

Iron uptake in *Neisseria meningitidis* during infection may be involved in the duality between carriage and invasiveness

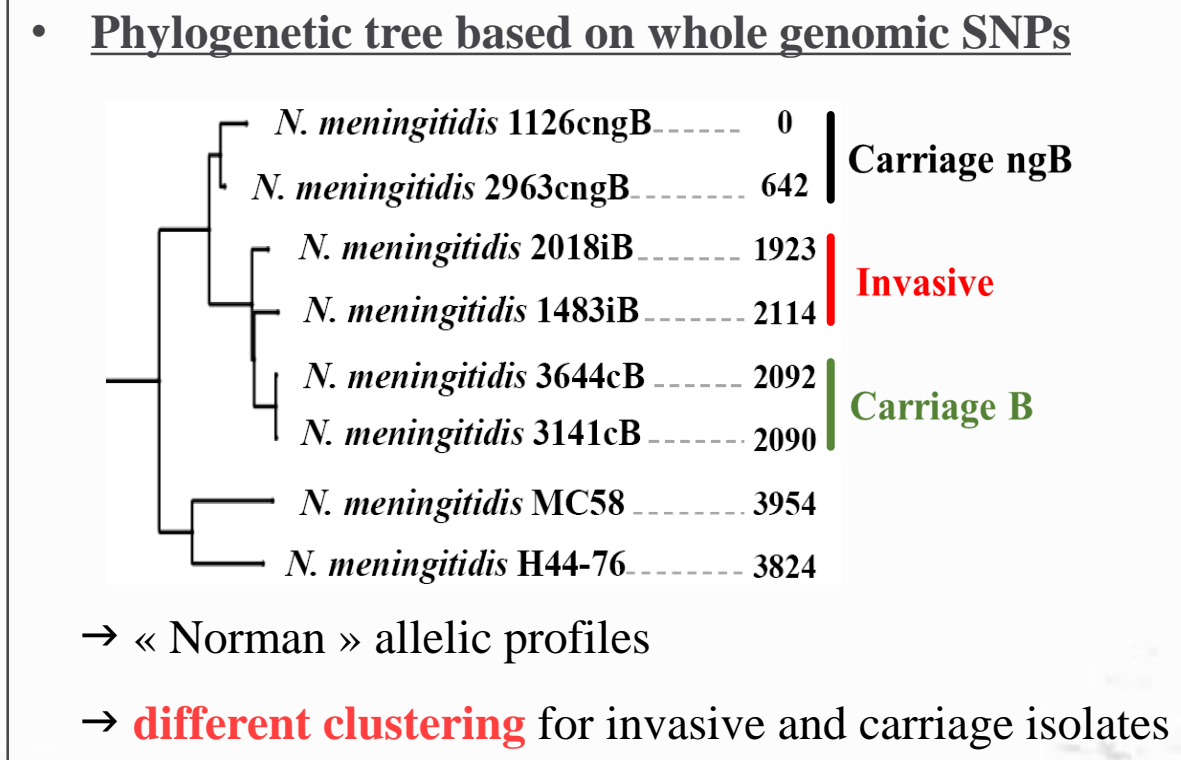
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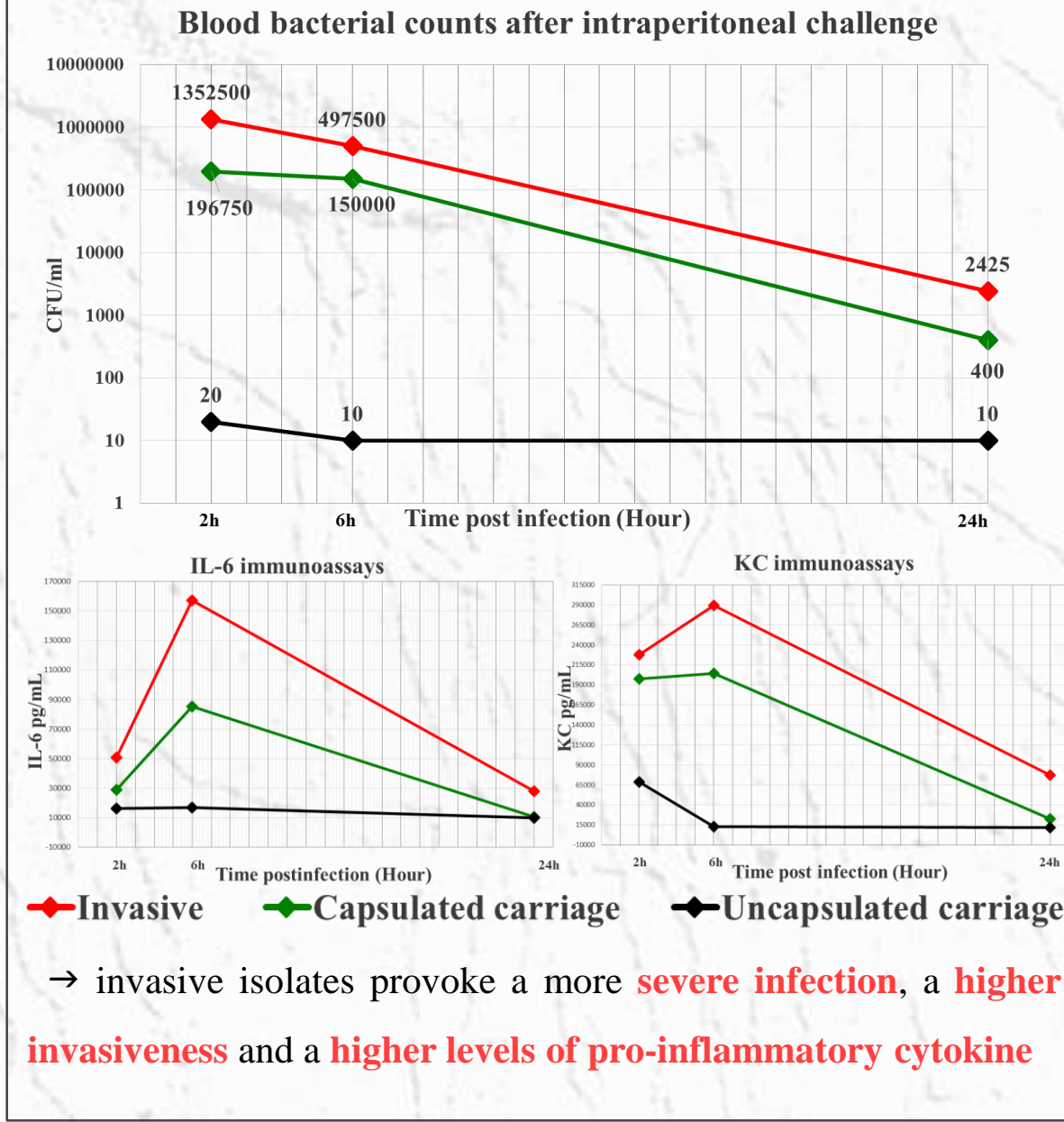
Background:
 During Nm clonal outbreaks, isolates apparently identical by conventional typing methods are founded from diseased subjects and asymptomatic carriers. The aim of this study was to detect potential determinants that can be involved in this differential behaviors of meningococcal isolates.

