**Single nucleotide polymorphisms in virulence genes and efflux pump related genes common to isolates CSF3053, 46-5069 and 43-13838**

**Table S1. Single nucleotide polymorphisms in virulence genes**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Position | Nucleotide change | Amino acid change | Protein variation effect | Gene | Function/Description | | | Virulence References |
| 200379 | C>T | Ala162Val | Deleterious | *mce1B* | Mammalian cell entry proteins | | | (Gioffre et al. 2005) |
| 206339 | T>C | Leu370Pro | Neutral | *mce1F* | Mammalian cell entry proteins | | | (Gioffre et al. 2005) |
| 206481 | C>G | Pro417Pro |  | *mce1F* | Mammalian cell entry proteins | | | (Gioffre et al. 2005; Pantel et al. 2012) |
| 206484 | G>T | Gly418Gly |  | *mce1F* | Mammalian cell entry proteins | | | (Gioffre et al. 2005) |
| 495198 | A>G | Phe706Ser | Deleterious | *pknG* | Protein kinase G | | | (Cowley et al. 2004) |
| 495473 | C>T | Ser614Ser |  | *pknG* | Protein kinase G | | | (Cowley et al. 2004) |
| 541201 | A>G | Leu97Leu |  | *mmpL4* | Membrane transport protein | | | (Domenech et al. 2005) |
| 580008 | A>G | Leu220Leu |  | *senX3* | Two component system sensor | | | (Rickman et al. 2004) |
| 580336 | C>A | Arg330Arg |  | *senX3* | Two component system sensor | | | (Rickman et al. 2004) |
| 686972 | T>C | Phe51Ser | Neutral | *mce2A* | Mammalian cell entry proteins | | | (Marjanovic et al. 2010) |
| 687602 | C>A | Thr261Asn | Deleterious | *mce2A* | Mammalian cell entry proteins | | | (Marjanovic et al. 2010) |
| 690248 | C>A | Thr397Asn | Neutral | *mce2C* | Mammalian cell entry proteins | | | (Marjanovic et al. 2010) |
| 690450 | A>C | Ala464Ala |  | *mce2C* | Mammalian cell entry proteins | | | (Marjanovic et al. 2010) |
| 690465 | T>G | Leu469Leu |  | *mce2C* | Mammalian cell entry proteins | | | (Marjanovic et al. 2010) |
| 1037012 | T>C | Met5Thr | Neutral | *pstA1* | Inorganic phosphate-ABC transporter | | | (Rengarajan et al. 2005) |
| 1037911 | C>T | Arg305\* |  | *pstA1* | Inorganic phosphate-ABC transporter | | | (Rengarajan et al. 2005) |
| 1038500 | T>G | Gln472Pro | Neutral | *pknD* | Protein kinase D | | | (Be et al. 2012) |
| 1043136 | C>T | Thr341Ile | Deleterious | *pstS1* | Inorganic phosphate transporter | | | (Peirs et al. 2005) |
| 1079927 | C>A | Thr395Thr |  | *ctpV* | Copper efflux transporter P-type ATPase | | | (Ward et al. 2010) |
| 1080192 | G>A | Asp484Asn | Neutral | *ctpV* | Copper efflux transporter P-type ATPase | | | (Ward et al. 2010) |
| 1097023 | G>A | Gly70Ser | Deleterious | *mprA* | Two component system | | | (Zahrt & Deretic 2001) |
| 1098523 | T>A | Leu339His | Neutral | *mprB* | Two component system | | | (Zahrt & Deretic 2001) |
| 1443899 | T>C | Ala383Ala |  | *Rv1290c* | Conserved hypothetical protein | | | (McAdam et al. 2002) |
| 1694547 | A>C | Ter200Glu |  | *Rv1504c* | Conserved hypothetical protein | | | (Brodin et al. 2010) |
| 1726816 | G>T | Pro532Thr | Neutral | *pks5* | Probable Polyketide synthase | | | (Rousseau et al. 2003) |
| 1875886 | C>A | Leu195Met | Neutral | *pks7* | Probable Polyketide synthase | | | (Rousseau et al. 2003) | |
