The putative lytic transglycosylase VirB1 from *Brucella suis* interacts with the type IV secretion system core components VirB8, VirB9 and VirB11

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VirB1-like proteins are believed to act as lytic transglycosylases, which facilitate the assembly of type IV secretion systems via localized lysis of the peptidoglycan. This paper presents the biochemical analysis of interactions of purified *Brucella suis* VirB1 with core components of the type IV secretion system. Genes encoding VirB1, VirB8, VirB9, VirB10 and VirB11 were cloned into expression vectors; the affinity-tagged proteins were purified from *Escherichia coli*, and analyses by gel filtration chromatography showed that they form monomers or homo-multimers. Analysis of protein–protein interactions by affinity precipitation revealed that VirB1 bound to VirB9 and VirB11. The results of bicistron expression experiments followed by gel filtration further supported the VirB1–VirB9 interaction. Peptide array mapping identified regions of VirB1 that interact with VirB8, VirB9 and VirB11 and underscored the importance of the C-terminus, especially for the VirB1–VirB9 interaction. The binding sites were localized on a structure model of VirB1, suggesting that different portions of VirB1 may interact with other VirB proteins during assembly of the type IV secretion machinery.

**INTRODUCTION**

Type IV secretion systems (T4SS) are used by many Gram-negative bacteria to translocate virulence factors into eukaryotic cells or to mediate conjugative transfer of broad-host-range plasmids (Cascales & Christie, 2003; Celli & Gorvel, 2004; Llosa & O’Callaghan, 2004; Zupan et al., 2000). T4SS are crucial determinants of host–pathogen interactions, which enable bacterial survival in widely different habitats, such as the rhizosphere of plants (*Agrobacterium tumefaciens*) and intracellular compartments of mammalian cells (*Brucella* species). The best-studied model is *A. tumefaciens*; its T4SS comprises 12 components, VirB1–VirB11 and VirD4. Biochemical, genetic and cell biological experiments suggest that VirB2–VirB11 constitute a membrane-spanning pore, which connects the inner and the outer membrane through periplasmic interactions and homo-oligomer formation, and an extracellular pilus (Cascales & Christie, 2003; Christie, 2004). VirD4 links this channel to translocated substrates (Atmakuri et al., 2003; Kumar & Das, 2002). VirB6, VirB7, VirB8, VirB9 and VirB10 constitute the core of the T4SS and the substrate transfer route, although direct evidence for channel formation is still lacking. VirB2 and VirB5 are major and minor components of the extracellular pilus of *A. tumefaciens*, which probably mediates contact formation with the host cell (Eisenbrandt et al., 1999; Hwang & Gelvin, 2004; Schmidt-Eisenlohr et al., 1999). The role of the VirB3 protein is less well defined than those of other T4SS components, but its interaction with pilus components and localization in the outer membrane suggest that it may play a role during the assembly of this structure (Jones et al., 1994; Shamaei-Tousi et al., 2004; Yuan et al., 2005). VirB4 and VirB11 are multimeric inner-membrane-localized NTPases, which may traverse the inner membrane to contact periplasmic VirB proteins (Atmakuri et al., 2004; Dang & Christie, 1997; Middleton et al., 2005; Yeo et al., 2003; Yuan et al., 2005). They may either act as assembly factors for the T4SS or drive pilus subunits or substrate molecules across the cell envelope. VirB2–VirB11 are indispensable both for gene transfer from *A. tumefaciens* and for *Brucella*’s ability to reach the proper intracellular niche and to replicate within HeLa cells or macrophages (Berger & Christie, 1994; Comerci et al., 2001; O’Callaghan et al., 1999; Sieira et al., 2000).

**Abbreviations:** S2B, StreptII buffer; T4SS, type IV secretion system(s).
VirB1 is the only non-essential T4SS component. It was previously demonstrated that VirB1 homologues play an important role in the T4SS of *A. tumefaciens* and *Escherichia coli* strains harbouring plasmids pKM101 and R1. The efficiency of substrate transfer was reduced 10- to 1000-fold upon non-polar deletion of the encoding genes (Bayer et al., 1995; Berger & Christie, 1994; Fullner, 1998; Winans & Walker, 1985). An infection assay with signature-tagged *Brucella abortus* mutants demonstrated that mutagenesis of the virB1 gene causes attenuation of virulence (Hong et al., 2000). A more recent study demonstrated that survival of *B. abortus* in macrophage cell cultures was attenuated in strains carrying a non-polar virB1 mutation (den Hartigh et al., 2004). Thus the deletion of genes encoding VirB1 homologues generally has an attenuating effect on T4SS-related functions. The *Helicobacter pylori* VirB1 homologue HP0523 is an exception to this rule, as it was shown to be essential for bacterial virulence (Odenbreit et al., 2001; Rohde et al., 2003). Due to the presence of highly conserved sequence motifs, VirB1 was identified as a putative lytic transglycosylase, but its specific role for T4SS function was not elucidated in detail. *A. tumefaciens* and *Brucella suis* VirB1 both possess a signal sequence and are therefore directed to the periplasmic space by the general secretion pathway (Llosa et al., 2000; O’Callaghan et al., 1999). Their enzymatic activity probably leads to localized cell wall lysis, creating space for accommodation of the T4SS (Bayer et al., 2001; Mushegian et al., 1996; Zahrl et al., 2005). Despite the well-known area of lysozyme biochemistry, proposals for the catalytic mechanism of lytic transglycosylases were published only recently. Whereas the well-known lysozymes like hen egg white lysozyme break up murein by hydrolysis of the β(1→4)-glycosidic bond between the N-acetylmuramic acid (MurNAc)-C1 and the N-acetylglucosamine (GlcNAc)-C4, the lytic transglycosylases lyse this substrate in a transglycosylation reaction utilizing the C6-OH residue of the same MurNAc (Blackburn & Clarke, 2001). This is because no water is required for the reaction, which produces a 1,6-anhydromuramic acid terminal residue. Special features of the active site that distinguish the lytic transglycosylases from lysozymes must explain the mechanistic difference, and this question is subject to structural biological studies (Lehnerr et al., 1998; Leung et al., 2001; Mushegian et al., 1996; Thunnissen et al., 1994; van Asselt et al., 1999, 2000).