Methods:
 Invasive and carriage isolates previously collected during a French Nm outbreak were analysed. All belonged to the B:14:P1.7,16:F3-3:cc32. Six isolates; **2 invasive**, **2 capsulated carriage** strains (B:14:P1.7,16/ST-32) and **2 uncapsulated carriage** (NG:14:P1.7,16/ST-32) were selected. All this six isolates were compared by analysis of their whole genome profile (by Illumina® Next-Generation DNA Sequencing and PubMLST comparison) as well as the expression of the human transferrin gene (*htf*) in mice.

I. Genomic comparison and experimental infections:

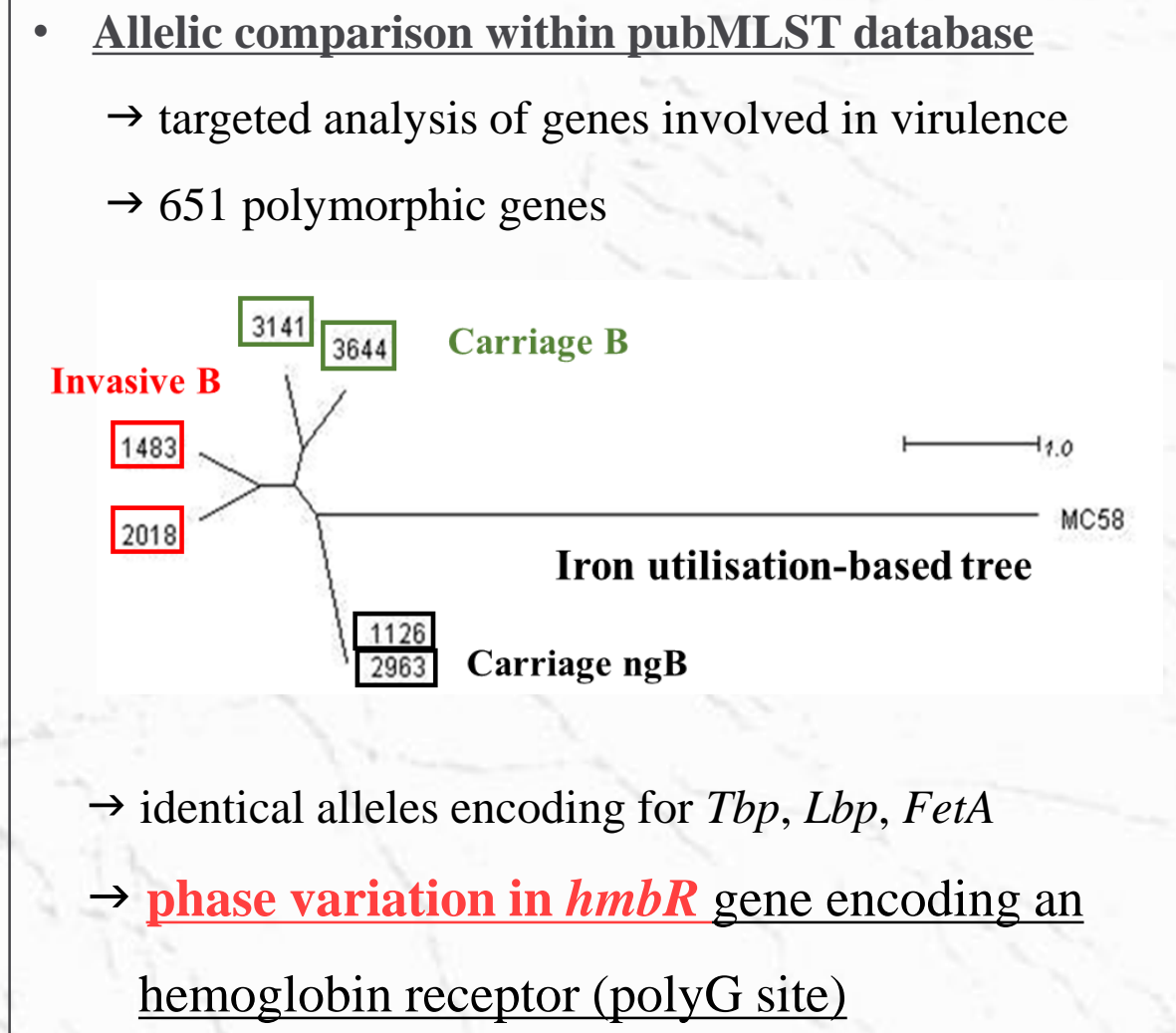


Transgenic mice (*htf*) and *in vivo* challenge



Conclusion: Whole Genome Sequencing combined with transgenic animal model allowed detecting different gene expression between invasive and carriage Nm isolates apparently identical, based on regular typing. Iron acquisition from several sources during infection seems to be crucial for Nm invasiveness and impacts on the duality of Nm between carriage and disease.

