| Protein(s) containing the identified peptide / NCBI/CGD accession number | aa before | Identified peptide sequencea | aa after | Functional class | Peptide mass (m/z) | Mascot searches | Trypsin | Semitrypsin & deamidation |
|---|---|---|---|---|---|---|---|---|
| Epa2 / CAGL0E05688g | F | TMLQGFTYK | A | Adhesin cluster I Epa | 1135 | 47 1 | 1135 | 47 1 |
| K | VSLFEK | D | | | | | |
| R | DNGALSLTLK | T | | | | | |
| L | FDTLPQANYR | T | | | | | |
| M | GCTSLFDTLPQANYR | T | | | | | |
| K | NGSLMELYSDYLLK | S | | | | | |
| T | NLGLMELYSDYLLK Deamidated (NQ) | S | | | | | |
| Epa6 / CAGL0C00110g | K | NGLSMELYSDYLLK | D | Adhesin cluster I Epa | 1695 | 95 1 | 1695 | 95 1 |
| T | SLFDTPQANYR | T | | | | | |
| TSFPDTLPQANYR | T | | | | | |
| K | VENAGNNFYPYAMGC | T | | | | | |
| Epa7 / CAGL0C05643g | R | EYDAELSLTLK | T | | | | 1281 | 66 8 |
| K | NGLSMELYSDYLLK | K | | | | | |
| K | NGLSMELYSDYLLK Deamidated (NQ) | K | | | | | |
| Epa22 / CAGL0K00170g | K | DYYVPIR | M | Adhesin cluster I Epa | 925 | 34 2 | 925 | 34 2 |
| K | VSLNLEK | D | | | | | |
| Epa3 and Epa22 | R | LGEYVAYDIWHVDSSK | N | | | | 1881 | 98 7 |
| K | MFFNNIGK | D | | | | | |
| Epa3 and Epa22 | R | LGEYVAYDIWHVDSSK Oxidation (M) | D | | | | 1947 | 104 8 |
| Epa3, 6, 7, 14a, 22 and Epa14/CAGL0L13552g | N | FGAGNFDCK | R | | | | 1246 | 74 2 |
| For L | GAGNFDCK | R or A | | | | | |
| Epa6 and 7 | T | AVWSQSTAK | Y | Adhesin cluster I Epa | 946 | 50 4 | 946 | 50 4 |
| Epa6 and 7 | K | DDLTHVLAGLPPYPR | I | non-unique peptides | 1860 | 90 25 | 1860 | 90 25 |
| Epa6 and 7 | R | ESSADDQFNYQAYAVWSQSTAK | D | | | | 2394 | 46 1 |
| Epa6 and 7 | K | ESSADDQFNYQAYAVWSQSTAK Deamidated (NQ) | K | | | | 2395 | 52 1 |
| Epa6, 7, 8, Epa22/CAGL0C000847g, Epa11/CAGL0L13299g, Epa12/CAGL0M00132g and Epa13/CAGL0L13332g | R | IFFNNR | D | | | | 809 | 28 3 |
| Epa7 and Epa1/CAGL0E08644g | K | VDGVTGNINNFYATK | G | | | | 1798 | 68 4 |
| Awp14 / CAGL0A04851g | K | APNSVPLVLGTLVLVLK | S | | | | 1654 | 72 1 |
| K | FEDDELLVLK | N | | | | | |
| K | FEDDELLVLK | N | | | | | |
| K | FSISHGFTYK | A | | | | | |
| K | GTFNVPFR | T | | | | | |
| L | LLGQKIDENGVFTMK | N | | | | | |
| L | LNLQAR | L | | | | | |