When VirB1 was identified as a lytic transglycosylase, its importance for the *A. tumefaciens* T4SS was largely attributed to its proposed catalytic activity. This notion was repeatedly confirmed by the observation that active-site mutants of the protein failed to fully complement virB1 deletion strains (Höppner et al., 2004; Mushegian et al., 1996). After export across the inner membrane, VirB1 of *A. tumefaciens* is further processed in the periplasm, yielding a processing product of the C-terminal 73 amino acids designated VirB1* (Baron et al., 1997). VirB1* and the N-terminus, representing the lytic transglycosylase domain, independently enhanced tumorigenicity, which implied an additional function of VirB1* (Llosa et al., 2000). Further evidence for this hypothesis was generated when it was shown by co-immunoprecipitation that VirB9 interacts with VirB1* in *A. tumefaciens* (Baron et al., 1997). A high-resolution dihybrid screen with protein components of the *A. tumefaciens* T4SS suggested self-interaction and a number of uni- and bidirectional interactions between VirB1 and VirB4, VirB8, VirB9, VirB10 and VirB11 (Ward et al., 2002). Direct biochemical evidence for the interactions was not presented in that study.

In spite of the low overall amino acid sequence identity of 22 %, the VirB1 homologue from *B. suis* complemented virB1 gene defects in *A. tumefaciens*, suggesting that it engages in similar interactions with T4SS components. Similarly, the *B. suis* VirB4 homologue complemented virB4 gene defects in *A. tumefaciens* (Yuan et al., 2005), which further supported the notion that the overall architecture of different T4SS is very similar (Christie, 2004; Yeo & Waksman, 2004). To directly test interactions of VirB1sp with T4SS core components we chose derivatives of VirB proteins from *B. suis*, (abbreviated VirB9 in the following – or VirBsp to indicate periplasmic domains without signal peptides or membrane domains), which are more readily amenable to overproduction and purification than those from *A. tumefaciens*. Using different biochemical methods (affinity precipitation, gel filtration, bicistron expression, peptide array analysis), we showed that purified *B. suis* T4SS core components undergo different interactions. VirB1sp was found to interact with VirB9sp, and whereas this interaction was the strongest among those we investigated, VirB1sp also bound to VirB8sp and VirB11s. The binding sites were localized in a structure model of VirB1sp, suggesting that a sequence of transient interactions guides lytic transglycosylase function during T4SS assembly.

### METHODS

#### Cultivation of bacteria

For overnight cultures all *E. coli* strains were grown in LB (1 % tryptone; 0.5 % yeast extract; 0.5 % NaCl) or LBON (1 % tryptone; 0.5 % yeast extract) under aerobic conditions at 37 °C in a laboratory shaker (modell Kühner, B. Braun) at 200 r.p.m. Carbenicillin (100 μg ml⁻¹) was included for selection of plasmid-carrying cells. Day cultures were inoculated to an OD600 of 0.05 in vessels of appropriate volume with the same media under vigorous shaking at 37 °C (Cerontmat-R, B. Braun Biotech International). The T7 promoter in the protein-overproducing strain GJ1158 (Bhandari & Gowrishankar, 1997) was induced at an OD600 of 0.4-0.8 by addition of 5 M NaCl stock solution to a final concentration of 0.3 M. Cultivation under aerobic conditions then proceeded at different temperatures for varying amounts of time for the overproduction of specific proteins as follows: VirB1s (C- or N-terminal tag) at 26 °C for 4 h, VirB1s/VirB8X (bicistron constructs) at 26 °C for 6 h, VirB7sp at 26 °C for 4 h, VirB8sp at 37 °C for 4 h, VirB9sp at 37 °C for 4 h, VirB10sp at 27 °C for 6 h, VirB11s at 27 °C for 18 h. The total culture volumes were 1 litre, in four 500 ml Erlenmeyer flasks each containing 250 ml LBON.

#### Molecular biology methods

Manipulations of DNA for plasmid isolation, PCR amplification, restriction, ligation and sequencing followed standard procedures, using enzymes from New England Biolabs and MBI Fermentas and *E. coli* JM109 as cloning host (Maniatis et al., 1982; Yanisch-Perron et al., 1985). PCR fragments
were first cloned into pCR2.1-TOPO (Invitrogen), followed by sequencing and further subcloning into expression vectors as described below.

**Construction of virB gene expression vectors.** Expression vectors for the production of VirBs proteins (Table 1) were constructed by PCR amplification of the genes with oligonucleotides, which introduced 5’ and 3’ restriction sites (sequences given in Table 2), followed by ligation into similarly cleaved vectors. Constructs for the overproduction of N-terminally tagged StrepII-VirB1sp and StrepII-VirB10sp were described previously (Yuan et al., 2005). The gene encoding VirB11sp was subsequently subcloned into pT7-H6TrxFus for expression as an N-terminally His6-TrxA-tagged fusion protein (pT7-H6TrxFus, pT7-H6TrxFus). The gene encoding VirB11s was subsequently subcloned using the same restriction sites into pT7-H6TrxFus for expression as an N-terminally His6-TrxA-tagged fusion protein (pT7-H6TrxFus, pT7-H6TrxFus). Constructs for the production of VirBs proteins (Table 1) were constructed as follows. In order to co-produce C-terminally His6-tagged VirB1sp with putative interaction partners, vector pET21BC was constructed by introducing a SalI/NotI DNA fragment encoding *Schizosaccharomyces pombe* Srb11 including the ribosome-binding site (Baumli et al., 2005). The first ORF of the pET21BC series encoded the putative interaction partner and was created by cleavage of the vector with *NheI/EcoRI* and insertion of PCR-amplified *virB8, virB9*, and *virB10* genes treated with the same restriction endonucleases. After excision of the Srb11-encoding gene by cleaving the vector with *NheI/NotI*, *virB10* was inserted using the same

