Crystal Structure of Glycoprotein C from a Hantavirus in the Post-fusion Conformation

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Abstract

Hantaviruses are important emerging human pathogens and are the causative agents of serious diseases in humans with high mortality rates. Like other members in the Bunyaviridae family their M segment encodes two glycoproteins, G\textsubscript{N} and G\textsubscript{C}, which are responsible for the early events of infection. Hantaviruses deliver their tripartite genome into the cytoplasm by fusion of the viral and endosomal membranes in response to the reduced pH of the endosome. Unlike phleboviruses (e.g. Rift valley fever virus), that have an icosahedral glycoprotein envelope, hantaviruses display a pleomorphic virion morphology as G\textsubscript{N} and G\textsubscript{C} assemble into spikes with apparent four-fold symmetry organized in a grid-like pattern on the viral membrane. Here we present the crystal structure of glycoprotein C (G\textsubscript{C}) from Puumala virus (PUUV), a representative member of the Hantavirus genus. The crystal structure shows G\textsubscript{C} as the membrane fusion effector of PUUV and it presents a class II membrane fusion protein fold. Furthermore, G\textsubscript{C} was crystallized in its post-fusion trimeric conformation that until now had been observed only in Flavi- and Togaviridae family members. The PUUV G\textsubscript{C} structure together with our functional data provides intriguing evolutionary and mechanistic insights into class II membrane fusion proteins and reveals new targets for membrane fusion inhibitors against these important pathogens.

Author Summary

Hantaviruses (family: Bunyaviridae) encompass pathogens responsible to serious human diseases and economic burden worldwide. Following endocytosis, these enveloped RNA viruses are directed to an endosomal compartment where a sequence of pH-dependent conformational changes of the viral envelope glycoproteins mediates the fusion between the viral and endosomal membranes. The lack of high-resolution structural information for the entry of hantaviruses impair our ability to rationalize new treatments and prevention strategies. We determined the three-dimensional structure of a glycoprotein C from Puumala virus (PUUV) using X-ray crystallography. The two structures (at pH 6.0 and 8.0) were determined to 1.8 Å and 2.3 Å resolutions, respectively. Both structures reveal a
class II membrane fusion protein in its post-fusion trimeric conformation with novel structural features in the trimer assembly and stabilization. Our structures suggest that neutralizing antibodies against G\(_C\) target its conformational changes as inhibition mechanism and highlight new molecular targets for hantavirus-specific membrane fusion inhibitors. Furthermore, combined with the available structures of other class II proteins, we remodeled the evolutionary relationships between virus families encompassing these proteins.

**Introduction**

The *Bunyaviridae* is a large and diverse virus family of human, animal and plant pathogens that encompasses five genera; *Phlebovirus*, *Orthobunyavirus*, *Hantavirus*, *Nairovirus* and *Tospovirus*. Members of the *Hantavirus* genus are rodent-borne zoonotic viruses and are important human pathogens responsible for severe illnesses such as hemorrhagic fever with renal syndrome (HFRS), and hantavirus pulmonary syndrome (HPS) [1–4]. Puumala virus (PUUV), the causative agent of a mild form of HFRS was first isolated in Finland [5]. In humans, PUUV infection is mostly asymptomatic or manifested with minor symptoms. However, outbreaks were recently reported in central Europe with growing numbers of affected patients [6–8]. The bank vole (*Myodes glareolus*) is the main reservoir of the virus and transmission to humans occurs typically via aerosols of the rodent excreta with no role for arthropod vectors.

Hantaviruses encompass a tripartite, negative sense ssRNA genome. The viral medium (M) segment encodes the two glycoproteins, G\(_N\) and G\(_C\), originating from a glycoprotein precursor (GPC) that is cleaved into N- and C-terminal fragments [9–11]. G\(_N\) and G\(_C\) assemble into a lipid bilayer envelope to form an outer protein shell. The non-continuous, pleomorphic envelope projects G\(_N\) and G\(_C\) as a spike complex bearing an apparent four-fold symmetry [12]. Recently, the atomic resolution structure of G\(_N\) was published and together with electron cryo-tomography data it was proposed to be located at the membrane distal part of the spike complex [13]. However the structure, orientation and stoichiometry of G\(_C\) within the spikes remain unclear.

To deliver their RNA genome into the host cell cytoplasm, hantaviruses must fuse their envelope with a cellular membrane. Like other enveloped viruses, hantaviruses rely on their glycoproteins to induce membrane fusion [14]. Following attachment to the host cell, hantaviruses usually undergo clathrin-mediated endocytosis (CME). Interestingly, clathrin-independent endocytosis was reported for some hantaviruses [15, 16], implying that different routes may be involved in these viruses entry. In both routes, however, the virus is directed to an endosomal compartment where the glycoproteins respond to the reduced pH of the compartment with a sequence of conformational changes [17]. These conformational changes expose a hydrophobic motif, which is inserted into the endosomal membrane [18, 19]. The glycoprotein then folds back on itself, forcing the cell membrane (held by the fusion motif) and the viral membrane (held by a transmembrane anchor) to proximity, inducing the viral and endosomal membranes to fuse [20–22].

