Autographa californica multiple nucleopolyhedrovirus ODV-E56 envelope protein is required for oral infectivity and can be substituted functionally by Rachiplusia ou multiple nucleopolyhedrovirus ODV-E56

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The Autographa californica multiple nucleopolyhedrovirus (AcMNPV) odv-e56 gene encodes an occlusion-derived virus (ODV)-specific envelope protein, ODV-E56. In a previous analysis, the odv-e56 gene was found to be under positive selection pressure, suggesting that it may be a determinant of virus host range. To assess the role of ODV-E56 in oral infectivity and host range, we constructed recombinant AcMNPV clones (Ac69GFP-e56lacZ and AcIEGFP-e56lacZ) in which ODV-E56 protein synthesis was eliminated by inserting a β-galactosidase (lacZ) expression cassette into the odv-e56 open reading frame. We also constructed a recombinant virus, Ac69GFP-Roe56, in which the native AcMNPV odv-e56 coding sequence was replaced with that of Rachiplusia ou multiple nucleopolyhedrovirus (RoMNPV), a closely related virus that is significantly more virulent towards some host species than AcMNPV. The odv-e56 recombinant viruses exhibited no alterations in polyhedron production and morphogenesis or in the production of infectious budded virus in cell culture. In bioassays using three lepidopteran host species, the oral infectivities of the odv-e56 mutant viruses Ac69GFP-e56lacZ and AcIEGFP-e56lacZ were profoundly impaired compared with those of wild-type and control recombinant viruses. Oral infectivity was restored fully by marker rescue of the odv-e56 mutant viruses with either the AcMNPV or the RoMNPV odv-e56 gene. In bioassays using two host species that are more susceptible to RoMNPV than to AcMNPV, Ac69GFP-Roe56 killed larvae with LC50 values similar to those of recombinant viruses expressing AcMNPV ODV-E56. This result indicated that replacement of the AcMNPV odv-e56 gene with the RoMNPV orthologue did not increase virulence against these two species.

INTRODUCTION

Baculoviruses are rod-shaped, occluded viruses with circular, double-stranded DNA genomes in the family Baculoviridae (Bonning, 2005; Jehle et al., 2006; Rohrmann, 2008). These viruses have been identified exclusively in arthropods, with most isolates identified from insects within the order Lepidoptera. A considerable amount of work has been done on baculoviruses due to their potential and realized applications as biopesticides and recombinant protein expression vectors (Kost et al., 2005; Moscardi, 1999; Summers, 2006; van Beek & Davis, 2007). Most studies on baculoviruses have focused on members of the genera Alphabaculovirus (lepidopteran nucleopolyhedroviruses, or NPVs) and Betabaculovirus (lepidopteran granuloviruses, or GVs). Virion morphogenesis of these baculoviruses, as well as mosquito baculoviruses (genus Deltabaculovirus), is distinguished by the production of two physically and biochemically distinct types of infectious virus particles: occlusion-derived virus (ODV) and budded virus (BV) (Braunagel & Summers, 1994; Volkman & Summers, 1977; Volkman et al., 1976). Both ODV and BV contain rod-shaped nucleocapsids that are assembled within the nucleus. ODV nucleocapsids are enveloped within the nucleus and occluded within a matrix of viral protein (polyhedrin or granulin) to form occlusion bodies (OB) or polyhedra/ granules. BV nucleocapsids exit the nucleus and acquire an envelope derived from the plasma membrane of the host cell upon budding through the membrane. ODV virions infect the host insect’s midgut epithelial cells when OBs are ingested by the host and solubilized in the midgut lumen, releasing the ODV. BV that is assembled during the primary infection of
midgut cells (and also during subsequent secondary infection of other tissues) serves as a vehicle to spread infection to other susceptible tissues in the host (Bonning, 2003; Rohrmann, 2008).

