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An integrated approach to determine the clade-specific signatures of invasive *Salmonella* Enteritidis

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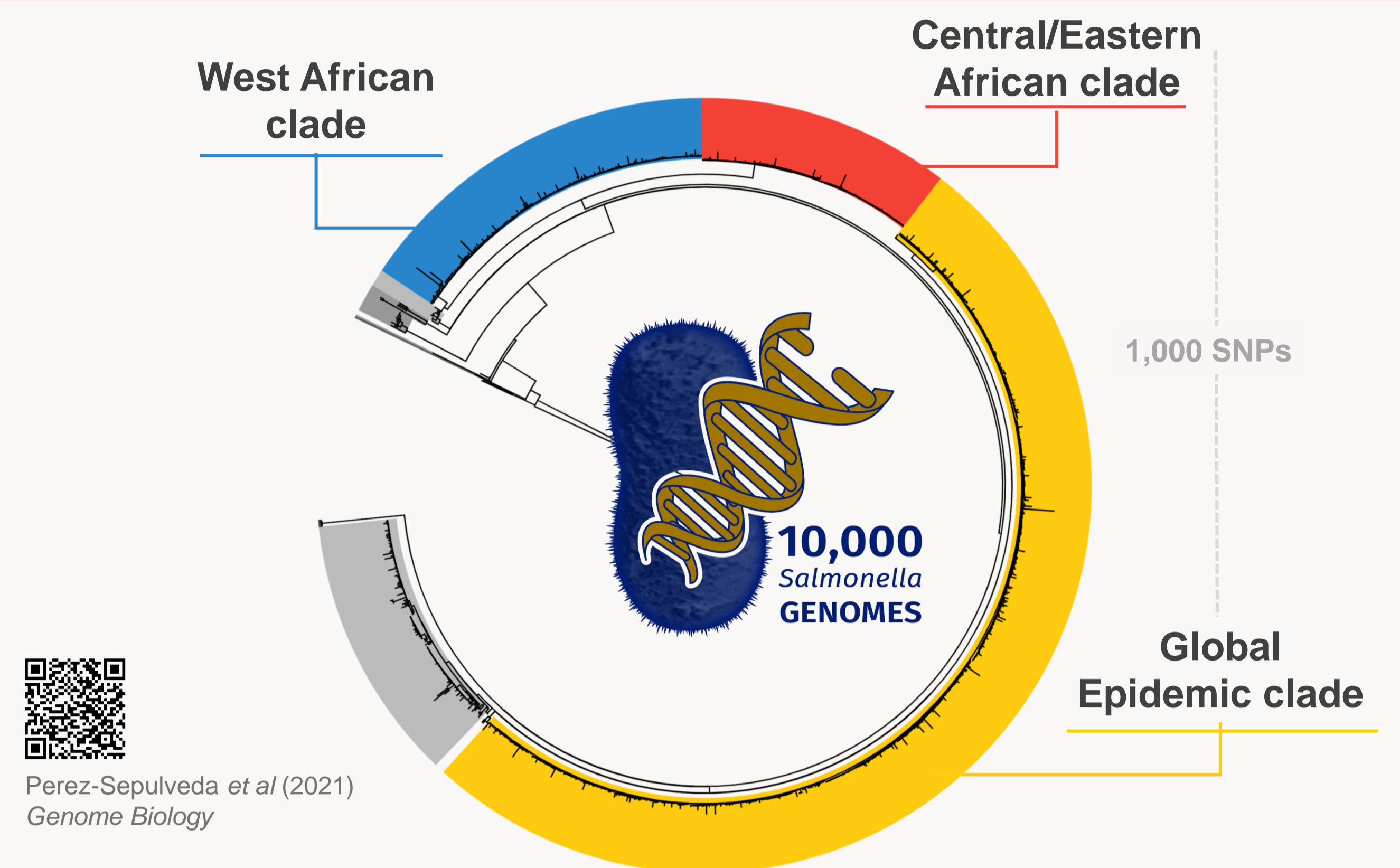
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Background

