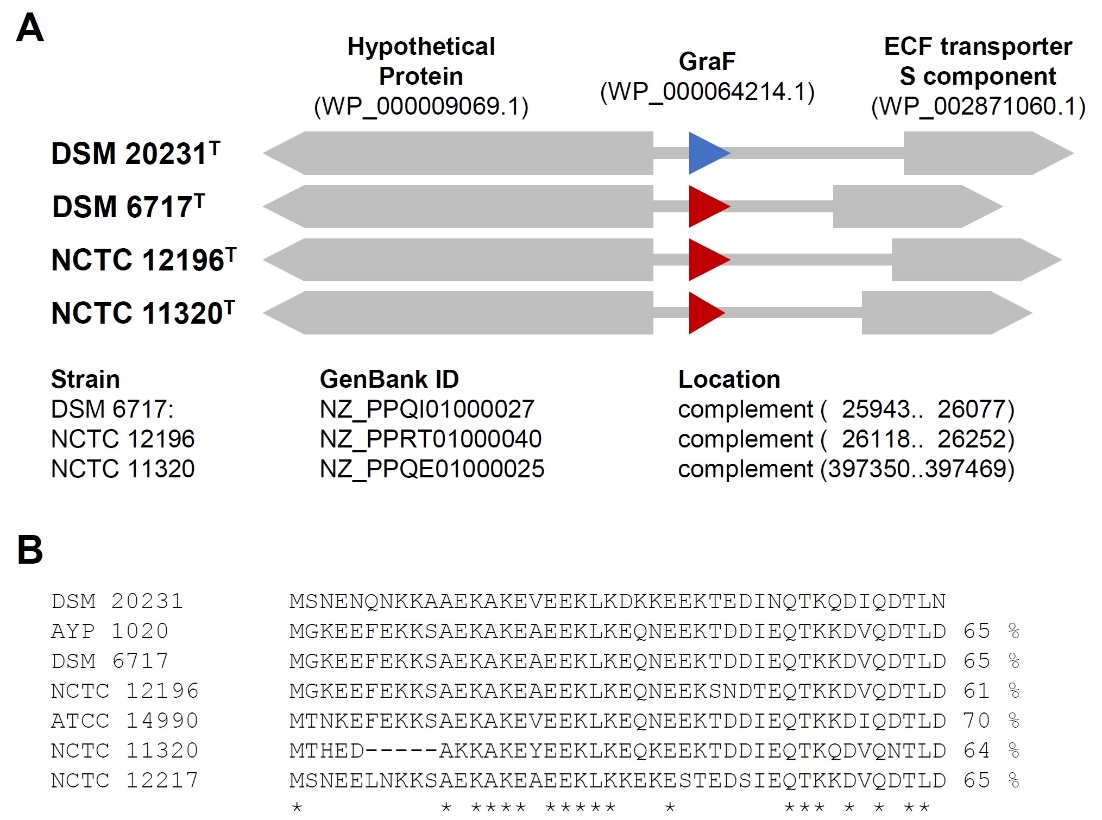
**Table 1.** Comparison chart of observed prominent MALDI peaks and calculated masses of significant proteins in *Cutibacterium* spectra. acn IA1: *C. acnes* subsp. *acnes* type IA1, acn IB: *C. acnes* subsp. *acnes* type IB, acn II: *C. acnes* subsp. *defendens* type II, acn III: *C. acnes* subsp. *elongatum* type III, mod: *C. modestum*, nam: *C. namnetense*, avi: *C. avidum*, gra: *C. granulosum*. Obs.: Observed m/z. Calc.: Calculated m/z. ND: Not detected. NP: Not present.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Protein name |  | Species/subspecies | |  |  |  |  |  |  |
|  |  | acn IA1 | acn IB | acn II | acn III | mod | nam | avi | gra |
| Putative sheep haemoglobin | Calc. | 15033.17 | 15033.17 | 15033.17 | 15033.17 | 15033.17 | 15033.17 | 15033.17 | 15033.17 |
| alpha chain -Met [M+H]+ | Obs. | *15041.93* | *15047.06* | *15045.41* | *15045.67* | ND | *15041.64* | *15052.29* | *15046.48* |
| 50S ribosomal prot L7/L12 -Met [M+H]+ | Calc. | 13571.41 | NP | 13571.41 | 13626.48 | 13586.42 | 13529.37 | 13572.39 | 13602.42 |
|  | Obs. | *13565.43* | ND | ND | ND | *13583.00* | ND | 13575.42 | *13601.29* |
| Lsr2-like prot -Met [M+H]+ | Calc. | 11651.76 | 11651.76 | 11651.76 | 11651.76 | 11712.76 | 11724.81 | 11629.67 | 11582.72 |
|  | Obs. | *11646.05* | *11649.39* | *11651.38* | *11648.23* | *11708.91* | ND | *11623.58* | *11581.71* |
| 10 kD Chaperonin GroS -Val [M+H]+ | Calc. | 10497.97 | 10497.97 | 10497.97 | 10497.97 | 10510.02 | 10497.97 | 10525.98 | 10497.97 |
|  | Obs. | *10493.82* | *10496.39* | *10495.79* | *10496.60* | *10507.86* | ND | ND | *10495.91* |
| DNA-binding prot HU [M+H]+ | Calc. | 9589.07 | 9589.07 | 9589.07 | 9589.07 | 9529.96 | 9529.02 | 9514.99 | 9601.09 |
|  | Obs. | *9586.01* | *9587.65* | *9587.41* | *9589.36* | *9528.55* | *9527.97* | *9518.68* | *9600.35* |
| Putative sheep haemoglobin | Calc. | 7517.09 | 7517.09 | 7517.09 | 7517.09 | 7517.09 | 7517.09 | 7517.09 | 7517.09 |
| alpha chain -Met [M+2H]2+ | Obs. | *7523.20* | ND | *7523.96* | ND | *7524.36* | *7524.85* | *7527.10* | *7524.27* |
| CsbD-like prot -Val/-Met [M+H]+ | Calc. | 7179.95 | 7179.95 | 7251.03 | 7237.98 | 7424.24 | 7283.97 | 7369.07 | NP |
|  | Obs. | *7179.01* | *7179.61* | *7250.54* | *7238.00* | *7424.35* | *7285.33* | *7372.75* | ND |
| 7 kD Antitoxin -Met [M+H]+ | Calc. | 7034.57 | 7004.55 | 6985.50 | 6971.52 | 6986.53 | 6940.46 | 7043.62 | 7017.54 |
|  | Obs. | *7033.48* | *7002.77* | *6985.48* | *6969.34* | *6986.52* | *6939.36* | *7047.01* | *7017.81* |
| 50S ribosomal prot L7/L12 -Met [M+2H]2+ | Calc. | 6786.21 | NP | 6786.21 | 6813.75 | 6793.72 | 6765.19 | 6786.70 | 6801.72 |
|  | Obs. | *6785.03* | ND | *6786.62* | ND | *6793.46* | ND | ND | *6801.65* |