The virulence of alphabaculoviruses against different species within the order Lepidoptera is highly variable. Although some genes that influence baculovirus virulence against individual species have been identified (Chen & Thiem, 1997; Clem & Miller, 1993; Clem et al., 1991; Crozier et al., 1994; Lapointe et al., 2004; Lu & Miller, 1996; Lu et al., 2003; Maeda et al., 1993; Popham et al., 1998), our understanding of the molecular determinants of baculovirus species-specific virulence and host range is incomplete. The accumulation of non-synonymous (amino acid-changing) nucleotide substitutions in specific baculovirus genes may facilitate adaptation to a new host species, or counter host defences to increase virulence against a particular host. Hence, it may be possible to identify candidate baculovirus genes that influence host range and virulence through an examination of non-synonymous (\(d_N\)) and synonymous (\(d_S\)) substitution rates to identify genes that have undergone positive selection, in which \(d_N > d_S\) (Aguilera et al., 2009; Yang, 2007). Selection pressure analysis carried out with gene sequences from other viruses has identified positively selected genes and codon sites within those genes that are involved in host immune recognition, receptor binding, antiviral drug resistance, epidemics and changes in virulence (Banke et al., 2003; Bennett et al., 2003, 2004; Brault et al., 2007; Holmes et al., 2002; Twiddy et al., 2002; Woelk & Holmes, 2001; Woelk et al., 2001; Zlateva et al., 2004). Mutations at a single positively selected site in the helicase gene of West Nile virus were sufficient to increase its virulence against American crows significantly (Brault et al., 2007). Hence, selection pressure analysis can potentially identify differences among highly conserved viral sequences that account for substantial differences in virulence, without prior knowledge of the contributions to pathogenesis by the sequences being analysed.

Selection pressure analysis of sequences from 83 NPV genes using codon-substitution models revealed nine baculovirus genes predicted to have undergone positive selection (Harrison & Bonning, 2004). One of the genes identified through this analysis was \(odv\text{-}e56\), a baculovirus core gene found in all baculovirus genomes examined to date (van Oers & Vlak, 2007). The \(odv\text{-}e56\) gene is expressed late during infection and encodes an ODV envelope protein (Braunagel et al., 1996; Theilmann et al., 1996). Five other ODV envelope proteins – P74, PIF-1, PIF-2, PIF-3 and PIF-4 – have been found to be required for oral infectivity of alphabaculovirus ODV (Fang et al., 2009; Faulkner et al., 1997; Kikhno et al., 2002; Kuzio et al., 1989; Ohkawa et al., 2005; Pijman et al., 2003; Song et al., 2008). These proteins have been referred to as per os infectivity factors (PIFs).

In this study, we examined the role of ODV-E56 in oral infectivity with recombinant clones of Autographa californica multiple nucleopolyhedrovirus (AcMNPV) in which expression of ODV-E56 had been eliminated. We also produced a recombinant virus in which the AcMNPV \(odv\text{-}e56\) coding sequence had been replaced with that of Rachiplusia ou multiple nucleopolyhedrovirus (RoMNPV) and tested for altered virulence in selected host species. AcMNPV and RoMNPV (which is a variant of Anagrapha falcifera multiple nucleopolyhedrovirus) are genetically very similar and have broad, overlapping host ranges (Harrison, 2009b; Harrison & Bonning, 1999; Hostetter & Puttler, 1991). However, individual species within their host ranges are significantly more susceptible to RoMNPV than to AcMNPV (Cardenas et al., 1997; Harrison & Bonning, 1999; Hostetter & Puttler, 1991; Lewis & Johnson, 1982; Vail et al., 1993). Among these species are Helicoverpa zea, the corn earworm, and Ostrinia nubilalis, the European corn borer (Harrison & Bonning, 1999). The production of BVs and OBs by the recombinant viruses created in this study was measured, and their virulence towards three species of lepidopteran hosts was evaluated to see whether ODV-E56 was required for oral infectivity and whether a recombinant AcMNPV clone expressing the RoMNPV \(odv\text{-}e56\) gene exhibited a higher degree of virulence towards Helicoverpa zea and Ostrinia nubilalis.

