**Table S3**. Orthologs of the differentially abundant proteins reported to be involved in pathogenesis, virulence or resistance mechanisms.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| # | Protein name | Locus IDa | Orthologs in pathogenesis/virulence/resistance | Interactionsb |
| 1 | Malonyl-CoA:acyl carrier protein transacylase (FabD) | Smlt1028 | Involved in biosynthesis of coronatine (*Pseudomonas syringae*) [1]Involved in resistance to trifluoroperazine (*Escherichia coli*) [2] | AccA AccC |
| 2 | Acetyl-CoA carboxylase, carboxyl transferase alpha subunit (AccA) | Smlt1490 |  | AccC FabD AcsA PdhB FadI |
| 3 | Acetyl-CoA carboxylase, biotin carboxylase subunit (AccC) | Smlt4241 | Downregulated by epinephrin (*Salmonella enterica*) [3] | AccA FabD AcsA PdhB FadI |
| 4 | Acetyl-CoA synthetase (AcsA) | Smlt4623 | Essential for growth on ethanol (*Pseudomonas aeruginosa*) [4,5] | AccC DntE FadI PdhB AccA |
| 5 | Pyruvate dehydrogenase, dihydrolipoamide acetyltransferase subunit (PdhB) | Smlt4121 | Involved in host interactions (*Mycoplasma pneumoniae*) [6]Belongs to core exoproteome of virulent strains (*Staphylococcus aureus*) [7]PDH complex required for pathogenesis (*Mycobacterium tuberculosis*) [8]Immunoreactive (*Bacillus* sp.) [9]Involved in type III secretion system-dependent cytotoxicity (*Pseudomonas aeruginosa*) [10] | AcsA AccC AccA FadI |
| 6 | Acetyl-CoA acetyltransferase (FadI) | Smlt0164 |  | AcsA AccA PdhB AccA SucB |
| 7 | 2-oxoglutarate dehydrogenase, dihydrolipoamide succinyltransferase subunit (SucB) | Smlt3198 | Involved in persister survival and tolerance to antibiotics and stress (*Escherichia coli*) [11]Immunoreactive (*Bartonella henselae*) [12] | FadI AcnB |
| 8 | Aconitate hydratase 2 (AcnB) | Smlt2245 | Involved in colonization (*Xanthomonas campestris*) [13]Involved in virulence (*Xanthomonas oryzae*) [14]Upregulated under oxidative stress together with virulence factors / involved in resistance to hydrogen peroxyde [15,16,17] | SucB |
| 9 | Methylmalonate-semialdehyde dehydrogenase (DntE) | Smlt0264 |  | AcsA Smlt0266 |
| 10 | Enoyl-CoA hydratase | Smlt0266 | Involved in virulence (*Pseudomonas aeruginosa*) [18] | DntE EtfB |
| 11 | Electron transfer flavoprotein, beta subunit (EtfB) | Smlt0646 |  | Bcd Smlt0266 |
| 12 | Butyryl-CoA dehydrogenase (Bcd) | Smlt3174 |  | EtfB |
| 13 | UDP-N-acetylglucosamine 1-carboxyvinyl-transferase (MurA) | Smlt1119 | Upregulation confers resistance to fosfomycin and to bromoacetate (*Escherichia coli*) [19,20]Required for intrinsic resistance to cephalosporin (*Enterococcus faecalis*) [21]Upregulated in biofilm (*Streptococcus suis*) [22] | GlyA |
| 14 | Serine hydroxymethyl-transferase (GlyA) | Smlt0718 | Upregulated by the QS system (*Pseudomonas aeruginosa*) [23] | PepA MurA PyrH |
| 15 | Leucine aminopeptidase (PepA) | Smlt0675 | Highly upregulated by the QS system together with virulence factors (*Pseudomonas aeruginosa*) [23,24] | GlyA |
| 16 | Uridylate kinase (PyrH) | Smlt1504 | Involved in biofilm, QS and virulence (*Pseudomonas aeruginosa*, *Vibrio vulnificus*) [25,26]Essential for in-host survival (*Vibrio vulnificus*) [27] | RpoA GlyA |
| 17 | DNA-directed RNA polymerase, alpha subunit (RpoA) | Smlt0931 | Involved in the activation of virulence factors (*Salmonella enterica*, *Brucella melitensis*) [28,29] | PyrH |