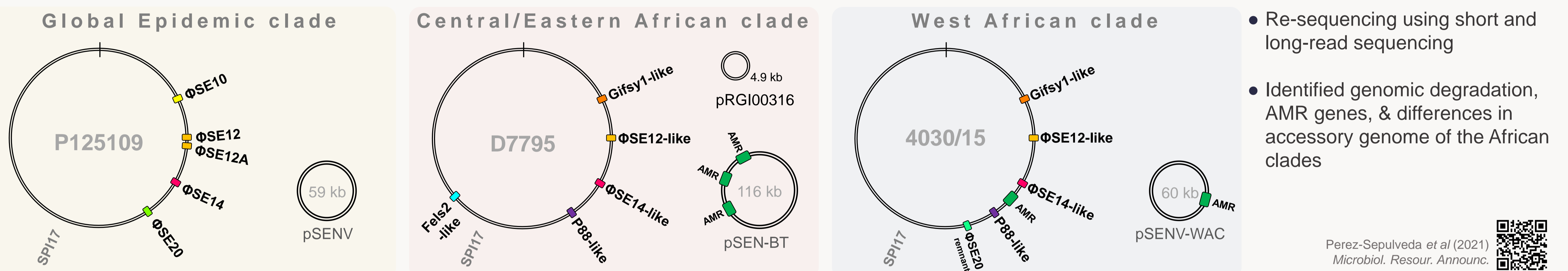
- Nontyphoidal *Salmonella* (NTS) has generally been associated with gastroenteritis in humans
- New lineages of invasive NTS (iNTS) serovars Typhimurium and Enteritidis are responsible for about 77,000 deaths per year worldwide, mostly in sub-Saharan Africa
- Research has mainly focused on *S. Typhimurium* ST313 lineages
- S. Enteritidis* is the other leading cause of iNTS disease in sub-Saharan Africa. Unlike *S. Typhimurium*, *S. Enteritidis* clades do not belong to a distinct sequence type, and little is known about their precise characteristics

We used a combination of comparative genomics, functional transcriptomics & phenotypic characterisation to investigate virulence determinants of emerging African *S. Enteritidis* clades

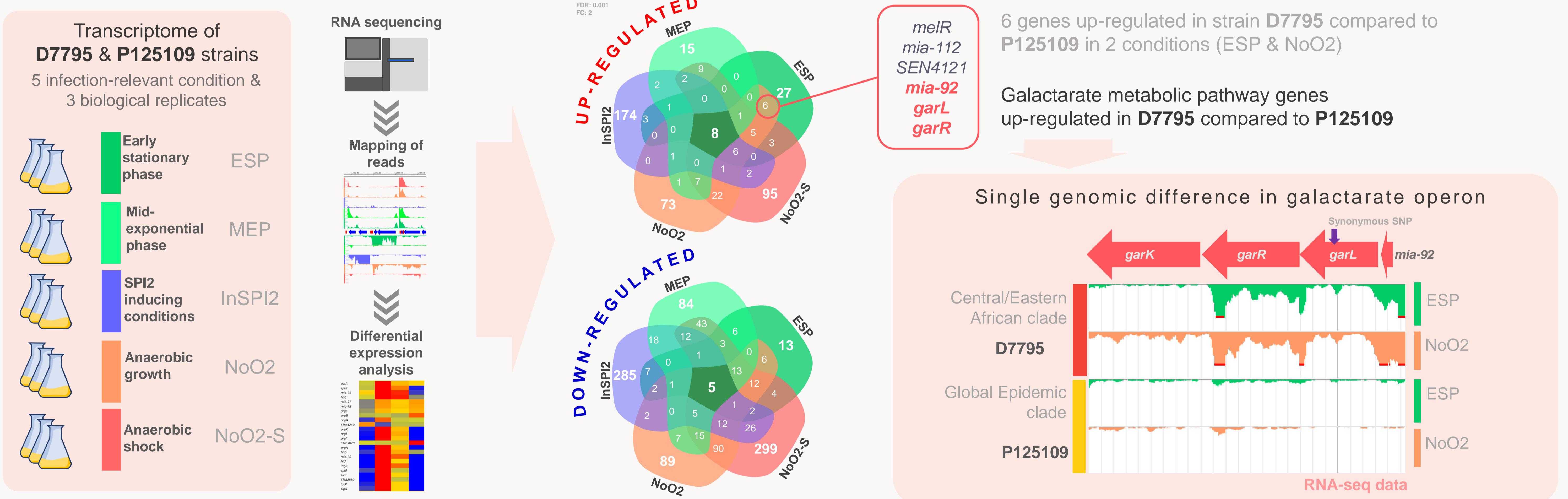
The global population structure of *Salmonella* Enteritidis