### RESULTS

**Characteristics of recombinant viruses**

Recombinant viruses carrying the \(hsp70\) promoter–\(lacZ\) expression cassette in the \(odv\text{-}e56\) open reading frame (ORF) in either orientation were produced successfully by standard co-transfection of parental viral DNA (AcMLF9.EGFP, AcIETV3.EGFP) with transfer vectors carrying the disrupted \(odv\text{-}e56\) ORF (Fig. 1a). Although marker rescue of the \(odv\text{-}e56\) mutant viruses was easily accomplished with a plasmid (pAcClal-F) carrying the wild-type \(odv\text{-}e56\) sequence, replacement of the native AcMNPV \(odv\text{-}e56\) ORF with the RoMNPV \(odv\text{-}e56\) ORF using an RoMNPV-derived amplifier was inefficient. Only one clone was obtained that contained enough of the RoMNPV \(odv\text{-}e56\) ORF sequence to include all of the amino acid substitutions that distinguish the AcMNPV and RoMNPV gene products (Fig. 1a, b). These differences include 12 amino acid substitutions and an insertion of two additional amino acids near the C terminus of the RoMNPV sequence (Fig. 1b). Two of the substitutions (S97G and I199N) were identified as sites under positive selection pressure (Harrison & Bonning, 2004), whilst a single other substitution (M344I) is located within a conserved hydrophobic region identified in an alignment of five ODV-E56 sequences (Theilmann et al., 1996). No other substitutions occur in a second conserved hydrophobic region identified in the sequence, or in conserved cysteine residues and a putative N-glycosylation site (Theilmann et al., 1996). Clones containing \(lacZ\) in the opposite orientation with respect to \(odv\text{-}e56\) in AcMLF9.EGFP (Ac69GFP-e56lacZ) and in the same
orientation as \textit{adv-e56} in AcIE1TV3.EGFP (AcIE1GFP-e56lacZ) were selected for further study, along with their accompanying marker-rescued viruses (Ac69GFP-e56R and AcIE1GFP-e56R; Fig. 1).

Western blot analysis of ODV protein from polyhedra derived from \textit{Heliothis virescens} larvae revealed that both Ac69GFP-e56lacZ and AcIE1GFP-e56lacZ were missing a protein migrating at 48 kDa that was present in the wild-

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Fig. 1. Construction of recombinant viruses used in this study. (a) Schematic diagram of the \textit{polh} and \textit{adv-e56} loci (centre and right columns, respectively) in wild-type and recombinant viruses used in this study. ORFs are indicated as arrows, with the direction of the arrow indicating the orientation of the ORF. The restriction enzyme sites into which EGFP and \textit{lacZ} reporter genes were inserted are indicated, as are the enhancer/promoter sequences and simian virus 40 (SV40) polyadenylation signal. (b) Schematic diagram of the \textit{adv-e56} ORF in AcMNPV-C6, RoMNPV-R1 and Ac69GFP-Roe56, showing positions of amino acid substitutions in the ODV-E56 sequences of these viruses, as well as two additional amino acids in the RoMNPV sequence (positions 350–351).
**Fig. 2.** Western blot analysis of ODV-E56 in samples from (a) total ODV protein derived from virus-killed *Heliothis virescens* larvae and (b) ODV envelope protein from infected *Trichoplusia ni* BTI-TN-5B1-4 cells. The identity of the virus for each protein sample is shown above each lane, and molecular mass marker lanes (M) and sizes (in kDa) of individual markers are indicated on the left of each panel. ODV-E56-specific bands are indicated by arrows.

**Fig. 3.** (a) Budded virus produced by *Sf*9 cells infected with AcMNPV-C6, RoMNPV-R1 and recombinant viruses derived from either AcMLF9.EGFP (left graph) or AcIE1TV3.EGFP (right graph), displayed as mean p.f.u. ml^-1 of three replicate samples per time point. (b) Polyhedra produced by *Sf*9 cells infected with the same viruses as in (a). Mean numbers of polyhedra per cell from three replicate infections per virus are shown. For both (a) and (b), error bars represent 1 SD. For (b), values with different letters are significantly different at P<0.05.
type AcMNPV and in the parental and marker-rescued viruses, indicating that insertion of the lacZ expression cassette had eliminated expression of ODV-E56 (Fig. 2a). Whilst the AcMNPV odv-e56 ORF encodes a protein of approximately 41 kDa, the relative mobility of ODV-E56-specific bands in SDS-PAGE gels of AcMNPV and Orygia pseudotsugata multiple nucleopolyhedrovirus has varied from 43 to 56 kDa in previous reports (Braunagel et al., 1996; Theilmann et al., 1996). No bands that could correspond to a partial protein product from the N-terminal part of the odv-e56 ORF upstream of the lacZ insertion were observed in the mutant odv-e56 virus lanes. A minor band migrating at 58 kDa was also missing from the lacZ insertion mutants. The ODV-E56 antibodies also bound to proteins of the same size in RoMNPV and Ac69GFP-Roe56 ODV, indicating that the AcMNPV ODV-E56 antibodies recognized the RoMNPV ODV-E56 protein. The same results were observed with total cellular protein from infected Sf9 and BTI-TN-5B1-4 cells and with clones of Ac69GFP-e56lacZ and AcIE1GFP-e56lacZ with the lacZ expression cassette inserted in opposite orientations (data not shown).