| 18 | dTDP-glucose 4,6-dehydratase (RfbB) | Smlt0647 | Involved in colonization and virulence (*Salmonella* Typhimurium) [30]Involved in colonization (*Vibrio cholerae*) [31]Upregulated by the QS system (*Pseudomonas aeruginosa*) [23] |  |
| 19 | LPS-assembly protein LptD | Smlt0821 | Δ mutants are leaky and produce little LPS, which is not in the surface (*Neisseria meningitidis*) [32] |  |
| 2021 | Putative TonB-dependent receptor | Smlt3444Smlt4151 | Involved in virulence (*Pseudomonas fluorescens*, *Neisseria meningitidis*, *Flavobacterium psychrophilum*, *Porphyromonas gingivalis*, *Escherichia coli*, *Bordetella avium*) [33,34,35,36,37,38] |  |
| 22 | Putative membrane protease, HflC subunit | Smlt3595 | Involved in tobramycin resistance (*Pseudomonas aeruginosa*) [39] |  |
| 23 | Putative long-chain fatty acid transport protein (FadL) | Smlt0423 | Involved in virulence (*Pseudomonas fluorescens*) [40]Involved in chlortetracycline resistance (down regulation in presence of CTC, but increased sensitivity of Δ mutant) (*Escherichia coli*) [41]Upregulated in response to erythromycin, kanamycin, tetracycline, streptomycin, and chloromycetin (*Vibrio alginolyticus*) [42] |  |
| 24 | Porin P (OprP) | Smlt3943 |  |  |
| 25 | Putative outer membrane protein W (OmpW) | Smlt4123 | Involved in virulence [43]Involved in resistance to tetracycline, ceftriaxone and oxidative stress (by downregulation) (*Acinetobacter baumannii*, *Salmonella* Typhimurium, *Escherichia coli*) [44,45,46]Involved in resistance to paraquat (by upregulation) (*Salmonella* Typhimurium) [47] |  |
| 2627 | Putative outer membrane protein A (OmpA) | Smlt0955Smlt1826 | Involved in virulence (*Acinetobacter baumannii*, *Francisella tularensis*) [48,49]Involved in adhesion/invasion (*Escherichia coli*, *Porphyromonas gingivalis*) [50,51,52] |  |
| 28 | Endopeptidase O (PepO) | Smlt3447 | Involved in virulence (*Aeromonas hydrophila*) [53]Involved in invasion/colonization (*Porphyromonas gingivalis*) [54] |  |
| 29 | Putative exported peptidase S9 | Smlt1246 |  |  |
| 30 | Xaa-Pro dipeptidase (PepQ) | Smlt3861 |  |  |
| 31 | L-Threonine 3-dehydrogenase (Tdh) | Smlt0961 |  |  |
| 32 | Adenylosuccinate lyase (PurB) | Smlt3193 | Involved i virulence (*Salmonella enterica*) [55]Involved in colonization (*Listeria monocytogenes*) [56]Involved in biofilm formation and virulence (*Streptococcus sanguinis*) [57] |  |
| 33 | NADH-quinone oxidoreductase, G subunit (NuoG) | Smlt3399 | Inhibits apoptosis of infected host cells (*Mycobacterium tuberculosis*) [58,59,60]Involved in virulence (*Salmonella* Gallinarum) [61] |  |
| 34 | Bifunctional molybdenum cofactor biosynthesis protein (MoaC) | Smlt2781 |  |  |
| 35 | Putative monooxygenase | Smlt1459 |  |  |
| 36 | Putative quorum-sensing factor Ax21 | Smlt0387 | Involved in regulation of motility, biofilm formation and virulence (*Xanthomonas oryzae*) [62,63]Involved in intraspecies signaling (non sulfation-dependent) (*Stenotrophomonas maltophilia*) [64] |  |
| 37 | UPF0234 family protein | Smlt4090 |  |  |
| 38 | Conserved hypothetical exported protein | Smlt3796 |  |  |

aLocus ID in *Stenotrophomonas maltophilia* K279a, GenBank code AM743169.

bInteraction partners within the list of differentially abundant proteins as given by STRING (<http://string-db.org/>), based on *Stenotrophomonas maltophilia* K279a using all prediction methods and a confidence threshold of 0.7.

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