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Towards an integrated approach for the annotation of ICEs and IMEs in bacterial genomes

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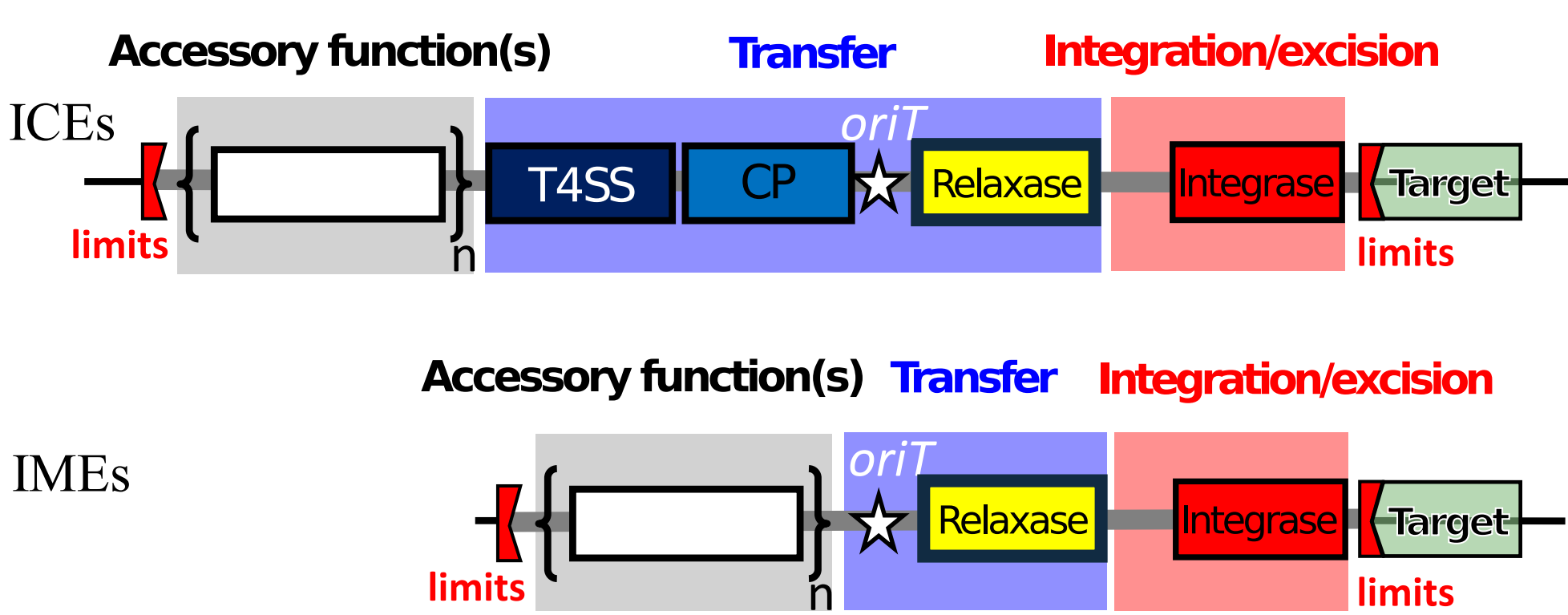
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Abstract

- Integrative Conjugative Elements (ICEs) are mobile genetic elements (MGE) that are **integrated in bacterial chromosomes** which encode their **own transfer by conjugation**.
- Integrative Mobilizable Elements (IMEs) are another type of bacterial integrated MGE, they lack a full conjugation system and **hijack co-resident conjugative elements** to promote their own transfer.
- ICEs and IMEs are poorly known and annotated but **play a key role in bacterial genome evolution** and the very few systematic investigations of these MGEs in bacterial genomes suggest that they have a **very high prevalence**.
- **Dedicated bioinformatics approaches are needed** for their identification and precise delineation.

In this poster, we present the first results from the comparison of the two currently existing strategies for the detection and delineation of ICEs: "ICE Finder" strategy^a and "CONJscan" strategy^b