| Lsr2-like prot -Met [M+2H]2+ | Calc. | 5826.39 | 5826.39 | 5826.39 | 5826.39 | 5856.89 | 5862.91 | 5815.34 | 5791.87 |
|  | Obs. | *5825.25* | *5826.89* | *5825.46* | *5824.34* | *5856.20* | ND | *5813.98* | *5791.43* |
| DUF3117 domain-containing protein | Calc. | 5712.64 | 5712.64 | 5712.64 | 5754.72 | 5692.65 | 5708.65 | 5678.58 | 5686.60 |
| -Met [M+H]+ | Obs. | *5712.45* | *5711.39* | 5710.68 | *5753.77* | *5692.28* | ND | 5681.95 | *5686.97* |
| 10 kD Chaperonin GroS -Val [M+2H]2+ | Calc. | 5249.49 | 5249.49 | 5249.49 | 5249.49 | 5255.52 | 5249.49 | 5263.50 | 5249.49 |
|  | Obs. | *5248.94* | *5248.13* | *5247.38* | *5248.20* | *5255.26* | ND | ND | *5250.86* |
| DNA-binding prot HU [M+2H]2+ | Calc. | 4795.04 | 4795.04 | 4795.04 | 4795.04 | 4765.48 | 4765.01 | 4758.00 | 4801.05 |
|  | Obs. | *4793.57* | *4792.28* | *4793.29* | *4794.08* | *4764.56* | *4762.25* | *4760.70* | *4801.21* |
| CsbD-like prot -Val/-Met [M+2H]2+ | Calc. | 3590.48 | 3590.48 | 3626.02 | 3619.50 | 3655.58 | 3584.95 | 3627.50 | NP |
|  | Obs. | *3587.20* | *3587.20* | *3622.35* | *3616.04* | ND | ND | ND | ND |
| 7 kD Antitoxin -Met [M+2H]2+ | Calc. | 3517.79 | 3502.78 | 3493.26 | 3486.27 | 3493.77 | 3470.74 | 3522.32 | 3509.28 |
|  | Obs. | *3513.32* | *3497.88* | *3489.62* | *3496.78* | *3490.74* | ND | ND | *3508.86* |
|  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |

**Table 2.** Comparison chart of observed prominent MALDI peaks and calculated masses of significant proteins in *Staphylococcus* spectra. aur: *S. aureus*, capi capi: *S. capitis* subsp. *capitis*, capi urea: *S. capitis* subsp. *urealiticus*, capr: *S. caprae*, epi: *S. epidermidis*, hom *S. hominis*, lug: *S. lugdunensis*. Obs.: Observed m/z. Calc.: Calculated m/z. ND: Not detected. NP: Not present.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Protein name |  | Species/subspecies | |  |  |  |  |  |
|  |  | aur | capi capi | capi urea | capr | epi | hom | lug |
| Putative sheep haemoglobin | Calc. | 15033.17 | 15033.17 | 15033.17 | 15033.17 | 15033.17 | 15033.17 | 15033.17 |  |
| alpha chain -Met [M+H]+ | Obs. | *15042.92* | *15046.25* | *15043.91* | *15044.56* | *15042.32* | *15041.76* | *15043.53* |
| 50S ribosomal prot L7/L12 -Met [M+H]+ | Calc. | 12580.36 | 12533.27 | 12533.27 | 12533.27 | 12519.25 | 12532.23 | 12475.18 |
|  | Obs. | *12577.10* | *12530.38* | ND | *12531.30* | ND | *12526.23* | ND |
| 30S ribosomal prot S15 -Met [M+H]+ | Calc. | 10478.07 | 10477.08 | 10477.08 | 10478.07 | 10507.11 | 10521.14 | 10409.99 |
|  | Obs. | *10479.53* | *10474.45* | *10473.15* | *10480.77* | *10501.76* | *10515.16* | *10409.12* |
| 30S ribosomal prot S16 -Met [M+H]+ | Calc. | 10104.68 | 10192.69 | 10192.69 | 10229.76 | 10229.76 | 10172.74 | 10217.85 |
|  | Obs. | *10101.38* | *10193.03* | *10190.21* | *10226.78* | *10227.07* | *10106.73* | *10213.89* |