ODV-E56 was also absent from ODV envelope protein samples prepared from BTI-TN-5B1-4 cells infected with the odv-e56 mutant viruses Ac69GFP-e56lacZ and AcIE1GFP-e56lacZ (Fig. 2b). The presence of ODV-E56 bands in the Ac69GFP-Roe56 ODV envelope protein sample suggested that the RoMNPV ODV-e56 protein was being assembled into AcMNPV ODV.

Quantification of BV produced by wild-type and recombinant viruses revealed that, whilst there were some small but significant differences between selected pairs of the viruses at some time points (Fig. 3a), eliminating expression of odv-e56 or replacing AcMNPV odv-e56 with the RoMNPV orthologue did not significantly affect production of infectious BV observed at 24 h post-infection (p.i.) and afterwards. There also was no effect on production of polyhedra (Fig. 3b). By 96 h p.i., Sf9 cell cultures infected with RoMNPV-R1 exhibited a visibly greater degree of cell lysis and number of free-floating polyhedra than cultures infected with wild-type AcMNPV and the AcMNPV recombinants, although there was not a consistently significant difference in numbers of polyhedra produced between these viruses (Fig. 3b). Ultrastructural observations on infected BTI-TN-5B1-4 cells indicated that elimination of ODV-E56 expression or replacement with RoMNPV ODV-E56 also did not appear to affect ODV morphogenesis and assembly into polyhedra (Fig. 4; compare b and d with a, c and f).

**Biological activity against larvae**

An initial attempt to produce a polyhedron stock for bioassays by orally inoculating fifth-instar *Heliothis virescens* larvae with cell culture-derived polyhedra revealed an impairment in the oral infectivity of the odv-e56 mutant viruses. Whilst a dose of $1 \times 10^6$ polyhedra from wild-type and recombinant viruses carrying an intact odv-e56 gene was sufficient to kill all larvae in a test population, little to no mortality was observed when larvae were fed this dose of polyhedra from viruses with the lacZ cassette inserted in odv-e56. To investigate further the biological activity of the recombinant viruses, droplet-feeding bioassays were carried out with polyhedron stocks produced by intrahaemocoelic injection of larvae with BV. Whilst viruses expressing ODV-E56 killed neonate *Heliothis virescens* larvae with LC$_{50}$ values ranging from $0.78 \times 10^5$ to $1.30 \times 10^5$ polyhedra ml$^{-1}$, <50% mortality was observed with AcIE1GFP-e56lacZ, even at a dose of $1.5 \times 10^9$ polyhedra ml$^{-1}$ (Table 1). Ac69GFP-e56lacZ was able to achieve mortalities >50% in bioassays, with LC$_{50}$ values that were approximately two orders of magnitude higher than those of viruses expressing ODV-E56. In additional bioassay data against fourth-instar larvae, two additional clones of Ac69GFP-e56lacZ and AcIE1GFP-e56lacZ that carried the lacZ expression cassette in opposite orienta-
Table 1. Dose—mortality response of neonate larvae infected with wild-type and recombinant AcMNPV and RoMNPV

For each host and group of viruses, values with different superscript letters (a–d) are significantly different at \( P<0.05 \). ND, Not determined due to <50% mortality at the highest dose.