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**Table 1. Plasmids**

<table>
<thead>
<tr>
<th>Plasmid</th>
<th>Genotype</th>
<th>Source or reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>pUC18VirB</td>
<td>CarbK, virB region from <em>B. suis</em> 1330</td>
<td>O'Callaghan et al. (1999)</td>
</tr>
<tr>
<td>pCR2-1-TOPO</td>
<td>CarbK, Kan8, for direct cloning of PCR fragments</td>
<td>Invitrogen</td>
</tr>
<tr>
<td>pET24d</td>
<td>Kan8, cloning and T7 expression vector</td>
<td>Novagen</td>
</tr>
<tr>
<td>p17-7StrepII</td>
<td>CarbK, for overexpression of N-terminally StrepII-tagged proteins</td>
<td>Balsinger et al. (2004)</td>
</tr>
<tr>
<td>p17-7StrepIIVirB8sp</td>
<td>p17-7StrepII with 492 bp Acc65I/PstI fragment of <em>virB8</em> from <em>B. suis</em></td>
<td>Yuan et al. (2005)</td>
</tr>
<tr>
<td>p17-7StrepIIVirB9sp</td>
<td>p17-7StrepII with 813 bp Acc65I/PstI fragment of <em>virB9</em> from <em>B. suis</em></td>
<td>Yuan et al. (2005)</td>
</tr>
<tr>
<td>p17-7StrepIIVirB10sp</td>
<td>p17-7StrepII with 1020 bp Acc65I/PstI fragment of <em>virB10</em> from <em>B. suis</em></td>
<td>Yuan et al. (2005)</td>
</tr>
<tr>
<td>p177-StrepIIVirB11s</td>
<td>p17-7StrepII with 1083 bp Acc65I/HindIII fragment of <em>virB11</em> from <em>B. suis</em></td>
<td>This work</td>
</tr>
<tr>
<td>p17-H6TrxFus</td>
<td>CarbK, for T7-based expression of N-terminal His6-TrxA (thioredoxin) fusions</td>
<td>Kromayer et al. (1996)</td>
</tr>
<tr>
<td>p17-H6TrxVirB7sp</td>
<td>p17-H6TrxFus with 126 bp XbaI/PstI fragment of <em>B. suis</em> virB7</td>
<td>This work</td>
</tr>
<tr>
<td>p17-H6TrxVirB8sp</td>
<td>p17-H6TrxFus with 492 bp Acc65I/PstI fragment of <em>B. suis</em> virB8</td>
<td>Yuan et al. (2005)</td>
</tr>
<tr>
<td>p17-H6TrxVirB9sp</td>
<td>p17-H6TrxFus with 813 bp Acc65I/PstI fragment of <em>B. suis</em> virB9</td>
<td>Yuan et al. (2005)</td>
</tr>
<tr>
<td>p17-H6TrxVirB10sp</td>
<td>p17-H6TrxFus with 1020 bp Acc65I/PstI fragment of <em>B. suis</em> virB10</td>
<td>Yuan et al. (2005)</td>
</tr>
<tr>
<td>p17-H6TrxVirB11s</td>
<td>p17-H6TrxFus with 1083 bp Acc65I/HindIII fragment of <em>virB11</em> from <em>B. suis</em></td>
<td>This work</td>
</tr>
<tr>
<td>p17-7StrepIIVirB1sp</td>
<td>p17-7StrepII with 654 bp Acc65I/PstI fragment of <em>virB1</em> from <em>B. suis</em></td>
<td>This work</td>
</tr>
<tr>
<td>pET21BC</td>
<td>Carb8, pET21 derivative with a DNA fragment encoding the <em>S. pombe</em> ribosome-binding site and Srb11 cloned with SalI/NotI into pET21b (with two RBS in the polylinker) for T7-driven bicistronic expression; determines His6-tagged C-terminus of second ORF</td>
<td>This work</td>
</tr>
<tr>
<td>pET24dVirB1spHis6</td>
<td>Kan8, pET24d with 654 bp NcoI/NotI <em>B. suis</em> virB1 fragment</td>
<td>This work</td>
</tr>
<tr>
<td>pET21BCVirB8sp-VirB1spHis6</td>
<td>pET21BC with 524 bp <em>NheI/EcoRI</em> virB8 and 654 bp NcoI/NotI <em>B. suis</em> virB1 fragment downstream</td>
<td>This work</td>
</tr>
<tr>
<td>pET21BCVirB9sp-VirB1spHis6</td>
<td>pET21BC with 776 bp virB9 and 654 bp <em>B. suis</em> virB1 fragment downstream</td>
<td>This work</td>
</tr>
<tr>
<td>pET21BCVirB10sp-VirB1spHis6</td>
<td>pET21BC with 1011 bp virB10 and 654 bp <em>B. suis</em> virB1 fragment downstream</td>
<td>This work</td>
</tr>
<tr>
<td>pET21BCVirB8sp</td>
<td>pET21BCVirB8sp-VirB1spHis6, virB1 gene removed with SalI/XhoI and religated</td>
<td>This work</td>
</tr>
<tr>
<td>pET21BCVirB9sp</td>
<td>pET21BCVirB9sp-VirB1spHis6, virB1 gene removed with SalI/XhoI and religated</td>
<td>This work</td>
</tr>
<tr>
<td>pET21BCVirB10sp</td>
<td>pET21BCVirB10sp-VirB1spHis6, virB1 gene removed with SalI/XhoI and religated</td>
<td>This work</td>
</tr>
</tbody>
</table>
restriction sites. This placed virB1 in-frame with the vector sequence encoding the C-terminal His$_6$-tag. A series of constructs for the expression of non-tagged proteins was generated to serve as controls, as these proteins did not bind avidly to affinity columns. Based on the pET21BC bicistron vectors, three constructs that served as negative controls were created by excision of virB1 with SalI/XhoI and religation of the vector. Untagged VirB8sp, VirB9sp or VirB10sp were produced upon induction of expression from these vectors.

Strep-Tactin Sepharose chromatography. Bacterial cells were resuspended in 4–8 ml StreplI buffer (S2B) without DTT (300 mM NaCl, 100 mM Tris/HCl, 1 mM EDTA, pH 7.0) and with 0·5 mM PMSF and passed three times through a French pressure cell (Amino) at 18 000 p.s.i. The lysate was centrifuged (SS34 rotor, 20 min, 13 000 r.p.m. at 4°C) to remove cell debris and unbroken cells, and the N-terminal StreplI-fusion protein was purified with a 1 ml Streptactin Sepharose column following the instructions of the manufacturer (IBA), using 2·5 mM desthiobiotin in the elution buffer. The fractions were subsequently purified by size-exclusion chromatography using S2B at a flow rate of 0·5 ml min$^{-1}$. Superdex 75 or Superdex 200 (Amersham Pharmacia Biosciences) was used depending on the molecular mass of the protein. The samples were dialysed for >12 h against 1 litre of PSB (S2B with 50% glycerol) in dialysis tubing (Visking, Roth) at 4°C and were stored at −20°C until further use. Protein concentrations were determined using the Bradford dye binding assay (Bio-Rad) with bovine serum albumin (Aminco) at 18 000 p.s.i. The lysate was centrifuged (SS34 rotor, 20 min, 13 000 r.p.m. at 4°C) to remove cell debris and unbroken cells, and the N-terminal Streptactin Sepharose pull-down assay. Samples were loaded onto Superdex 75 or Superdex 75 gel filtration columns in S2B; the flow rate was 0·5 ml min$^{-1}$ or 1·0 ml min$^{-1}$. To determine the molecular mass of proteins, the columns were calibrated with the Gel Filtration Calibration Kit (Amersham Pharmacia Biotech), which uses reference proteins in the range between 13·7 and 669 kDa.

