**Supplemental material**

**Table S1.** Evolution of the wild-colony morphotype of SA ATCC and SAI during 120 h of growth in TSA.

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SD - standard deviation

**Table S2***.* Detailed morphological description of the colonies produced by *S. aureus* strains after 48 h of growth on TSA.

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Form** | **Margin** | **Sheath** | **Type of Surface** | **Texture** | **Consistency** | **Elevation** | **Opacity** | **Size** | **Diameter (mm)** | **Colour** |
| **SA ATCC**  |  |  |  |  |  |  |  |  |  |  |  |
| WMT  | circular | Entire | absent | homogeneous | smooth | moist | flat | opaque | large  | 3.7±0.2 | beige |
|  |  |  |  |  |  |  |  |  |  |  |  |
| **SAI** |  |  |  |  |  |  |  |  |  |  |  |
| WMT | circular | Entire | absent | homogeneous | smooth | moist | flat | opaque | large | 2.5±0.5 | beige |
| SCV | circular | Entire | absent | homogeneous | smooth | moist | flat | opaque | small | 0.7±0.2 | beige |
|  |  |  |  |  |  |  |  |  |  |  |  |
| **PAO1** |  |  |  |  |  |  |  |  |  |  |  |
| WMT | circular | Undulate | present | homogeneous | rough | dry | flat | opaque | large | 14±0,5 | yellow |
|  |  |  |  |  |  |  |  |  |  |  |  |
| **PAI** |  |  |  |  |  |  |  |  |  |  |  |
| WMT | circular | entire | absent | homogeneous | rough | dry | flat | iridescent | large | 5.24±0.3 | blue-green |
| SCV | circular | undulate | absent | heterogeneous | smooth/rough | dry | flat | iridescent | small | 2.4±0.2 | blue-green |

WMT – wild-colony morphotype; SCV – small colony variants

**Table S3.** Oligonucleotide sequences of the primers used for gene expression quantification by qPCR and target gene function.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Primer | Forward | Reverse | Melting Temperature (ºC) | Amplicon size (bp) | Priming efficiency (%) | Gene Function |
| *16S* | GGAGAAAGTGGGGGATCTTC | CCGGTGCTTATTCTGTTGGT | 59.87 | 316 | 90. 6 | Housekeeping |
| *lasR* | *AAGGACAGCCAGGACTACGA* | *GTAGATGGACGGTTCCCAGA* | 59.87 | 156 | 94.5 | *QS* |
| *pqsE* | *ATGATGACCTGTGCCTGTTG* | *GTCGTAGTGCTTGTGGGTGA* | 59.75 | 188 | 97.9 | *QS* |
| *rhlR* | *TGGATGTTCTTGTGGTGGAA* | *GTTGCATGATCGAGTTGCTG* | 60.42 | 193 | 92.7 | *QS* |