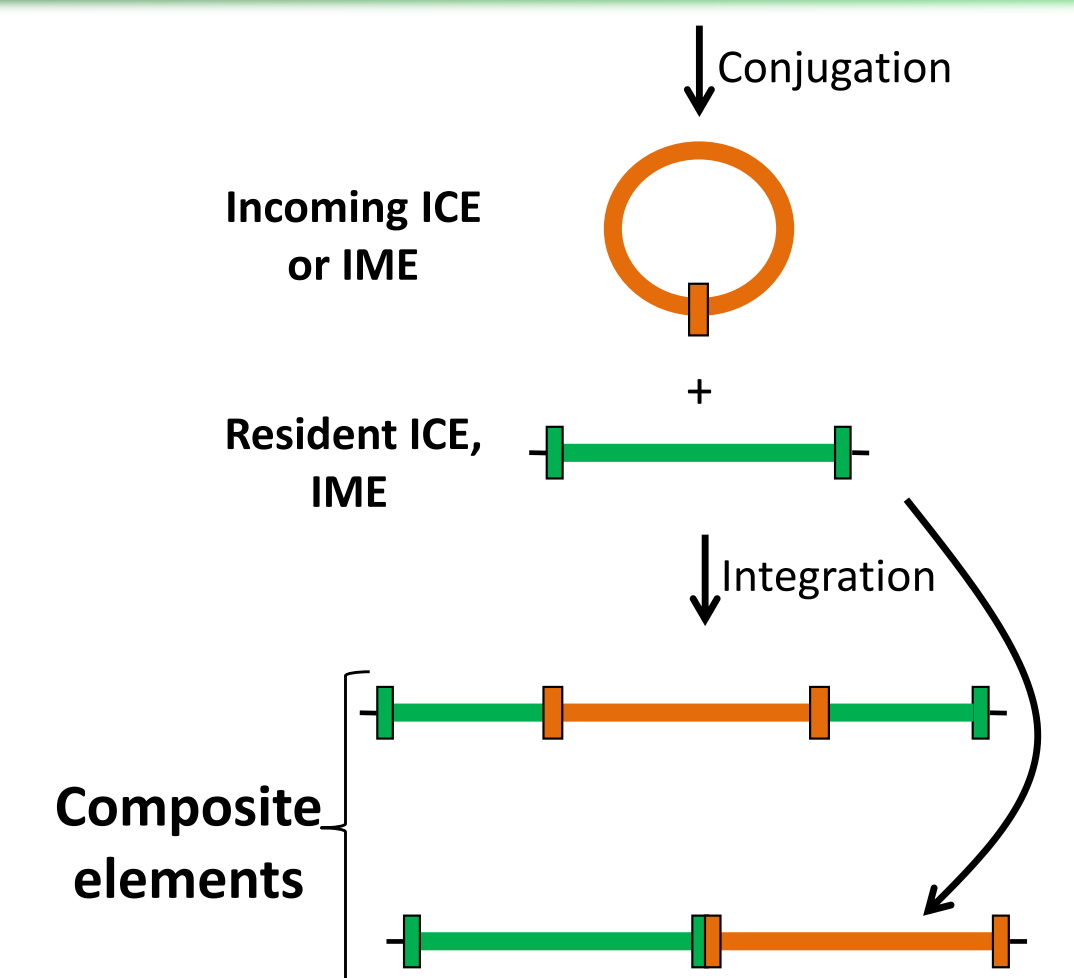
Modular structure



- Genes involved in the same biological function are grouped into modules
- ICE Finder searches 3 genes of the **transfer module** and 1 gene of the **integration module**
- CONJscan searches up to 6 genes of the **transfer module** and **don't search the integration module**

"ICE Finder"	Comparison of strategies	"CONJscan"
Detection		
✓ automatic	Transfer module	automatic ✓
✓ automatic	Integration module	don't search ✗
✓ manual	Target gene	don't search ✗
Delineation		
✓ manual	Simple element	automatic ✓
✓ manual	Composite element	no ✗
Streptococci only	Organism	All bacteria
1	Genomes	at least 4

Composite elements



Many composite elements result from the insertion of an incoming element into another or into one of its ends

"ICE Finder" strategy

- **Automatic** detection of "signature" proteins of the **transfer** and **integration** modules using **BlastP**. A **manually curated database** of known elements in **streptococci**^a is used.
- **Manually annotate and delineate simple and composite elements** at the **nucleotide level** through the research of the **target gene**.
- In many cases, the target gene contains one of the definite boundaries of the element.

