytogenes* isolates [6] revealed at least six different cgMLST groups, all of which contained variable amino acid sequences of well-known virulence factors of the master regulator PrfA regulon, compared to 10403S (**Figure 7**).



Pathogenicity of Fecal Isolates

A subset of *L. monocytogenes* isolates exhibited equal or enhanced pathogenicity against the mammalian cell lines [4], Caco-2 epithelial cells for human colon invasion (**Figure 5**) and mouse L2 fibroblasts for animal cell-to-cell spread (**Figure 6**), compared to the *L. monocytogenes* reference strain 10403S, signifying a subclass of hyper-virulence serotypes.



References

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