SDS-PAGE and Western blotting. Proteins were separated in denaturing SDS gels using the Laemmli system (Laemmli, 1970) followed by transfer to PVD membranes (Immobilon-P, Millipore) in a vertical blot device (Trans Blot Cell, Bio-Rad; blot buffer 192 mM glycine, 25 mM Tris, 20% methanol) at 90 V for 1 h or 30 V for 16 h (Harlow & Lane, 1988). Proteins attached to peptide array membranes (see below) were transferred in a semi-dry blot device (Fast-Blot, Biometra) onto PVD membranes following a specialized protocol, followed by regeneration of the membrane as suggested by the manufacturer (Jerini). Proteins were detected with goat anti-rabbit IgG-HRP (Bio-Rad), a chemiluminescence detection system (Lumi Light, Roche Diagnostics) and X-ray film (Harlow & Lane, 1988).
Peptide array experiments. The entire sequence of VirB1sp from *B. suis* (GenBank accession no. NP_699276) without the signal peptide was displayed on a cellulose membrane as seventy 13-mers, covalently bound at the C-terminus and with N-terminal acetylation, shifting three amino acid positions each time, beginning with peptide 1 (AAIVQVESGFNPY), peptide 2 (QVESGFPYPAIG), etc., to peptide 70 (PPPGKDNTDGVVVF). The protocol for 'Mapping of discontinuous epitopes' from the manual of the supplier (Jenini) was followed. The peptide array membrane, which features all possible linear epitopes of VirB1sp, was precleaned for 30 min in TBS-T (20 mM Tris/Cl, 137 mM NaCl, 0.1% Tween-20; pH 8.0), transferred into blocking solution (Roche) for 1 h, washed again with TBS-T for 10 min and then incubated in blocking solution containing 1–5 μg/ml of different proteins (StrepIIVirB1sp, StrepIIVirB8sp, StreplVirB9sp or StreplVirB11s) for 12 h at 4 °C. Before transfer of the attached proteins onto PVDF membranes with a semi-dry blot device (see above), the peptide array membrane was washed three times in TBS-T for 10 s to remove non-specifically bound protein.

Generation of polyclonal antisera. Soluble SteplIIVirB11s and H₄TrxAVirB7 were purified by affinity chromatography as described above, whereas SteplIIVirB1sp was obtained from a preparation of inclusion bodies, separated by SDS-PAGE, excised from the gel and subjected to electroelution. Approximately 0.5 mg of each protein was lyophilized and used for immunization of rabbits (BioGenes) to generate specific antisera. The other antisera used in this study were described elsewhere (Yuan et al., 2005).

Graphical data processing. To capture images of polyacrylamide gels and chemoluminograms, they were digitized using a UMAX UTC-6400 scanner, followed by processing with Photoshop 6.0 (Adobe) and Canvas 7.0 (Deneba Systems).

Protein sequence analysis. The CLUSTAL W (version 1.82) algorithm for multiple sequence alignment (Higgins, 1994) (http://www.ebi.ac.uk/clustalw) or EMBOSS for alignment of two less conserved amino acid sequences (Needleman & Wunsch, 1970; Smith & Waterman, 1981) (http://www.ebi.ac.uk/emboss/align) were applied. Sequence information was processed with NORSp (Liu & Rost, 2003) (http://cubic.bioc.columbia.edu/services/NORSp) in order to discover long regions without regular secondary structure. Predictions of secondary structure were obtained with the PHD algorithm (Rost, 1996) (http://www.embl-heidelberg.de/predictprotein). To create a conservation plot of sequence alignment, the alignment data were transferred to the AMAS server (Livingstone & Barton, 1993) (http://barton.ebi.ac.uk/servers/amas_server.html) using standard default values. All structure images were generated with DINO 9.0 (http://cobra.msh.unibas.ch/dino/intro.php).

**RESULTS**

Purification and characterization of affinity-tagged *B. suis* VirBs proteins

To analyse interactions of VirB1s with *B. suis* VirBs the region of virB1 encoding the predicted periplasmic domain of the protein without signal peptide was PCR-amplified and cloned into pT7-7-StrepII for expression with an N-terminal SteplII peptide (StrepIIVirB1sp) or into pET24d for expression with a C-terminal His₆ tag (VirB1spHis₆). The gene encoding full-length VirB1s was PCR-amplified and cloned into pT7-7StrepII for expression with an N-terminal SteplII peptide (StrepIIVirB11s). Similar clones for expression of SteplIIVirB8sp, SteplII-VirB9sp and SteplIIVirB10sp were described previously (Yuan et al., 2005). The proteins were overproduced and purified via affinity columns, followed by gel filtration over a Superdex 200 column for further purification and analysis of their molecular masses. Analysis with a specific antiserum showed that both N- and C-terminally tagged variants of VirB1sp eluted in a broad molecular mass range; we have indicated the predicted sizes of monomers, dimers, tetramers and hexamers in Fig. 1. The relative distribution between the different forms varied between experiments and the hexameric form was not always prominent, suggesting a dynamic equilibrium between different multimeric forms. In addition, large portions of VirB1sp (70–80 %) eluted in the void volume in high-molecular-mass complexes (Fig. 1). The elution of lytic transglycosylases in high-molecular-mass complexes has also been observed by others and was shown to be due to binding of the proteins by GroEL (Zahril et al., 2005). The possibility that GroEL binds to VirB1sp was therefore assessed by Western blot analysis of the samples eluted from the gel filtration column using specific antiserum, and we indeed detected co-elution of VirB1sp variants with GroEL in the void volume (not shown). Analysis of the molecular masses of the other VirBs proteins by gel filtration showed that they eluted as apparent monomers (StrepII-VirB8sp and SteplIIVirB9sp), dimers (StrepIIVirB10sp) or hexamers (StrepIIVirB11s) (Table 3). Varying degrees of high-molecular-mass aggregates eluting in the void volume of gel filtration columns were observed in all cases. The amounts varied in different overexpression experiments and could not be reduced by the addition of DTT or increased NaCl concentrations (not shown). Whereas we cannot exclude that these aggregates are of physiological relevance,
Table 3. Molecular masses of StrepIIVirB proteins

<table>
<thead>
<tr>
<th>Protein analysed</th>
<th>Expected mass of the monomer (kDa)</th>
<th>Mass determined by gel filtration (kDa)</th>
<th>Tertiary structure determined by gel filtration</th>
</tr>
</thead>
<tbody>
<tr>
<td>StrepIIVirB1sp</td>
<td>27</td>
<td>Various to 160</td>
<td>Monomer, dimer, tetramer, hexamer</td>
</tr>
<tr>
<td>and VirB1spHis6</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>StrepIIVirB8sp</td>
<td>22</td>
<td>26</td>
<td>Monomer</td>
</tr>
<tr>
<td>StrepIIVirB9sp</td>
<td>33</td>
<td>41</td>
<td>Monomer</td>
</tr>
<tr>
<td>StrepIIVirB10sp</td>
<td>43</td>
<td>92</td>
<td>Dimer</td>
</tr>
<tr>
<td>StrepIIVirB11s</td>
<td>41</td>
<td>242</td>
<td>Hexamer</td>
</tr>
</tbody>
</table>

we did not consider this as very likely and used only the lower-molecular-mass fractions for the following studies.