"CONJscan" strategy

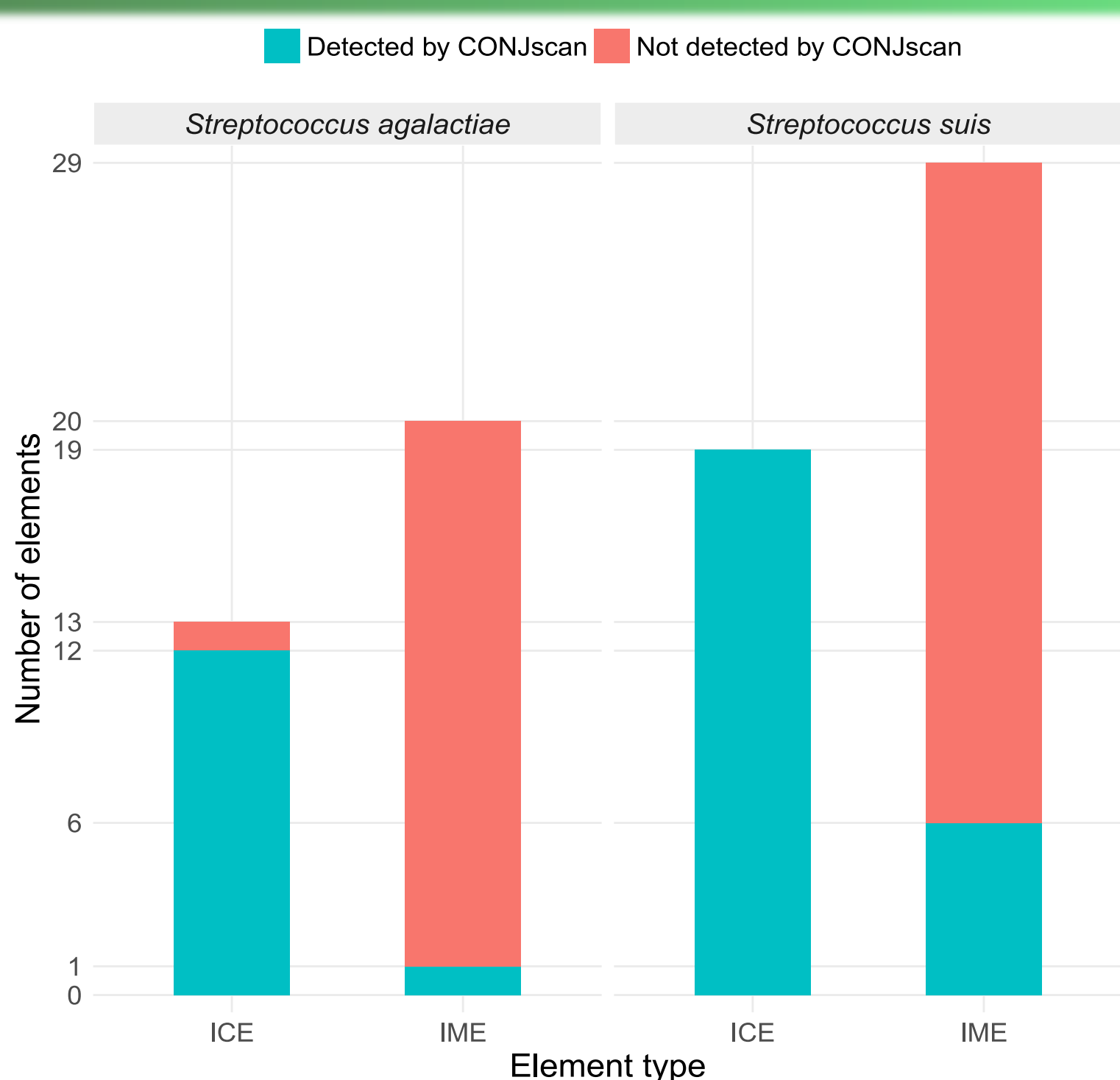
- It is a pipeline that delineates **ICEs only** in **all bacterial genomes** by using the **core genes** that surrounds them^{b,c}.
- This procedure is based on the detection of **one module only (transfer module)** using the CONJscan module of MacSyFinder software^{d,e}.
- It needs **at least 4 different closely-related** genomes to enable ICE annotation.