| R | RPQYMNQVGK | V | | | | | |
| K | SFSIGDPR | K | | | | | |
| K | TDGGYFQFNLFR | I | | | | | |
| K | VLDWGFSHATTIK | F | | | | | |
| Awp6 / CAGL0G01017g and Awp7 / CAGL0C00020g | R | VNMIQGAYLADIK | G | Adhesin cluster IV | 1620 | 82 1 | 1620 | 82 1 |
| Awp2 / CAGL0K00110g | K | GGALYYVINNK | Q | | | | 1227 | 43 1 |
| K | GTSFKPQR | L | | | | | |
| K | IHGYSYNYVFVR | Y | | | | | |
| S | SSIPSWTR | D | | | | | |
| F | VFNLQYVK | R | | | | | |
| Awp2a/Awp8 / CAGL0B00154g | K | GGALYYVNDYLSGF | I | Adhesin cluster III | 1183 | 55 5 | 1183 | 55 5 |
| K | GGGYLYNLGNQGDFIESK Deamidated (NQ) | H | | | | | |
| K | GTSANMPQILK | L | | | | | |
| K | HALFVSFVFR | N | | | | | |
| Awp2b/Awp9 / CAGL0B00561g | K | GGALYYVINNK | Q | | | | 1207 | 55 5 |
| K | GGSYLYNLGNQGDFIESK Deamidated (NQ) | H | | | | | |
| K | GTSANMPQILK | L | | | | | |
| K | HALFVSFVFR | N | | | | | |
| Awp2c/Awp10 / CAGL0F00099g | K | NPIEWVGCVGTVKENFVK Deamidated (NQ) | D | | | | 1183 | 55 5 |
| K | STSIVGK | I | | | | | |
| K | SVNTGTFYSIK | G | | | | | |
| R | YNGSPRNASPSCR | P | | | | | |
| R | YNGSPRNASPSCR Deamidated (NQ) | P | | | | | |
| Awp2d/Awp11 / CAGL0J12067g | K | GTSSSKPQQLK | I | Adhesin cluster V | 1370 | 32 1 | 1370 | 32 1 |
| Awp2f/Awp9 / CAGL0C00170g | K | GGSYLYNLGNQGDFIESK | H | | | | 2074 | 60 2 |
| K | GGSYLYNLGNQGDFIESK Deamidated (NQ) | H | | | | | |
| K | GTSANMPQILK | L | | | | | |
| K | HALFVSFVFR | N | | | | | |
| Awp4 / CAGL0M00121g | K | YSGALPPQFKQQLK | I | | | | 1160 | 43 8 |
| K | YSGALPPQFKQQLK | I | | | | | |
| Awp4 and CAGL0D00143g | K | GAQLYNYINDLQSF | S | | | | 1552 | 92 1 |
| K | LAFQIMTVLQYTPVR | F | | | | | |
| F | QDMTVFQYTVR | D | | | | | |
| K | ACVQEPFQFTK | V | | | | | |
| K | GKPQPPASPICK | A | | | | | |
| Awp4 and CAGL0D00143g | K | GTNAAARPQQLK | I | | | | 1183 | 40 4 |
| Awp4 and CAGL0D00143g | K | INDGSFTNTGMPQPSQ Deamidated (NQ) | G | | | | 1131 | 40 4 |
| Awp4 and CAGL0D00143g | K | LISTSAGSKW | R | | | | 93 5 |
| Awp4 and CAGL0D00143g | K | VNOQGALYYIMNLK Deamidated (NQ) | G | | | | 68 1 |
| Awp4 and CAGL0D00143g | K | VNOQGALYYIMNLK Deamidated (NQ) | G | | | | 68 1 |
| Awp4 and CAGL0D00143g | K | VNOQGALYYIMNLK Deamidated (NQ) | G | | | | 68 1 |