Analysis of interactions by gel filtration

As a first approach to assess interactions between purified StrepIIVirB proteins, mixtures of these proteins were co-incubated to allow complex formation. The samples were then subjected to gel filtration chromatography over a Superdex-200 column. Complex formation was assumed to lead to shifts of the elution volumes, but we did not observe changes in any case. This suggested that these proteins do not interact, or that the affinities are not high enough to form complexes stable during gel filtration (not shown).

We subsequently followed an alternative strategy based on the observation that recombinant proteins produced in *E. coli* are often insoluble or misfolded, and one reason for this is that their natural binding partners are absent. One method to circumvent this problem is the co-expression of the genes encoding such proteins together with genes encoding potential interaction partners (Lutzmann et al., 2002). To this end, the potential interactions of VirB1sp with other components of the *B. suis* T4SS were tested by expression from vectors encoding C-terminally tagged VirB1spHis6, fusion proteins and their putative interaction partners VirB8sp, VirB9sp or VirB10sp. In order to co-produce His6-tagged VirB1sp with putative interaction partners, vector pET21BC was constructed to permit expression of bicistronic mRNAs. The first ORF of the pET21BC series encoded the putative interaction partners VirB8sp, VirB9sp and VirB10sp, and the second one VirB1spHis6. In addition, a series of pET21BC-derived monocistronic constructs for the expression of the non-tagged interaction partners VirB8sp, VirB9sp or VirB10sp without VirB1spHis6 was generated to serve as controls.

The proteins encoded on the pET21BC-derived vectors were overproduced in *E. coli*, followed by cell lysis, purification over a His6-tag-specific affinity column and Superdex 200 gel filtration for analysis of complex formation. In spite of the two-step separation procedure, the untagged VirB8sp proteins from both monocistronic and bicistronic expression experiments were detected in the gel filtration eluates, indicating that VirB8sp, VirB9sp and VirB10sp had non-specific binding affinity to the column. In order to distinguish between co-elution due to similar molecular masses and co-elution as an effect of an interaction, we compared the elution after expression from a bicistronic expression vector with that after expression from a monocistronic vector. VirB8sp eluted as a monomer in fractions 24–28 from the gel filtration in both cases, and VirB1spHis6 eluted in fractions 17–21, supposedly the tetrameric and dimeric form (Fig. 2a). The co-expression with *virB8* thus had no apparent effect on the elution of VirB1spHis6 and vice versa, suggesting that these two proteins did not interact. When VirB1spHis6 was produced from the bicistronic vector with VirB10sp it eluted in fractions 17–19, which corresponded to the molecular mass expected for the tetramer (Fig. 2c). VirB10sp produced in strains carrying the monocistronic as well as the bicistronic vector eluted in fractions 17–19 as a dimer. As the molecular masses of VirB1spHis6 and VirB10sp were very similar, this experiment did not give any evidence for an interaction. In contrast, when VirB1spHis6 was produced from the bicistronic vector with VirB9sp it eluted from the column in three forms (Fig. 2b). First, it was detected in fractions 6–9, representing a large complex that had a lower molecular mass than that of VirB1spHis6 when it was expressed from a monocistronic vector. Second, it eluted in fractions 15–17, corresponding to a complex markedly larger than the hexamer of 160 kDa, and third, it was detected in fractions 21–23, corresponding to a size between the dimer and tetramer. VirB9sp eluted in fractions 6–9 and 15–17 but the largest portion of the protein was monomeric (fractions 22–25). In contrast, when VirB9sp was expressed from the monocistronic vector, it predominantly eluted in fractions 22–25, which corresponded to the supposed monomer. It is evident from the comparison of the elution profiles that the co-expression with VirB9sp affected the oligomeric state of VirB1spHis6 and vice versa. Whereas this method did not permit the unambiguous identification of hetero-oligomer formation, the results support a direct interaction between the two proteins. Alternative methods were employed in the following to further assess this possibility.

Analysis of interactions by affinity precipitation

An alternative way to demonstrate protein–protein interactions is a pull-down assay that exploits the affinity of the
Fig. 2. Coelution of VirB1spHis6 with other T4SS components: Superdex 200 gel filtration analysis of the molecular masses of VirB8sp (a), VirB9sp (b) and VirB10sp (c) expressed alone or from bicistronic vectors (bc) together with VirB1spHis6 after overproduction and purification by affinity chromatography. After gel filtration, the proteins in the eluted 2 ml fractions were separated by SDS-PAGE followed by Western blotting and detection with specific antisera. Upper panels were probed with VirB1sp-specific antiserum, whereas lower panels were probed with antisera specific for VirB8sp (a), VirB9sp (b) and VirB10sp (c), respectively, as indicated by arrows. A dashed line marks the Superdex 200 void volume at >600 kDa. Arrowheads point to the expected size of monomeric (M), dimeric (D) and tetrameric (T) proteins. VirB1spHis6 was detected in a complex of typical molecular mass (X), which was larger than the hexamer, exclusively after co-expression with VirB9sp. Molecular masses of SDS-PAGE marker proteins are given on the right in kDa; the elution of gel filtration reference proteins with their associated molecular masses (MM) from the Superdex 200 column is indicated below the chemilumograms. All experiments were performed up to three times with similar results and the results of one set of representative experiments is shown.

StrepII tag for the Strep-Tactin Sepharose affinity matrix. The VirBs proteins that were tested for their capacity to bind StrepIIVirB1sp were affinity-purified as His6-tagged thioredoxin fusions (His6TrxA) and their co-precipitation with StrepII-tagged VirB1sp bound to the affinity matrix was determined. His6TrxAVirB7sp, which was not expected to interact with VirB1sp, was included as a negative control for non-specific binding of the His6TrxA affinity tag. Equimolar mixtures of StrepIIVirB1sp were incubated with His6TrxAVirB7sp, His6TrxAVirB8sp, His6TrxAVirB9sp, His6TrxAVirB10sp or His6TrxAVirB11s, followed by sedimentation of the affinity matrix, washing and elution of StrepIIVirB1sp and attached binding partners with biotin, SDS-PAGE and Western blot analysis. His6TrxAVirB7sp and His6TrxAVirB10sp did not co-precipitate with StrepIIVirB1sp, showing that these proteins did not interact under these conditions (Fig. 3). These results also demonstrated that the His6TrxA tag had no affinity for the matrix utilized here. A different observation was made in the case of His6TrxAVirB8sp, which bound to the matrix irrespective of the presence of StrepIIVirB1sp. Since even extensive washing could not remove the protein from the Strep-Tactin matrix, it was impossible to use this method to assess this interaction. Co-fractionation with StrepIIVirB1sp was demonstrated in the case of His6TrxAVirB9sp and His6TrxAVirB11s (Fig. 3). These results substantiate the interaction of VirB1sp with VirB9sp observed above and suggest that VirB11s may be another interaction partner. Since our experiments gave evidence for interactions of VirB1sp with VirB9sp and VirB11s, and VirB8sp may also interact with VirB1sp (Ward et al., 2002), we next analysed the binding site(s) on VirB1sp using peptide array experiments.