Understanding the chromosome & accessory genome of *Salmonella* Enteritidis

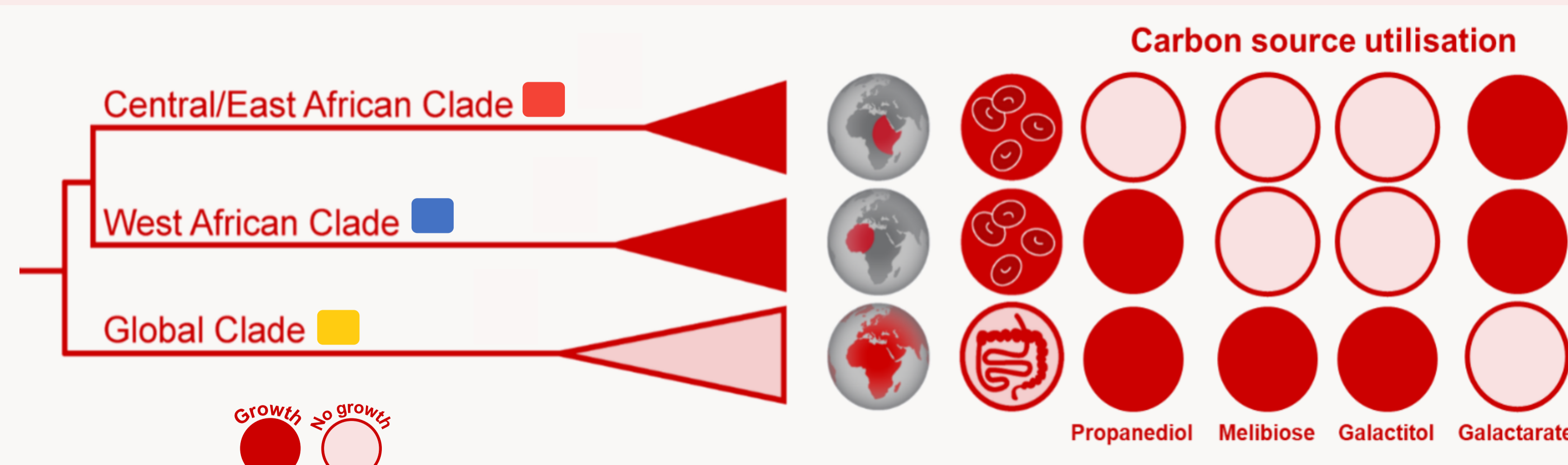


Functional transcriptomics of *Salmonella* Enteritidis Central/Eastern African & Global Epidemic clade representatives



Clade-specific utilisation of carbon sources by *Salmonella* Enteritidis isolates

- Phenotypic characterisation of carbon utilisation of 149 strains from 3 clades, tested in minimal media with 28 different carbon sources
- Specific carbon utilisation could be associated to gastrointestinal colonisation & intra-macrophage replication



TAKE-HOME MESSAGE

Identification of key metabolic defects in invasive *Salmonella* Enteritidis relied on an integrated approach