<table>
<thead>
<tr>
<th>Host/virus</th>
<th>LC50* ( \times 10^5 ) (95% CL)</th>
<th>Slope (± SEM)</th>
<th>Heterogeneity</th>
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<tbody>
<tr>
<td><em>Heliothis virescens</em></td>
<td></td>
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<tr>
<td>AcE1TIV3.EGFP</td>
<td>1.20a (0.85–1.65)</td>
<td>1.95 (± 0.331)</td>
<td>0.28</td>
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<td>AcE1GFP-e56lacZ</td>
<td>ND</td>
<td></td>
<td></td>
</tr>
<tr>
<td>AcE1GFP-e56R</td>
<td>1.30a (0.95–1.77)</td>
<td>2.00 (± 0.312)</td>
<td>0.77</td>
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<td>AcML9P.EGFP</td>
<td>0.89a (0.63–1.20)</td>
<td>2.10 (± 0.293)</td>
<td>0.67</td>
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<tr>
<td>Ac69GFP-e56lacZ</td>
<td>320.0b (210.2–449.2)</td>
<td>1.96 (± 0.409)</td>
<td>0.33</td>
</tr>
<tr>
<td>Ac69GFP-e56R</td>
<td>0.84ad (0.35–1.49)†</td>
<td>2.16 (± 0.323)</td>
<td>2.44</td>
</tr>
<tr>
<td>Ac69GFP-Roe56</td>
<td>0.78ad (0.53–1.06)</td>
<td>2.09 (± 0.318)</td>
<td>0.91</td>
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<td><em>Helicoverpa zea</em></td>
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<tr>
<td>AcMNPV-C6</td>
<td>3.40a (2.44–4.98)</td>
<td>1.52 (± 0.261)</td>
<td>0.15</td>
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<tr>
<td>RoMNPV-R1</td>
<td>0.54b (0.38–0.71)</td>
<td>1.90 (± 0.303)</td>
<td>0.33</td>
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<tr>
<td>AcML9P.EGFP</td>
<td>2.90a (1.90–4.43)</td>
<td>1.25 (± 0.189)</td>
<td>0.33</td>
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<tr>
<td>Ac69GFP-e56lacZ</td>
<td>249.5b (177.1–358.3)</td>
<td>1.60 (± 0.227)</td>
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<tr>
<td>Ac69GFP-e56R</td>
<td>1.52cd (0.50–3.29)</td>
<td>1.18 (± 0.188)</td>
<td>1.13</td>
</tr>
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<td>Ac69GFP-Roe56</td>
<td>2.75cd (0.91–7.85)</td>
<td>1.10 (± 0.181)</td>
<td>1.38</td>
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<tr>
<td><em>Ostrinia nubilalis</em></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AcMNPV-C6</td>
<td>4339.5a (2289.2–14091.6)</td>
<td>1.58 (± 0.257)</td>
<td>1.43</td>
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<td>RoMNPV-R1</td>
<td>185.7b (133.7–337.8)</td>
<td>2.14 (± 0.438)</td>
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<td>AcML9P.EGFP</td>
<td>3259.9b (1248.7–7362.7)</td>
<td>1.26 (± 0.294)</td>
<td>1.56</td>
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<tr>
<td>Ac69GFP-e56lacZ</td>
<td>ND</td>
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<td></td>
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<tr>
<td>Ac69GFP-e56R</td>
<td>2675.5b (1995.4–3483.0)</td>
<td>2.45 (± 0.387)</td>
<td>0.04</td>
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<td>Ac69GFP-Roe56</td>
<td>3059.9b (2023.2–4369.5)</td>
<td>1.71 (± 0.323)</td>
<td>0.65</td>
</tr>
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</table>

*Values are no. polyhedra ml\(^{-1}\), reported with 95% confidence limits (CL).
†90% CL.