Peptide array analysis of VirB1sp interactions

The analysis of binding to peptide arrays constitutes a high-resolution method to narrow down interaction site(s) on a protein, which has been used successfully for antibody epitope mapping and for the analysis of protein–protein interaction sites (Burns-Hamuro et al., 2003; Knoblauch et al., 1999; Llanos et al., 1999; Reimer et al., 2002; Reineke et al., 1999). The analysis of multiple binding partners of different binding affinities in parallel permits a direct comparison of the bound region(s) and enables positive and negative control experiments. To this end, the binding of StrepIIVirB8sp, StrepIIVirB9sp and StrepIIVirB11s to 70 peptides displayed on membranes (13 amino acids long, three amino acids overlap) which represented the entire sequence of the processed form of VirB1sp, was analysed. Three identical membranes were used in parallel experiments, and they retained StrepIIVirBs proteins in every case. Western blots from five independent experiments, which determined the binding of an interaction partner to specific peptides, were graphically superimposed to obtain a representative mean result (Fig. 4a–c). The intensity of the signal for each spot was categorized from 1 (weak) to 4 (very strong). By aligning the sequences of the bound peptides, which overlapped by three amino acids, it was possible to identify domains of VirB1 that bind the respective VirBsp protein (Fig. 4d). When more than one spot defined an interacting domain in the sequence, the highest value of signal intensity present was assigned to the entire domain.
The three studied proteins StrepIIVirB8sp, StrepIIVirB9sp and StrepIIVirB11s bound to peptides from different regions of VirB1sp and the binding strengths were different, as indicated by the numbers of bound peptides and the signal intensity on the chemoluminogram. StrepIIVirB9sp bound to the highest number of VirB1sp peptides, but StrepIIVirB8sp and StrepIIVirB11s also bound to a defined set of VirB1sp peptides. To place this information in the context of the protein structure, a prediction of the VirB1sp secondary structure was done with the PHD algorithm and the proposed secondary structure is also shown in Fig. 4(a–c). Weak binding of StrepIIVirB8sp occurred to a region C-terminal to the catalytic Glu27 residue, which is predicted to be a loop/β-sheet region (Fig. 4a). StrepIIVirB8sp strongly interacted with another loop region N-terminal to the C-terminus. StrepIIVirB9sp bound to different amino acid stretches throughout the entire sequence of VirB1 (Fig. 4b). Interactions of intermediate strength occurred with three parts of the VirB1sp sequence that are only three amino acids long. StrepIIVirB9sp bound to the first three amino acids following the predicted signal peptide of VirB1, a loop region C-terminal to a short β-sheet and N-terminal to the conserved GIAQ motif, which is characteristic of all soluble lytic transglycosylases. An extended domain bound with intermediate strength by StrepIIVirB9sp was localized to the C-terminus of VirB1. Strong interactions with the amino acids C127–Y128–Y129 were observed, which are predicted to participate in the formation of an α-helix N-terminal to the C-terminus. Very strong binding to a loop region shortly after the GIAQ motif and N-terminal to the start of the C-terminus was detected. In addition, two long amino acid sequence stretches in the C-terminus were strongly recognized by StrepIIVirB9sp (Fig. 4b). StrepIIVirB11s bound only to a limited set of peptides on the VirB1sp array membrane (Fig. 4c). A weak interaction of StrepIIVirB11s with the VirB1sp sequence was apparent in a loop/β-sheet region C-terminal to the catalytic Glu27. Strong binding to an α-helix/loop region and to a loop region in the amino acid sequence constituting the second half of the lytic transglycosylase domain was detected. A very strong interaction of StrepIIVirB11s was observed with a short loop region C-terminal to the GIAQ motif. These results further substantiated the interactions of VirB1sp with other T4SS components shown by different methods above. Interacting amino acids are often found in external loop regions, but a structure of VirB1sp was not available. To further assess the biological relevance of these interactions it was necessary to place the information on bound peptides in the context of a three-dimensional structure, and a model of the VirB1sp structure was generated next.

Modelling of the VirB1 structure and localization of its VirB protein interaction site(s)

To assess whether the sequence stretches of VirB1sp that interact with other proteins are spatially clustered and are conserved among different VirB1-like proteins, the X-ray structure of the soluble lytic transglycosylase Slt70 from E. coli was used as a model to approximate the structure of B. suis VirB1. To identify residues conserved among VirB1-like proteins, several of them were aligned with E. coli Slt70 (Fig. 5a). Next, the AMAS algorithm was used to assign values expressing the degree of conservation to all amino acid positions in a multiple sequence alignment, ranging from A (identical) to 8 (weakly conserved). One of the sequences in this alignment was a protein with known tertiary structure (here E. coli Slt70) and the other was B. suis VirB1. To identify residues conserved among VirB1-like proteins, several of them were aligned with E. coli Slt70 (Fig. 5a). Next, the AMAS algorithm was used to assign values expressing the degree of conservation to all amino acid positions in a multiple sequence alignment, ranging from A (identical) to 8 (weakly conserved).
VirB1. The software DINO was next applied to create a map of conserved residues on the surface of the known three-dimensional model (Fig. 5b, c). It is assumed that conserved patches on the surface are likely to interact either with partner proteins or substrate(s). Following the modelling we found that many of the amino acids conserved between VirB1 and Slt70 were not exposed on the surface but rather seem to stabilize the structurally conserved lysozyme fold. The most prominent conserved surface patch was the active-site cleft with the catalytic Glu residue, which is ubiquitously found throughout all lysozyme-like enzymes (Fig. 5b, c). The C-terminus of VirB1s did not align with Slt70 and it is thus not part of the model.

Next, the model was used to localize the interaction sites with StrepIIVirB8sp, StrepIIVirB9sp and StrepIIVirB11s on the surface of the VirB1sp model (Fig. 5d). The peptide array experiments yielded signals of different intensities corresponding to peptides featuring parts of the VirB1sp sequence. The corresponding sequences were aligned, and defined regions of interaction. For each interacting region, the intensity of the signals constituting it was categorized into four classes, from ‘weak’ to ‘very strong’.