Comparison design

Results obtained with "ICE Finder" strategy are the reference

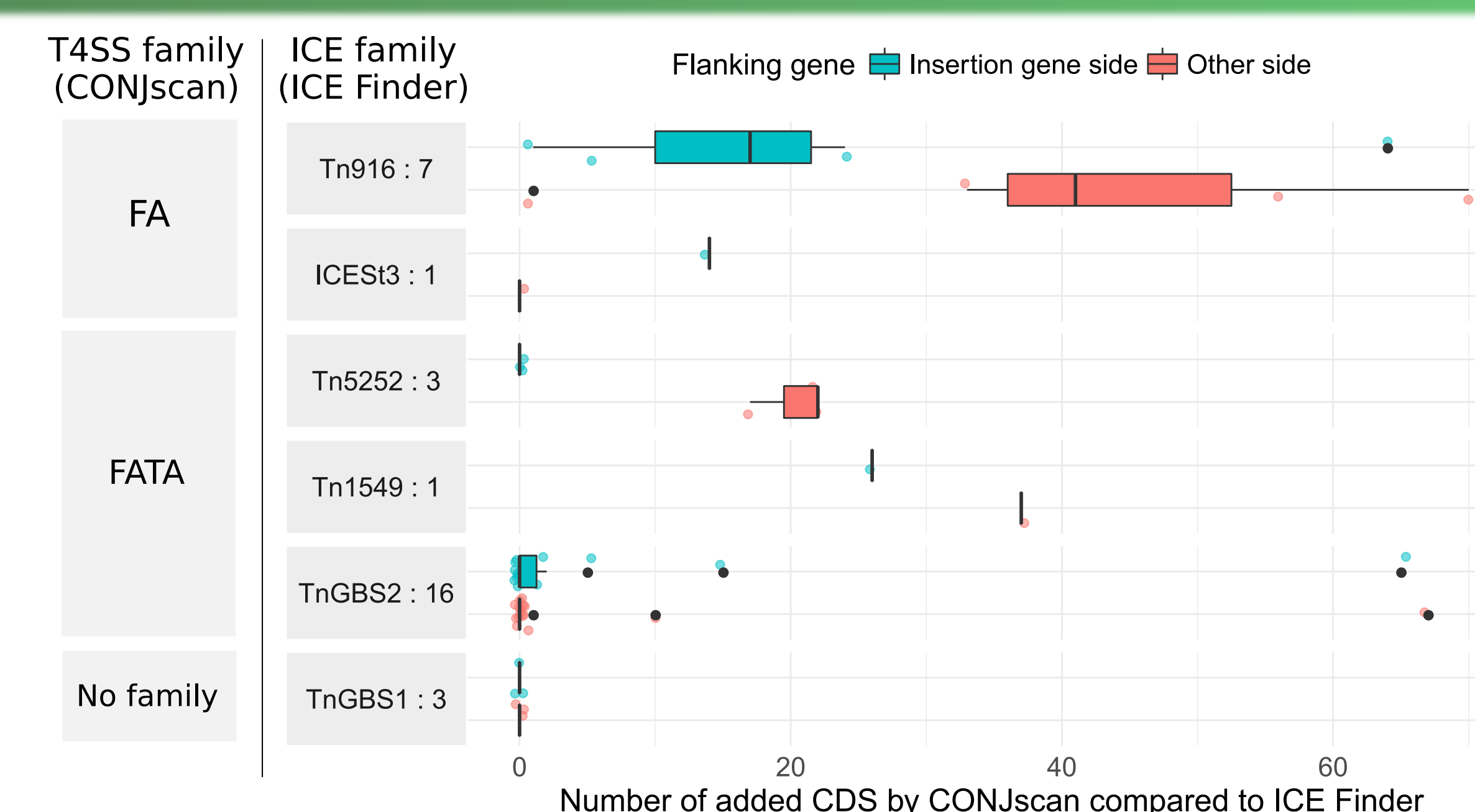
- **Dataset:** 15 genomes of *Streptococcus suis* and 7 genomes of *Streptococcus agalactiae*
- **Detection of transfer module by "CONJscan" strategy is assessed:** Is T4SS families of CONJscan consistent with ICE families of ICE Finder?
- **Is delineation of ICEs with "CONJscan" strategy and "ICE Finder" strategy similar?**

Detection of the transfer module



- ICE Finder detects the transfer module of all known ICEs and IMEs of *Streptococci*.
- CONJscan detects the transfer module of **most ICEs and of some IMEs**. It **does not have dedicated method for IME detection**.

Delineation results: CONJscan compared to ICE Finder



- ICE Finder delineates ICEs at the **nucleotide level**.
- CONJscan delineates **automatically** ICEs at the **gene level**.
- CONJscan **cannot delineate an element within another element and frequently failed to delineate elements that are integrated in tandem**.
- CONJscan **cannot delineate IMEs**.

Integration module and target gene

- "CONJscan" strategy cannot find the target gene because dedicated research of the insertion module is lacking.
- Unlike CONJscan, "ICE Finder" strategy search specifically the integration module (by BlastP of the integrase protein).

Conclusion

- CONJscan has a **more specific definition of the T4SS**.
- CONJscan does not specifically detect the integration module and does not detect most of transfer module from IMEs in *Streptococci*.
- Boundaries obtained with "CONJscan" strategy are not as precise as the ones obtained with "ICE Finder" strategy. But CONJscan always delineate elements with transfer module.

New strategy proposed:

- 1) Detection of **transfer module AND integration module** with MacSyFinder^d:
Development of a **mixed model "CONJscan + Integrase"** including more HMM profiles of transfer protein (of IMEs) that are **not presently searched by CONJscan**.
- 2) Get **first approximate delineation** with "CONJscan" strategy.
- 3) **Refine delineation** with the "ICE Finder" strategy.

References

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