**DISCUSSION**

There are many baculovirus proteins in the ODV envelope, but only a small proportion have been examined with respect to their role in oral infectivity (Braunagel & Summers, 2007; Rohrmann, 2008; Slack & Arif, 2007). The results presented above indicate that ODV-E56 is required for oral infectivity, but not production of infectious BV, much like the PIF proteins P74, PIF-1, PIF-2, PIF-3 and PIF-4. Electron micrographs of odv-e56 mutants indicate that ODV-E56 is not required for virion morphogenesis or occlusion assembly. In a previous study, Braunagel et al. (1996) generated a recombinant AcMNPV in which the odv-e56 ORF was replaced with a fusion between the N terminus of ODV-E56 and β-galactosidase. Electron micrographs of cells infected with this virus also did not show any obvious defects in ODV or occlusion body morphogenesis.

The RoMNPV odv-e56 gene was able to substitute functionally for the AcMNPV orthologue in AcMNPV ODV, as Ac69GFP-Roe56 killed *Heliothis virescens* larvae with LC\(_{50}\) values similar to those of AcMNPV viruses with intact odv-e56 genes. This suggests that the amino acid substitutions encoded by the RoMNPV orthologue affect neither interactions of ODV-E56 with host proteins that may act as a receptor for ODV in midgut cells, nor...
ODV-E56 is a per os infectivity factor

interactions with other ODV envelope or capsid proteins that are required for infectivity. Replacing AcMNPV odv-e56 with the RoMNPV ORF also did not alter biological activity towards two host species that differ in their susceptibility to AcMNPV and RoMNPV. Of the 13 codon positions in odv-e56 that were identified previously as being under positive selection pressure (Harrison & Bonning, 2004), only two (S97 and I199) differ in the RoMNPV amino acid sequence (Fig. 1b). It may be the case that odv-e56 has not been under a significant amount of positive selection pressure in the lineage containing AcMNPV and RoMNPV, or has not undergone sufficient changes since the divergence of these NPVs to alter its function. It may be that several genes (perhaps those under positive selection pressure) would need to be swapped between AcMNPV and RoMNPV before host range and species-specific virulence would be altered detectably. Alternatively, ODV-E56 may influence virulence against host species other than Heliothis zeae and Ostrinia nubilalis.

Research is under way to characterize further the role of ODV-E56 as a PIF, including determining whether ODV-E56 is directly required for binding to midgut cells and fusion with the cell membrane.

METHODS

Cells, viruses and insects. The Spodoptera frugiperda Sf9 cell line (Vaughn et al., 1977) was maintained in TNN-FH medium (Sigma) supplemented with 10 % fetal bovine serum (Invitrogen), antibiotics (10 U penicillin, 0.1 mg streptomycin and 0.25 μg amphotericin B ml⁻¹; Sigma) and 0.1 % Pluronic F-68 (JRH Biosciences). Trichoplusia ni BTI-TN-5B1-4 ('High Five'; Wickham et al., 1992) cells were maintained in Ex-Cell 405 medium (SAFC Biosciences) supplemented with antibiotics as described above.

The wild-type AcMNPV strain C6 (Possee, 1986), RoMNPV strain R1 (Smith & Summers, 1987) and the recombinant viruses described in this study were propagated in Sf9 cells and titrated by plaque assay on Sf9 cells as described by Summers & Smith (1987). AcBacPAK6 (Kitts & Possee, 1993) was used as the parental virus for the first round of recombinant virus construction in this study.

Eggs of Heliothis virescens and Helicoverpa zea were obtained from Bio-Serv. Eggs of Ostrinia nubilalis were obtained from the USDA-ARS Corn Insects and Crop Genetics Research Unit in Ames, IA, USA. Larvae for all three species were reared at 28 °C and a 14:10 light:dark cycle on species-specific diets obtained from Southland Products.

Construction of recombinant viruses. The plasmid pAcP (+)IE1eGFP, a gift from Dr Don Jarvis (University of Wyoming, Laramie, WY, USA), was constructed by ligating the BglII–NotI fragment from plasmid pEGFP-N1 (Clontech) containing the enhanced green fluorescent protein (EGFP) coding sequence into the corresponding sites in AcMNPV transfer vector pAcP (+)IE1TV3 (Jarvis et al., 1996). To construct transfer vector pAcMLP9.EGFP, a subclone containing the EGFP coding sequence was produced by ligating a SpeI–SalI fragment from pAcP (+)IE1eGFP into pBluescript II KS(+) (Stratagene) to produce plasmid pEGFP. A BglII fragment from this plasmid containing the EGFP coding sequence was subcloned into the BglII site of AcMNPV transfer vector pACMLP9 (Harrison & Bonning, 2000; GenBank accession no. EF050536).