This classification did not compare signal intensities between peptide array experiments with different proteins and therefore, a ‘strong’ interaction of VirB1sp peptides with StrepIIVirB8sp might be classified as ‘intermediate’ in a peptide array with StrepIIVirB9sp. The studies are therefore semi-quantitative and need to be followed up by more quantitative methods in future. StrepIIVirB8sp and StrepIIVirB9sp apparently interacted with surface-exposed loop regions of VirB1sp that are most probably situated on different sides of the protein, and StrepIIVirB11s may bind to a part of the protein that connects these two (Fig. 5d). Interestingly, both StrepIIVirB9sp and StrepIIVirB11s bound strongly to peptides representing a not well-conserved part of the protein C-terminal to the second region, which is probably required for enzymic activity (boxed in Fig. 5a). Similarly, both StrepIIVirB8sp and StrepIIVirB9s bound strongly C-terminal to the third region implicated in enzyme activity of lytic transglycosylases (boxed in Fig. 5a). Most of the proposed interactions between VirB1sp and StrepIIVirB9sp could not be visualized in this model since they map to the C-terminal region of VirB1sp, which lacks a counterpart in Slt70. Nevertheless, the identification of binding sites for other T4SS components in a structure
model of VirB1sp constitutes a substantial advance in our understanding of the biological role of this protein. Our work lays the foundation for detailed structure–function analyses in future.

**DISCUSSION**

A role of VirB1 as nucleation centre for T4SS assembly has been suggested before, but hitherto, the interactions of VirB1 with T4SS components had only been demonstrated in the yeast dihybrid system (Ward et al., 2002). Here we have directly studied the interaction of VirB1sp with most of its proposed interaction partners. This analysis was possible because the *B. suis* T4SS components are more amenable to biochemical experiments than their counterparts from the *A. tumefaciens* T4SS. Many of its components are relatively easy to purify, because in contrast to those from *A. tumefaciens*, they can be overexpressed in a soluble form with high yield, followed by affinity purification. This feature was exploited to conduct biochemical experiments to assess the suggested interactions. A portion of StrepII-VirB1sp and VirB1spHis6, eluted from gel filtration columns in a multimeric protein complex (or aggregate) together with GroEL. We did not pursue the analysis of this complex further, as we did not consider it as the physiologically relevant form. Apart from that, VirB1spHis6 was mainly present in the dimeric and tetrameric state and with reduced prominence as a hexamer. A larger portion of StrepII-VirB1sp was present in the high-molecular-mass complex, but it was also detected as lower-molecular-mass multimer. The available data suggest that StrepII-VirB1sp forms homomultimeric assemblies, probably dimers and tetramers. The molecular sieving effect of the murein layer prohibits diffusion of globular proteins or protein assemblies larger than 55 kDa (Höltje, 1998). Since the permeation of the

![Fig. 5. Prediction of conserved surface residues in different lytic transglycosylases and regions of VirB1sp peptide arrays bound by StrepII-VirB1s proteins. (a) Multiple sequence alignment of VirB1-like proteins. Residues identical to *A. tumefaciens* VirB1 are shaded; conserved residues implicated in the enzymic activity are indicated by black frames. The putative active-site Glu is labelled with a star; the cleavage site of *A. tumefaciens* VirB1 is indicated with a black arrowhead. The alignment of the VirB1 orthologues was generated with the MegAlign program, the SLT domain of *E. coli* Slt70 was aligned to *B. suis* VirB1 with EMBOSS (Needle algorithm) and fitted into the alignment. Amino acids conserved between the lytic transglycosylase domain of *B. suis* VirB1 and *E. coli* Slt70 (b) or *A. anser* LysG and *E. coli* Slt70 (c) are displayed on the surface of the Slt70 soluble lytic transglycosylase domain. The results from an EMBOSS alignment were processed and submitted to the AMAS server to validate the degrees of conservation. Identical residues in each of the two pairs are shown in dark green [A+], high similarity [A] in green, and lower similarity is in yellow [9] and light yellow [8]. The figure was prepared with DINO and the active-site Glu residue is indicated. (d) View of the Slt70 lytic transglycosylase domain surface structure taken as a model for VirB1sp. Interactions with StrepII-VirB8sp, StrepII-VirB9sp and StrepII-VirB11sp as defined by the peptide array experiments are shown. A grey colour indicates no significant interaction; orange colour indicates strong and red colour very strong interaction.
murein layer might be important for the function of lytic transglycosidase in the periplasm, the formation of dimers (approx. 50 kDa) appears to be more plausible in the natural biological context than the formation of tetramers (approx. 100 kDa), which may not permeate the murein layer.

The purified \textit{B. suis} VirB proteins were then used to systematically assess the predicted interactions with VirB1sp. Some of those interactions were confirmed here, whereas others were only weak or not observed. Using co-elution and pull-down assays we did not get any evidence for an interaction between VirB1sp and VirB8sp or VirB10sp, which had been predicted from a previous yeast two-hybrid study (Ward \textit{et al.}, 2002). In contrast, data from the peptide array experiment suggested that a set of VirB1sp peptides interacted with StreplIIVirB8sp, which supports the notion that these two proteins interact at least transiently. The evidence is not as substantial as that in case of StreplIIVirB9sp discussed below, suggesting that the interaction is weaker and/or may need additional interaction partners. These results are in line with the supposed role of VirB8 as nucleation factor, which undergoes transient interactions with many T4SS components (Kumar & Das, 2001; Yuan \textit{et al.}, 2005). The \textit{in vitro} data therefore argue against the postulated mechanism implying the VirB8–VirB1 interaction as key step for T4SS assembly (Ward \textit{et al.}, 2002), but we can not rule out that the interaction is stronger \textit{in vivo}.

Similar to VirB8sp, we obtained evidence for an interaction of the hexameric ATPase VirB11s with VirB1sp using peptide array as well as pull-down experiments. The interaction between VirB1sp and VirB9sp was demonstrated using a variety of different assays such as a pull-down assay and co-elution of the two proteins following their co-expression in a bicistronic construct. Peptide array experiments identified several StreplIIVirB9sp-interacting peptides throughout the VirB1sp sequence, and a considerable portion of them was in the C-terminus. Whereas this might argue for non-specific binding of StreplIIVirB9sp to the VirB1sp-derived peptides, we do not favour this interpretation for the following reasons. First, we have tested the binding of StreplIIVirB9sp to a pepspot membrane displaying the VirB5sp sequence, and, in line with other results showing that it does not bind strongly to VirB5sp, no non-specific binding to the membrane was observed (unpublished observations). Second, we observed non-specific binding of StreplIIVirB1sp as reflected by binding to most peptides on the VirB1sp pepspot membrane. Both the extent and strength of the signal were drastically elevated as compared to the relatively modest signal of bound StreplIIVirB9sp (unpublished observations). Finally, the peptide array data are very much consistent with the results of a previous study in intact cells, which demonstrated the interaction of the VirB1 C-terminus with VirB9 in \textit{A. tumefaciens} (Baron \textit{et al.}, 1997). We therefore conclude that the binding by StreplIIVirB9sp to many peptides of VirB1sp is likely to be of biological relevance.