| DNA-binding prot HU [M+H]+ | Calc. | 9627.02 | 9641.09 | 9641.09 | 9627.02 | 9627.02 | 9656.04 | 9643.07 |
|  | Obs. | *9624.58* | *9639.03* | *9639.62* | 9625.35 | *9625.37* | *9653.78* | *9640.08* |
| Putative sheep haemoglobin | Calc. | 7517.09 | 7517.09 | 7517.09 | 7517.09 | 7517.09 | 7517.09 | 7517.09 |
| alpha chain -Met [M+2H]2+ | Obs. | *7523.76* | *7524.89* | *7524.35* | *7524.22* | *7522.63* | *7522.85* | *7522.40* |
| CsbD-like prot -Met [M+H]+ | Calc. | 6888.51 | 6711.31 | 6711.31 | 7045.60 | 6681.33 | 6476.11 | 7355.01 |
|  | Obs. | *6888.04* | *6711.29* | *6712.02* | *7045.60* | *6679.67* | *6473.92* | *7353.52* |
| 50S ribosomal prot L32 -Met [M+H]+ | Calc. | 6354.36 | 6371.39 | 6371.39 | 6385.41 | 6398.41 | 6398.41 | 6371.39 |
|  | Obs. | *6353.70* | *6370.44* | *6371.43* | *6385.44* | *6396.83* | *6396.33* | *6370.26* |
| 5.5 kD Hypothetical prot -Met [M+H]+ | Calc. | 5525.00 | 5098.48 | 5098.48 | 5213.52 | 5338.87 | 5237.68 | 5165.57 |
|  | Obs. | *5524.85* | *5098.60* | *5098.86* | *5213.87* | *5337.31* | *5236.04* | *5164.67* |
| Glycopeptide resistance- | Calc. | 5032.49 | 5041.45 | 5041.45 | 5014.38 | 5112.57 | 4564.92 | 4953.38 |
| . associated prot GraF –Met [M+H]+ | Obs. | *5032.46* | *5041.61* | *5041.85* | *5015.48* | *5111.36* | *4563.08* | *4952.56* |
| DNA-binding prot HU [M+2H]2+ | Calc. | 4814.02 | 4821.05 | 4821.05 | 4814.02 | 4814.02 | 4829.03 | 4822.04 |
|  | Obs. | *4813.80* | *4822.65* | *4821.11* | *4812.46* | *4813.13* | *4827.57* | *4821.12* |
| 50S ribosomal prot L36 [M+H]+ | Calc. | 4306.37 | 4292.34 | 4292.34 | 4292.34 | 4292.34 | 4292.34 | 4292.34 |
|  | Obs. | *4305.95* | *4292.22* | *4292.43* | *4292.43* | *4290.37* | *4290.72* | *4291.35* |
| CsbD-like prot -Met [M+2H]2+ | Calc. | 3444.76 | 3356.16 | 3356.16 | 3523.31 | 3341.17 | 3238.56 | 3678.01 |
|  | Obs. | *3443.31* | *3356.11* | *3355.13* | *3522.30* | *3338.78* | *3236.21* | *3676.55* |

**Figure S1.** Identification of ORFs encoding GraF in *Staphylococcus* strains. A. Flanking region of the *GraF* gene. The *GraF* gene is located between two ORFs encoding ‘Hypothetical protein’ and ‘ECF transporter S component’ in the genome of DSM 20231T. The GenBank IDs for the genomic sequences and the locations of the predicted *GraF* gene in the strains, DSM 6717T, NCTC 12196T, and NCTC 11320T, were shown below. B. An alignment of predicted amino acid sequences of GraF. Sequence similarity scores (%) to the GraF protein in DSM 20231T were shown right.



**Reference**

1. Becher D, Hempel K, Sievers S, Zühlke D, Pané-Farré J, OttoA, Fuchs S, Albrecht D, Bernhardt J, Engelmann S, Völker U, van Dijl JM, Hecker M. 2009. A proteomic view of an important human pathogen – towards the quantification of the entire *Staphylococcus aureus* proteome. PLoS ONE 4: e8176. doi: 10.1371/journal.pone.0008176.