**SUPPLEMENTARY TABLE S1.** MS/MS identification of cell wall proteins in hyperadhesive *C. glabrata* isolate PEU1221.
Awp2 (ST: Awp2e and CAGL0L20277g)

| Peptide | Gene 1 | Gene 2 | Description | Start | End | Score |
|---------|--------|--------|-------------|-------|-----|-------|
| Awp2b (ST: Awp2e and CAGL0L20277g) | R | NVGTYVDVR | Adhesin cluster V | 1082 | 2 | 1 |
| Awp2b and Awp2d | N | SVPYQTVR | non-unique peptides | 1079 | 2 | 1 |
| Awp2c (ST: AWP4 and CAGL0L00227g) | K | GGALYYINNNLK | | 1339 | 52 | 2 |
| Awp2e or CAGL0L00227g | F | VFQNDGTVVVDDR | Deamidated (NQ) | 1463 | 98 | 1 |
| Awp2e or CAGL0L00227g | F | VFQNDGTVVVDDR | Deamidated (NQ) | 1464 | 59 | 1 |

Cwp1.1 / CAGL0G31271g

| Peptide | Gene 1 | Gene 2 | Description | Start | End | Score |
|---------|--------|--------|-------------|-------|-----|-------|
| Cwp1.1 and 1.2 | N | SGSPVQTVNPDT/DINIS/E/QINGALVK | Adhesin cluster VII | 1340 | 117 | 2 |
| Cwp1.1 and 1.2 | N | SGSPVQTVNPDT/DINIS/E/QINGALVK | Deamidated (NQ) | 1341 | 53 | 1 |

Cwp1.1 / CAGL0F08383g

| Peptide | Gene 1 | Gene 2 | Description | Start | End | Score |
|---------|--------|--------|-------------|-------|-----|-------|
| Cwp1.1 and 1.2 | E | ITHSGSPVQNTPV/DINIS/E/QINGALVK | Adhesin cluster VIII | 2262 | 45 | 1 |
| Cwp1.1 and 1.2 | L | IHSHSGSPVQNTPV/DINIS/E/QINGALVK | Deamidated (NQ) | 2263 | 60 | 3 |

Cwp1.2 / CAGL0G05751g

| Peptide | Gene 1 | Gene 2 | Description | Start | End | Score |
|---------|--------|--------|-------------|-------|-----|-------|
| Cwp1.1 and 1.2 | E | EVNLINNNRR | Ecm33 family | 1295 | 66 | 3 |
| Cwp1.1 and 1.2 | E | EGSVPQTVNPDT/DINIS/E/QINGALVK | non-unique peptides | 1297 | 50 | 1 |

Crh1 / CAGL0G81444g

| Peptide | Gene 1 | Gene 2 | Description | Start | End | Score |
|---------|--------|--------|-------------|-------|-----|-------|
| Crh1 | K | ADHSPVQTVNPDT/DINIS/E/QINGALVK | Ecm33 family | 1195 | 48 | 2 |

Gas2 / CAGL0M18448g

| Peptide | Gene 1 | Gene 2 | Description | Start | End | Score |
|---------|--------|--------|-------------|-------|-----|-------|
| Gas2 | R | DAFVFQQLGINTIR | | 1623 | 97 | 1 |

Gas3 / CAGL0F02869g

| Peptide | Gene 1 | Gene 2 | Description | Start | End | Score |
|---------|--------|--------|-------------|-------|-----|-------|
| Gas3 | R | DAFVFQQLGINTIR | | 1623 | 97 | 1 |

Pst1 / CAGL0E04620g

| Peptide | Gene 1 | Gene 2 | Description | Start | End | Score |
|---------|--------|--------|-------------|-------|-----|-------|
| Pst1 | R | ALSYQFFPTLYR | | 1506 | 64 | 2 |

Scw4 / CAGL0G03089g

| Peptide | Gene 1 | Gene 2 | Description | Start | End | Score |
|---------|--------|--------|-------------|-------|-----|-------|
| Scw4 | K | QGTLQAVPISK | Ecm33 family | 1069 | 71 | 1 |

Utr2 / CAGL0G02211g

| Peptide | Gene 1 | Gene 2 | Description | Start | End | Score |
|---------|--------|--------|-------------|-------|-----|-------|
| Utr2 | K | FDYSSK | | 893 | 47 | 2 |

Scw6 / CAGL0F08696g

| Peptide | Gene 1 | Gene 2 | Description | Start | End | Score |
|---------|--------|--------|-------------|-------|-----|-------|
| Scw6 | K | ALATSFSENFTSEK | | 1624 | 96 | 1 |

Scw7 / CAGL0G07575g

| Peptide | Gene 1 | Gene 2 | Description | Start | End | Score |
|---------|--------|--------|-------------|-------|-----|-------|
| Scw7 | K | AVDGEINGR | Deamidated (NQ) | 1731 | 47 | 2 |

Scw8 / CAGL0G08019g

| Peptide | Gene 1 | Gene 2 | Description | Start | End | Score |
|---------|--------|--------|-------------|-------|-----|-------|
| Scw8 | K | GNTATYDR | | 905 | 50 | 1 |

Scw9 / CAGL0G08475g

| Peptide | Gene 1 | Gene 2 | Description | Start | End | Score |
|---------|--------|--------|-------------|-------|-----|-------|
| Scw9 | K | IEYTDGQLSLGTK | | 1509 | 75 | 1 |

CaZy GH72

| Peptide | Gene 1 | Gene 2 | Description | Start | End | Score |
|---------|--------|--------|-------------|-------|-----|-------|
| CaZy GH72 | R | ALHSGSPVQTVNPDT/DINIS/E/QINGALVK | | 1353 | 50 | 1 |