The interaction with VirB9sp via the C-terminus is intriguing and this domain appears to play an important role for the functionality of the protein. Sequence analyses of a number of VirB1 homologues demonstrated special properties of the C-terminal part. The processed \textit{A. tumefaciens} VirB1 C-terminus VirB1* (Baron \textit{et al.}, 1997) and also the C-termini of \textit{B. suis} VirB1 and pKM101 TraL were classified as NORS regions. These are regions of more than 70 amino acids in length that show less than 12 % secondary structure elements and an amino acid composition different from loop regions. It was demonstrated that these very flexible regions show similar degrees of conservation as other domains in similar proteins, and that they are more abundant in proteins with functions as regulators or transcription factors than in those with functions in biosynthesis or energy metabolism-related proteins (Liu & Rost, 2003). This implies important functional roles, most likely for transient protein–protein interactions with different partners. Only 4 % of all prokaryotic proteins contain NORS regions, and among the VirB proteins from \textit{A. tumefaciens} and \textit{B. suis}, channel component VirB10, which is supposedly involved in a high number of interactions (Cascales & Christie, 2003, 2004), is the only other protein that possesses such a region. Most interacting amino acid stretches identified here constitute loop or NORS regions, which are especially suited for establishing transient protein–protein interactions, suggesting that the interaction sites are biologically relevant.

To assess the biological relevance of the interactions and binding site(s) identified here, we pursued a modelling approach based on the known X-ray structure of a soluble lytic transglycosylase enzyme. To date, the structures of 18 murein-lytic lysozymes from different organisms have been solved. In addition, the three structures of the lytic transglycosylases LaL from bacteriophage \(\lambda\), Slt35 and Slt70 (both from \textit{E. coli}) are also available (Leung \textit{et al.}, 2001; Thunnissen \textit{et al.}, 1994; van Asselt \textit{et al.}, 2000). The enzymic action of lysozymes and soluble lytic transglycosylases differs, but the protein fold is highly conserved (Mushegian \textit{et al.}, 1996). Sequence comparison of \textit{B. suis} VirB1 with two murolytic enzymes, whose X-ray structure was known, yielded intriguing results. The soluble lytic transglycosylase portion of Slt70 from \textit{E. coli} ranges from amino acid P494 to A620 and has a significant degree of sequence similarity to \textit{B. suis} VirB1 (identical, 23-1 %; similar, 38-1 %; gaps, 35-6 %). Other proteins like the lysozymes LysG from \textit{Anser anser} (identical, 18-0 %; similar, 33-1 %; gaps, 23-8 %) and \textit{Gallus gallus} LysC are less similar, although they were previously chosen to model the structure of \textit{A. tumefaciens} VirB1 (Mushegian \textit{et al.}, 1996). Structural superposition shows that despite an almost identical tertiary structure of LysG and Slt70 (Koraimann, 2003), their sequence similarity (identical, 22-0 %; similar, 36-3 %; gaps, 32-7 %) is less than that between Slt70 and VirB1. It was therefore appropriate to use the surface model of Slt70 to visualize regions of VirB1sp interaction with other VirB proteins. If the amino acids identified here by peptide array analysis were important for interactions they would be expected to localize on the surface of a protein. We indeed localized the
Table 4. Suggested and proven interactions of VirB1

The data for the predicted VirB protein localizations and interactions detected with dihybrid assays are from other publications as indicated and refer to the A. tumefaciens T4SS. IM, inner membrane; OM, outer membrane; ND, Not determined.

<table>
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<th>Protein</th>
<th>Localization (Cascales &amp; Christie, 2003)</th>
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<td>Dihybrid analysis (Ward et al., 2002)</td>
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binding sites for StrepIIVirB8sp, StrepIIVirB9sp and Strep-IIVirB11s on the surface of StrepIIVirB1sp, and these amino acids were not involved in the stabilization of the tertiary structure, which further substantiates the validity of the model. The model suggests that there was no apparent interference with the active-site cleft, but all three proteins bound C-terminally to residues likely to be involved in enzyme activity (regions 2 and 3 boxed in Fig. 5a). Thus, the binding may modulate enzyme activity; this possibility will be directly addressed in future.

Taken together, the results presented here suggest that VirB1s is a self-interacting protein that establishes transient contacts with other VirB proteins, such as VirB8s, VirB9s and VirB11s. A comparison of these results with predictions and results of previous studies is given in Table 4. A large amount of information on the role of VirB1-like proteins was collected in previous studies (Baron et al., 1997; Höppner et al., 2004; Llosa et al., 2000; Mushegian et al., 1996; Ward et al., 2002; Zahrl et al., 2005). Together with this analysis of protein interactions of VirB1s from the B. suis T4SS and the results from functional studies conducted with both the A. tumefaciens and B. suis T4SS, the following model was designed describing the function(s) of VirB1. Upon expression of the virB operon, all VirB proteins possessing an N-terminal signal peptide are exported into the periplasm or partially traverse the inner membrane. VirB1 may form a 50 kDa homodimer, which may render the active site inaccessible. The predicted pore size of the peptidoglycan layer permits diffusion of globular proteins smaller than 55 kDa, and therefore VirB9, VirB7, VirB5, VirB2 and the VirB1 dimer probably diffuse freely in the periplasm. The contact between VirB1 and VirB9 may be mediated by the C-terminus of VirB1 and lead to activation of the lytic transglycosylase activity of VirB9-bound VirB1. Transient interactions of VirB1 with VirB8 and VirB11 may facilitate this process, which may lead to a conformational change, followed by processing of VirB1 at its VirB1* cleavage site. The enzyme activity may be modulated by binding of VirB8, VirB9 or VirB11 close to active-site residues. Assembly of VirB7 and VirB9, which subsequently recruit other channel components such as VirB10 and VirB8, may accompany the opening of the cell wall. The N-terminal lytic transglycosylase domain of VirB1 (B1N) may subsequently be degraded in order to protect cellular integrity, whereas the C-terminal domain may remain attached to VirB9. VirB1* may exert an additional function in host cell recognition. As VirB1-like proteins can apparently be exchanged between different T4SS (Höppner et al., 2004; Zahrl et al., 2005), the results of these studies will probably be applicable to a wide variety of VirB1-like proteins from T4SS and other secretion systems (Koraimann, 2003).

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