| 1876739 | T>G | Val479Gly | Deleterious | *pks7* | Probable Polyketide synthase | | | (Rousseau et al. 2003) | |
| 2066471 | T>C | Gly5Gly |  | *secA2* | Accessory SecA protein | | | (Kurtz et al. 2006) | |
| 2154724 | C>A | Arg463Leu | Neutral | *katG* | Catalase-peroxidase | | | (Ng et al. 2004; Wilson et al. 1995) | |
| 2209465 | G>A | Ala47Thr | Neutral | *Mce-3* | Mammalian cell entry proteins | | | (Senaratne et al. 2008) | |
| 2211826 | A>G | Lys67Lys |  | *mce3C* | Mammalian cell entry proteins | | | (Senaratne et al. 2008) | |
| 2215712 | G>A | Leu152Leu |  | *mce3F* | Mammalian cell entry proteins | | | (Senaratne et al. 2008) | |
| 2216370 | G>C | Gly372Arg | Deleterious | *mce3F* | Mammalian cell entry proteins | | | (Senaratne et al. 2008) | |
| 2216443 | C>A | Ala396Glu | Neutral | *mce3F* | Mammalian cell entry proteins | | | (Senaratne et al. 2008) | |
| 2222308 | T>C | Asp286Gly | Neutral | *Rv1979c* | Region of difference 2 | | | (Kozak et al. 2011) | |
| 2278507 | G>A | Ser142Ser |  | *hspX* | Dormancy associated protein | | | (Yuan et al. 1998) | |
| 2296042 | G>A | Pro3649Ala | Neutral | *pks12* | Probable Polyketide synthase | | | (Sirakova et al. 2003) | |
| 2631641 | T>G | Pro153Pro |  | *plcA* | Probable phospholipase C | | | (Raynaud et al. 2002) | |
| 2672514 | C>G | Leu1108Leu |  | *mbtB* | ABC iron transporter | | | (De Voss et al. 1999) | |
| 3244126 | | G>A | Val144Ile(N) | Neutral | *fadD26* | Fatty acid coA synthase | | | (Camacho et al. 1999; Cox et al. 1999; Rousseau et al. 2004) | |
| 3285318 | | C>T | Ala83Ala |  | *mmpl7* | Transmembrane transport protein | | | (Cox et al. 1999) | |
| 3293423 | | A>G | Asp977Asp |  | *pks1* | Probable Polyketide synthase | | | (Tsenova et al. 2005) | |
| 3296809 | | G>A | Asp344Asp |  | *pks15* | Probable Polyketide synthase | | | (Reed et al. 2004) | |
| 3447480 | | A>C | Leu316Arg(D) | Deleterious | *VirS* | Transcriptional regulator | | | (Singh et al. 2003) | |
| 3518167 | | A>G | Ile474Met(N) | Neutral | *nuoG* | Type I NADH dehydrogenase subunit | | | (Velmurugan et al. 2007) | |
| 3518555 | | A>G | Thr604Ala(N) | Neutral | *nuoG* | Type I NADH dehydrogenase subunit | | | (Velmurugan et al. 2007) | |
| 3984321 | | G>A | His375His |  | *cyp125* | Putative cytochrome P450 | | | (Chang et al. 2009) | |
| 3984926 | | G>A | Leu174Leu |  | *cyp125* | Putative cytochrome P450 | | | (Chang et al. 2009) | |
| 4112429 | | T>C | Ile363Val(N) | Neutral | *Rv3671c* | Serine protease | | | (Vandal et al. 2008) | |
| 4289953 | | A>G | Val526Ala(N)\ | Neutral | *mmpL8* | Integral membrane transport protein | | | (Converse et al. 2003) | |
| 4290564 | | G>T | Ala322Ala |  | *mmpL8* | Integral membrane transport protein | | | (Converse et al. 2003) | |
| 4290827 | | C>G | Gly235Arg(N) | Neutral | *mmpL8* | Integral membrane transport protein | | | (Converse et al. 2003) | |
| 4344058 | | T>C | Ser249Pro(D) | Deleterious | *Rv3868* | Secretion system Esx-1 C or S | | | (Lewis et al. 2003) | |
| 4345682 | | C>T | Ser215Leu(N) | Neutral | *Rv3869* | Secretion system Esx-1 C or S | | | (Lewis et al. 2003) | |
| 4348418 | | G>A | Leu646Leu |  | *Rv3870* | Secretion system Esx-1 C or S | | | (Lewis et al. 2003) | |