CaZy GH72

| Peptide | Gene 1 | Gene 2 | Description | Start | End | Score |
|---------|--------|--------|-------------|-------|-----|-------|
| CaZy GH72 | R | ALHSGSPVQTVNPDT/DINIS/E/QINGALVK | | 1354 | 50 | 1 |

CaZy GH16

| Peptide | Gene 1 | Gene 2 | Description | Start | End | Score |
|---------|--------|--------|-------------|-------|-----|-------|
| CaZy GH16 | K | EVNVLNINNNR | | 1298 | 66 | 3 |

CaZy GH16

| Peptide | Gene 1 | Gene 2 | Description | Start | End | Score |
|---------|--------|--------|-------------|-------|-----|-------|
| CaZy GH16 | K | GAIQGDSFVCK | | 1183 | 76 | 3 |

CaZy GH17

| Peptide | Gene 1 | Gene 2 | Description | Start | End | Score |
|---------|--------|--------|-------------|-------|-----|-------|
| CaZy GH17 | R | ALSYQFFPTLYR | | 1503 | 64 | 2 |

CaZy GH17

| Peptide | Gene 1 | Gene 2 | Description | Start | End | Score |
|---------|--------|--------|-------------|-------|-----|-------|
| CaZy GH17 | R | ALSYQFFPTLYR | | 1503 | 64 | 2 |
| Protein | Accession | Start | End | Mascot Score | MS/MS Fragmentation |
|---------|-----------|-------|-----|--------------|---------------------|
| CAGLD011748g | R        | NAFEATTR | N | family | 909 | 54 | 3 |
| CAGLD016182g | K        | APNDPVGAVSCK | V | Pir family | 1214 | 78 | 14 |
| CAGLD038492g | K        | DPNDPVGAVSCK | V | Pir family | 1272 | 43 | 1 |
| CAGLD061600g | K        | IAECISPNLIEVVSVDKC | - | Pir family | 2045 | 118 | 2 |
| CAGLD01463g | K        | GIEALP艰苦 | L | Srp1/Tip1 family | 840 | 62 | 12 |
| CAGLD01485g | M        | QAELNAVMEDLX Oxidation (M) | T | Srp1/Tip1 family | 1489 | 77 | 2 |
| CAGLD006413g | N        | GNSDAAYTFK | N | unknown function | 1144 | 86 | 1 |

*Indicated for each peptide is the Mascot score and the number of times the peptide was selected for MS/MS fragmentation.

Blue color indicates semi-trypic (ST) peptides.

N-term of mature protein as predicted by SignalP.

Mascot assignment of semi-trypic peptides containing the sequence tags TPVDSQNGALVLK (Cwp1.1) or TPVNSENGALVLK (Cwp1.2) suggests that both proteins are present but is not unambiguous, therefore we have listed these peptides as "Cwp1.1 and 1.2."
**SUPPLEMENTARY TABLE S2.** Oligonucleotides used in this study.

| Name of primer<sup>a</sup> | Sequence 5'-3'<sup>b</sup> | Function |
|---------------------------|-----------------------------|----------|
| AWP14-KpnI-F              | CACAGGTACCGAGCTGGATTTCATGAGC | Cloning AWP14 upstream flank. |
| AWP14-XhoI-R              | CACACTCGAGCATGAACAAATGAATATTAGG | Cloning AWP14 downstream flank. |
| AWP14-NcoI-F              | CACAGCGGCCGCATTCCAGAACAGATGATGG | |
| AWP14-SacI-R              | CACAGAGCTCGTATCCACCGTATTGATAAC | |
| pSFS1-5'-R               | ATTTGAAGTTTTTACTTGGC | Checking genomic integration of the cassette together with AWP14 external primers. |
| pSFS1-3'-F               | ACAATCAAAGGTGGTCTGC | |
| AWP14-ext-F              | ATGTCCCAACCAGAG | Checking integration and excision of the cassette and deletion of AWP14. |
| AWP14-ext-R              | GGTTCGATGATAGGTATG | |
| AWP14-int_F              | GACGTATGAAAAACAAAAATTG | |

<sup>a</sup>F, forward; R, reverse.  
<sup>b</sup>Restriction enzyme sites used for cloning are underlined.