Recombinant viruses were generated by co-transfection of Sf9 cells with virus DNA and transfer vector plasmids by liposome-mediated transfection using Cellfectin (Invitrogen) following the manufacturer’s instructions, followed by plaque assay of the cell medium 5 days post-transfection. To produce viruses AcMLP9.EGFP and AcIE1TV3.EGFP (Fig. 1), Sf9 cells were co-transfected with pAcMLP9.EGFP or pAcP (+)IE1eGFP, respectively, together with AcBacPAK6 DNA that had been linearized by digestion with Bsu361. To produce recombinant viruses with insertional inactivated odv-e56 genes, AcMLP9.EGFP and AcIE1TV3.EGFP viral DNAs were co-transfected with transfer vectors pAcodev-e56-hspLacZ(+) and pAcodev-e56-hspLacZ(−), respectively. To generate marker-rescued versions of the odv-e56 inactivation mutants, Ac69GFP-e56lacZ and AcIE1GFP-e56lacZ, viral DNAs were linearized by digestion with Bsu361, which cuts within the lacZ sequence, and co-transfected with pAcClai-F to make viruses Ac69GFP-e56R and AcIE1GFP-e56R, respectively. To produce recombinant AcMNPV in which the native odv-e56 coding sequence was replaced with the RoMNPV-R1 coding sequence, Bsu361-linearized Ac69GFP-e56lacZ and AcIE1GFP-e56lacZ DNAs were co-transfected with a PCR amplifier consisting of the RoMNPV-R1 odv-e56 ORF (nt 12682–12781) of the RoMNPV-R1 genome sequence; Harrison & Bonning, 2003). The single usable clone recovered from these co-transfections was called Ac69GFP-Roe56 (Fig. 1).

Methods for selection and plaque purification of recombinant viruses were followed essentially as described by Summers & Smith (1987). For AcMLP9.EGFP and AcIE1TV3.EGFP, an occlusion-positive/lacZ-negative plaque phenotype was selected against an occlusion-negative/lacZ-positive background. For Ac69GFP-e56lacZ and AcIE1GFP-e56lacZ, an occlusion-positive/lacZ-negative plaque was selected against an occlusion-negative/lacZ-positive background. For Ac69GFP-e56R and AcIE1GFP-e56R, an occlusion-negative/lacZ-positive phenotype was selected against an occlusion-positive/lacZ-negative background. Plaque purification was carried out for at least three rounds, or until no plaques with a parental phenotype could be seen on the dish. Recombinant viruses were checked for proper integration of marker genes and the absence of second-site recombination by restriction endonuclease digestion and PCR amplification and sequencing of the odv-e56 locus.

Western blotting of ODV protein. Monolayer cultures of BTI-TN-5B1-4 cells were infected at an m.o.i. of 1 with wild-type and recombinant viruses. Cells and free-floating polyhedra were collected by centrifugation 5 days p.i. Polyhedra were extracted from cell pellets and purified as described by Braunagel & Summers (1994). Polyhedra for each virus were pelleted and resuspended in 28 ml 0.1 M Na₂CO₃/50 mM NaCl (pH 10.9), then incubated at 37 °C for 1.5 h. Insoluble material was pelleted by centrifugation in a tabletop centrifuge (1320 g for 10 min) and the supernatant was transferred to a
Beckman SW28 ultracentrifuge tube. The solubilized polyhedron solution was neutralized by the addition of 1 M Tris/HCl (pH 7.6) to a final concentration of 0.1 M. A 3 ml 25 % (w/v) sucrose pad prepared in PBS was layered underneath the solubilized polyhedra, and ODV were pelleted through the sucrose pad by ultracentrifugation (124 000 g for 75 min). The ODV pellet was resuspended in 150–200 μl 10 mM Tris/HCl (pH 8.5) and quantified by Bradford assay with the Coomassie Plus Bradford assay reagent (Thermo Scientific). An envelope protein fraction was prepared from approximately 100–250 μg ODV as described by Braunagel & Summers (1994), except that Triton X-100 at a concentration of 0.1% was used in place of NP-40 and insoluble material from the extraction was pelleted by brief microcentrifugation prior to loading and centrifugation on a 30–70% (w/v) continuous glycerol gradient. Envelope protein was collected from the top of the gradient and concentrated using an Amicon Ultra centrifugal filter with a 3 kDa molecular mass cutoff point (Millipore).