II. Allelic profiling and *ex vivo* experiments:

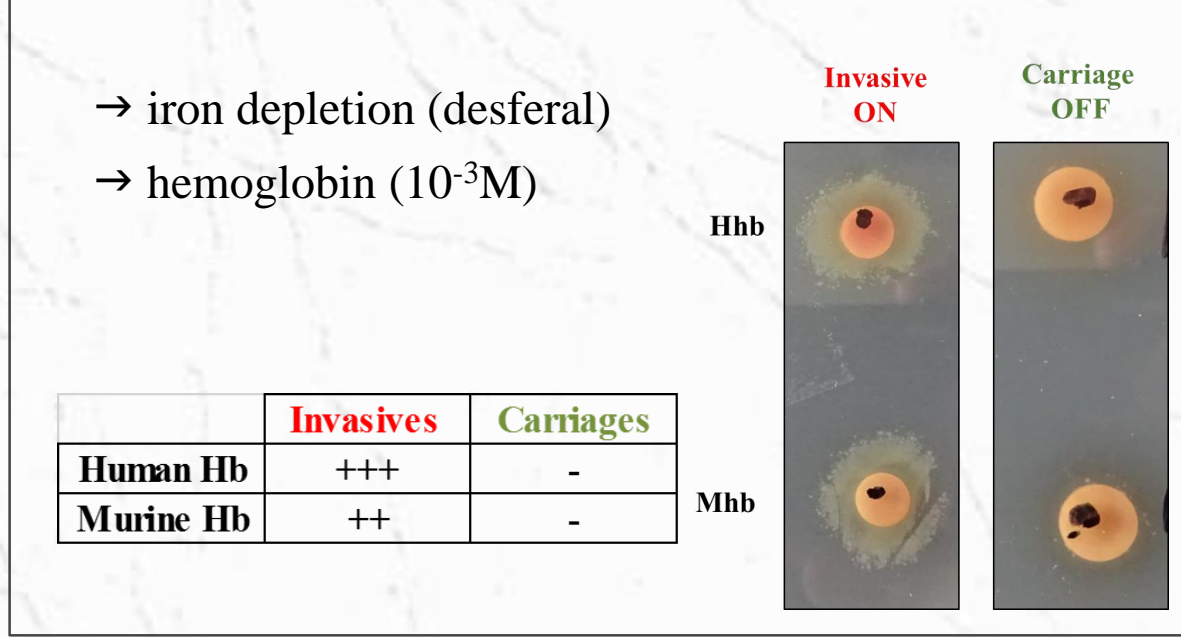


***hmbR*: Off in carriage isolates**
***hmbR*: On in invasive isolates**

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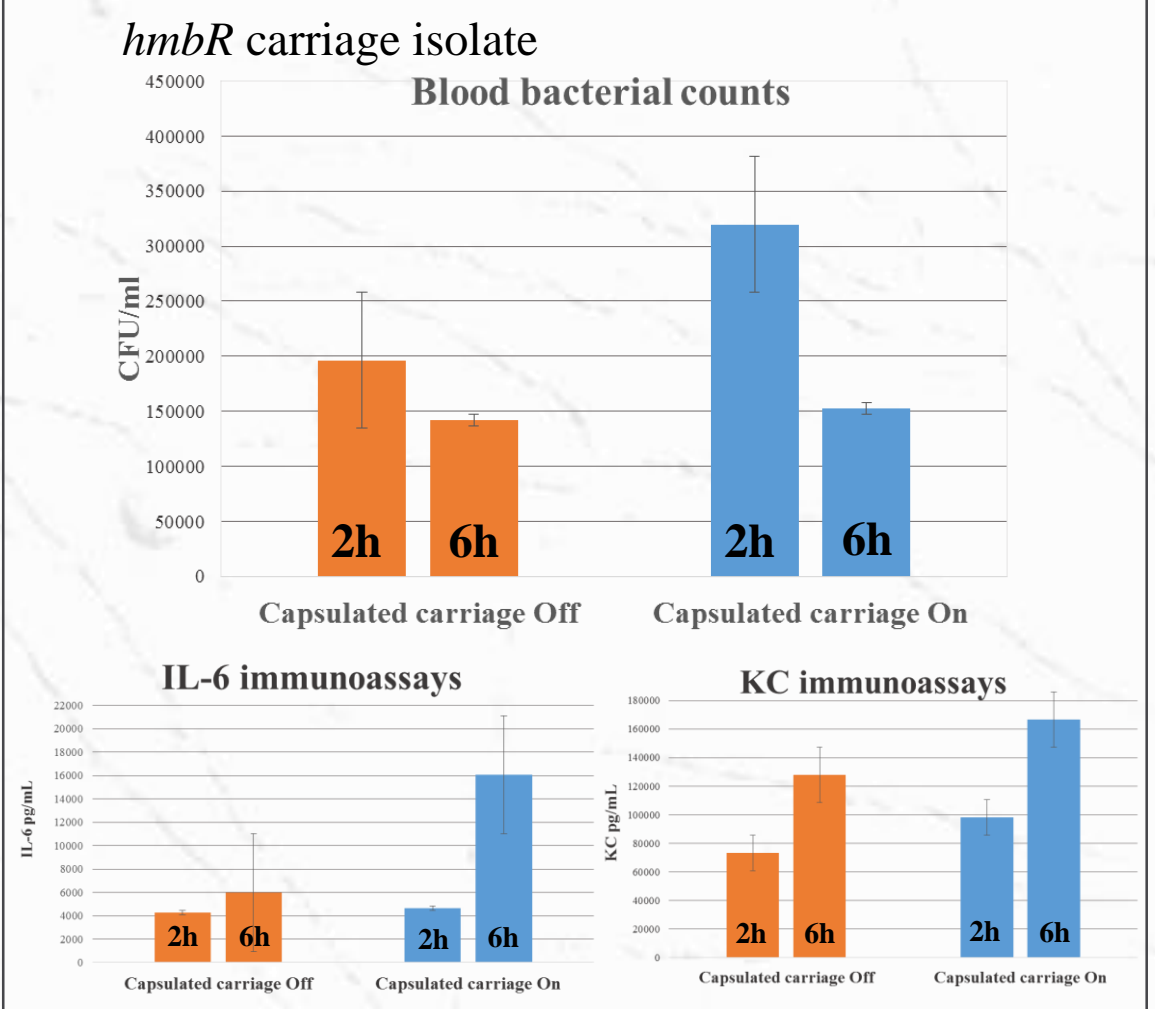
10G
TCGGTIGCAACTC--ggggggggggCGACACGGCT
12G
TCGGTIGCAACTCGGGGGGGGGGGCGACACGGCT
    
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Phenotypical characterization of iron utilization from heme



III. Impact of iron acquisition on virulence (*hmbR*):

***In vivo* challenge of On/Off carriage strains**
 → selection of an “On” revertant from an “Off”



→ recovery of **virulence in transgenic mice**

Histological section of infected spleen