Based on bioinformatic studies and *in vitro* experiments using synthetic peptides it was postulated that hantavirus G\(_C\) adopts a class II membrane fusion protein fold [23, 24]. Until recently, viral class II fusion proteins were thought to be restricted to members of the *Flavivirus* genus (family: *Flaviviridae*) and the *Togaviridae*. However, the crystal structure of G\(_C\) from Rift Valley fever virus (RVFV—family *Bunyaviridae*, genus: *Phlebovirus*) showed that the class II fold extends beyond these two families [25]. Interestingly, not all *Flaviviridae* members
contain a class II membrane fusion protein as bovine viral diarrhea virus (BVDV, genus: Pestivirus) E2 protein and hepatitis C virus E2 (HCV, genus: Hepacivirus) exhibit completely different folds in their proposed fusion proteins [26, 27]. In the absence of high-resolution structures for the complete E1 proteins from these viruses this data suggests that BVDV and HCV (flavivirus) fusion proteins do not adopt a class II fold.

The transition of class II membrane fusion proteins from their pre-fusion homo- or heterodimers on the virus surface to a post-fusion homotrimer has been shown to depend on the acidification of the virus’ environment [21, 28–30]. Recently, Acuña and colleagues have shown that G\textsubscript{C} from Andes virus (ANDV, genus: Hantavirus) forms trimers in response to acidic environment at pH 5.5 [17]. Hantavirus fusion activity was also demonstrated by syncytia formation upon low pH treatment of Vero E6 cells expressing G\textsubscript{N} and G\textsubscript{C} glycoproteins [14, 31]. In this cellular context, a pH of 5.9 was found to activate fusion of Andes virus while a pH of 6.3 was reported as the activation threshold for Hantaan virus [14, 32].

In the absence of experimental high-resolution structural data for G\textsubscript{C}, the molecular basis of membrane fusion in hantaviruses remains obscure. Here we present the first high-resolution structure of a fusogen from the hantavirus genus.

Results and Discussion

PUUV G\textsubscript{C} is a class II membrane fusion protein

The ectodomain of PUUV G\textsubscript{C} spans residues 659–1114 (GPC numbering, 1–456 in G\textsubscript{C} numbering). To obtain soluble protein for structural studies, we expressed only PUUV G\textsubscript{C} residues 659–1106 (1–448, soluble G\textsubscript{C} or sG\textsubscript{C}) using baculovirus expression system and purified it to homogeneity (see material and methods). During the elution step of ion exchange (IEX) chromatography we obtained two populations (termed sG\textsubscript{C\textsubscript{XF1}} and sG\textsubscript{C\textsubscript{XF2}}) that each crystallized in a distinct crystal form. We then determined the crystal structures of sG\textsubscript{C\textsubscript{XF1}} and sG\textsubscript{C\textsubscript{XF2}} to 1.8 Å and 2.5 Å resolution, respectively, with excellent crystallographic statistics (Table 1). Although sG\textsubscript{C\textsubscript{XF1}} crystals appeared in pH 6.0 and sG\textsubscript{C\textsubscript{XF2}} in pH 8.0, in both crystal forms PUUV sG\textsubscript{C} adopts the three-domain architecture of the post-fusion conformation of class II viral fusion proteins. It is not unprecedented that some class II membrane fusion proteins were crystallized in their post-fusion conformation without low pH triggering [33, 34], however we cannot exclude that for sG\textsubscript{C\textsubscript{XF2}} the pH was not changed during the crystallization period. The overall structure in both crystal forms is similar so to simplify our discussion we will refer mainly to the sG\textsubscript{C\textsubscript{XF1}} unless mentioned otherwise.

Viral class II membrane fusion proteins were found previously only in flaviviruses, alphaviruses, rubivirus and more recently in a phlebovirus [25, 35–37] (Figs 1, S1). The crystal structure of PUUV sG\textsubscript{C} spans residues 666–1076 (GPC numbering), lacking seven N-terminal and 30 C-terminal residues of the expressed ectodomain. Domain I, an eight-stranded \(\beta\)-sandwich (with strands termed \(B_0-I_0\)), is the center of the structure that arranges domain II and III around it (Fig 1). Two insertions in domain I between strands \(D_0-E_0\) and strands \(H_0-I_0\) form the elongated, mostly \(\beta\)-stranded domain II. The putative fusion loop, the endosomal membrane anchor, is located on the part of domain II that is distal to domain I. Domain III is an IgC-like module with six \(\beta\)-strands and is followed by a segment of eight amino acids of the so-called stem region.