Unfractionated ODV protein was prepared from polyhedra extracted from baculovirus-killed Heliothis virescens larvae. Larvae that had moulted to fifth instar were inoculated by intrahaemocoelic injection with 5 μl (approx. 50–200 p.f.u.) BV. Virus-killed cadavers were collected at 5–7 days p.i. and stored at -20 °C. Cadavers were homogenized and polyhedra isolated as described previously (Harrison, 2009a). Polyhedron pellets were resuspended in 28 ml 0.1 M Na2CO3 and incubated at 37 °C for 15 min. ODV were pelleted through a sucrose pad, resuspended in 10 mM Tris/HCl (pH 8.5) and quantified by Bradford assay as described above.

ODV proteins were separated by SDS-PAGE using a Mini-PROTEAN 3 cell (Bio-Rad) according to the manufacturer’s instructions. Approximately 7.5 μg ODV protein samples from polyhedra prepared from Heliothis virescens larvae and 15 μg ODV envelope protein from polyhedra isolated from BTI-TN-5B1-4 cells and loaded on an SDS-PAGE gel (10%) along with ECL DualVue Western blotting markers (Amersham/GE Healthcare). Protein was transferred to an Amersham Hybond-P PVDF membrane (GE Healthcare) using a Mini Trans-Blot Electrophoretic Transfer Cell (Bio-Rad) according to the manufacturer’s instructions, and immunoblot analysis was carried out using the Amersham ECL Plus Western blotting detection system (GE Healthcare) with the primary antibody consisting of a 1 : 2000 dilution of rabbit anti-ODV-E56 serum (Braunagel et al., 1996). Fluorescent Western blot signals were visualized with a Typhoon 9410 Variable Mode Imager set at an excitation wavelength of 532 nm.

**Measurement of BV and OB production.** Six-well plates were seeded with 0.8 × 106 S99 cells per well. Three wells per virus were infected with wild-type and recombinant viruses at an m.o.i. of 5. Aliquots of budded virus were harvested from each well at 24, 48 and 72 h.p.i. and the cells and free-floating polyhedra of each separate infection were harvested at 96 h p.i. Infectious virus (p.f.u. ml-1) at each time point was quantified by plaque assay. Polyhedra were purified following the procedure of O’Reilly et al. (1992) and counted with a Neubauer haemocytometer. The total numbers of polyhedra produced per cell in each well were calculated. Variation in BV and polyhedron production was examined by one-way analysis of variance (ANOVA) with significance evaluated by pairwise two-tailed t-test.

**Electron microscopy.** BTI-TN-5B1-4 cells were seeded into 75 cm2 flasks at a density of 9 × 104 cells per flask and infected with wild-type and recombinant viruses at an m.o.i. of 5. Cells were harvested at 72 h p.i. and fixed, embedded in resin, sectioned and stained as described previously (Harrison & Summers, 1995), except that resin infiltration was carried out by incubation with a series of increasing concentrations of Spurr’s resin in acetone. Stained ultrathin sections were examined with an H-7000 Hitachi electron microscope at 75 kV.

**Bioassays.** Polyhedron stocks prepared from Heliothis virescens cadavers (see above) were used to set up droplet-feeding bioassays as described previously (Hughes & Wood, 1981; Sparks et al., 2008) to assess the biological activity of polyhedra for each virus. Five doses producing a mortality range of 10–90% were used to infect neonate larvae of Heliothis virescens, Helicoverpa zea and Ostrinia nubilalis. Bioassays were repeated at least twice. Dose–mortality relationships were analysed by probit analysis using Polo Plus version 2.0 (LeOra Software). Comparison of LC50 values was carried out as described by Robertson et al. (2007).

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**REFERENCES**


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