The positions, nucleotide change , amino acid change and effect of single nucleotide polymorphisms in virulence genes that are common to isolates CSF3053, 46-5069 and 43-13838. The protein variation was determined by Protein Variation Effect Analyzer (PROVEAN), a web based protein variation analysis tool (Choi et al. 2012)

**Table S2 Single nucleotide polymorphisms in efflux pump related genes**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Position | Nucleotide change | Amino acid change | Protein variation effect | Gene | Reference |
| 41151 | C>A | Ala18Ser | Neutral | *Rv0037c* | (De Rossi et al. 2002) |
| 227098 | T>C | Met74Thr | Neutral | *Rv0194* | (Danilchanka et al. 2008) |
| 412280 | T>G | His481Gln | Neutral | *iniA* | (Colangeli et al. 2005) |
| 541201 | A>G | Leu97Leu |  | *mmpL4* | (Domenech et al. 2005) |
| 938246 | A>G | Leu45Leu |  | *Rv0842* | (Li et al. 2015) |
| 947176 | C>G | Ala374Gly | Neutral | *Rv0849* | (De Rossi et al. 2002) |
| 1362006 | T>C | Gln243Arg | Neutral | *Rv1218c* | (Balganesh et al. 2010) |
| 1395010 | A>G | Arg278Gly | Neutral | *Rv1250* | (De Rossi et al. 2002) |
| 1406312 | A>G | His343His |  | *Rv1258c* | (Ainsa et al. 1998) |
| 1839260 | T>G | Leu31Leu |  | *Rv1634* | (De Rossi et al. 2002) |
| 1839329 | G>A | Arg54Arg |  | *Rv1634* | (De Rossi et al. 2002) |
| 1839759 | G>C | Gly198Arg | Neutral | *Rv1634* | (De Rossi et al. 2002) |
| 1897646 | G>C | Pro188Ala | Deleterious | *Rv1672c* | (Li et al. 2015) |
| 1897938 | G>A | Val90Val |  | *Rv1672c* | (Li et al. 2015) |
| 2062922 | T>C | Ile603Val | Neutral | *Rv1819c* | (Gupta et al. 2006) |
| 2127523 | G>A | Leu540Leu |  | *Rv1877* | (De Rossi et al. 2002) |
| 2538793 | G>A | Gly32Ser | Neutral | *Rv2265* | (Zhang et al. 2013) |
| 2608117 | G>T | Asp69Tyr | Neutral | *Rv2333c* | (Ramon-Garcia et al. 2007) |
| 3005185 | G>T | Pro156Thr | Neutral | *Rv2688c* | (Pasca et al. 2004) |
| 3154414 | A>G | Ile73Thr | Neutral | *efpA* | (Doran et al. 1997) |
| 3273138 | C>G | His309Asp | Neutral | *drrA* | (Choudhuri et al. 2002) |
| 3274545 | G>A | Leu158Leu |  | *drrC* | (Choudhuri et al. 2002) |
| 3285318 | C>T | Ala83Ala |  | *mmpL7* | (Pasca et al. 2005) |
| 3351472 | G>A | Trp68\* |  | *Rv2994* | (De Rossi et al. 2002) |
| 3614982 | T>C | Leu874Leu |  | *Rv3239c* | (De Rossi et al. 2002) |

The positions, nucleotide change , amino acid change and effect of single nucleotide polymorphisms in efflux pump related genes that are common to isolates CSF3053, 46-5069 and 43-13838. The protein variation was determined by Protein Variation Effect Analyzer (PROVEAN), a web based protein variation analysis tool (Choi et al. 2012)

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