Compared to fusion proteins from flaviviruses and alphaviruses, PUUV G\textsubscript{C} has a longer stem region connecting domain III to the transmembrane (TM) domain. The stem region of PUUV G\textsubscript{C} spans approximately 44 residues, including two conserved cysteines (S2 Fig). Due to its disordered nature we could not detect electron density for most of this region. However, the first eight residues of the stem (1068–1076) could be modeled in both, sG\textsubscript{C\textsubscript{XF1}} and sG\textsubscript{C\textsubscript{XF2}}. The
The last residue visible in both of our structures is T1076, which lays ~30 Å from the fusion loop (Fig 1). The remaining 38 residues connecting to the TM anchor can easily cover the distance to the fusion loop. The overall domain organization (in particular the position of domain III), the parallel trimeric assembly and the stem peptide directionality imply that our structure represents sGC in its post-fusion conformation, or at least in the final stages of the fusion between the viral and the host-cell membranes.

PUUV sGC from both preparations (sGC\textsuperscript{XF1} and sGC\textsuperscript{XF2}) is a monomer in solution as determined by size exclusion chromatography (SEC) (S3A Fig). To investigate the oligomeric state of sGC at different pHs, we used size exclusion chromatography combined with multiangle

| Table 1. Crystallographic data collection and refinement statistics. |
|-----------------|-----------------|-----------------|-----------------|
|                 | sG\textsubscript{C}\textsuperscript{XF1} | sG\textsubscript{C}\textsuperscript{XF2} |
| **Data collection** | **SIRAS\textsubscript{native}** | **SIRAS\textsubscript{Hg}** | **Native** |
| Space group | R 3 2: H | R 3 2: H | R 3 2: H | I 2, 3 |
| a, b, c (Å) | 96.4, 96.4, 246.3 | 96.4, 96.4, 246.2 | 96.4, 96.4, 247.1 | 138.5, 138.5, 138.5 |
| α, β, γ (°) | 90, 90, 120 | 90, 90, 120 | 90, 90, 120 | 90, 90, 90 |
| Wavelength (Å) | 1.8 | 1.009 | 0.97949 | 0.97949 |
| Resolution (Å)\textsuperscript{a} | 50–2.5 (2.6–2.5) | 50–2.7 (2.8–2.7) | 48–1.8 (1.9–1.8) | 49–2.5 (2.53–2.5) |
| Unique reflections | 29,580 (3304) | 23,488 (2416) | 41,365 (6027) | 15391 (525) |
| R\textsubscript{merge} (%)\textsuperscript{b} | 14.9 (114.7) | 11.9 (144.2) | 9.4 (138) | 7.5 (78.3) |
| I/σ(I) \textsuperscript{a} | 15.8 (2.5) | 15 (1.03) | 14.65 (1.38) | 14.43 (2.15) |
| Completeness (%)\textsuperscript{a} | 100 (100) | 99.9 (99.5) | 99.9 (99.9) | 99.6 (99.6) |
| Redundancy\textsuperscript{a} | 14.83 (14.66) | 9.8 (5.33) | 9.93 (9.01) | 5.46 (5.5) |
| Overall figure of merit | 0.49 |

| **Refinement** | | |
| Resolution (Å) | 48.2–1.8 | 49–2.5 |
| No. reflections | 41,357 | 14,611 |
| R\textsubscript{work} / R\textsubscript{free} \textsuperscript{c} | 18.3/20.9 | 20.8/25.8 |
| Averaged B factor (Å\textsuperscript{2})\textsuperscript{e} | 38.48 / 3534 | 63.63 / 3238 |
| macromolecules\textsuperscript{a} | 37.62 / 3143 | 63.23 / 3149 |
| ligands\textsuperscript{a} | 65.31 / 70 | 106.6 / 44 |
| solvent\textsuperscript{a} | 41.02 / 321 | 49.78 / 45 |

| **R.M.S deviations**\textsuperscript{d} | | |
| Bond lengths (Å) | 0.009 | 0.008 |
| Bond angles (°) | 0.893 | 1.271 |

**Ramachandran analysis**

| In preferred regions (%) | 97.1 | 94 |
| In allowed regions (%) | 2.7 | 5.3 |
| Outliers (%) | 0.2 | 0.7 |

**Synchrotron Beamline**

| BESSY 14.1 | ESRF ID30B | DLS I04 | DLS I04 |

\textsuperscript{a} Highest resolution shell is shown in parentheses.

\textsuperscript{b} R\textsubscript{merge} = \sum_{hkl} \Sigma_{i} <I_{hkl}> / \Sigma_{hkl} <I_{hkl}>, where I_{hkl} is the intensity of a reflection and <I_{hkl}> is the average of all observations of the reflection.

\textsuperscript{c} R\textsubscript{work} / R\textsubscript{free} with 10% of F\textsubscript{obs} sequestered before refinement.

\textsuperscript{d} R.M.S., root mean square.

\textsuperscript{e} The number on the right is the number of atoms that the b-factor was calculated for.

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Structure of Puumala Virus Gc
light scattering (SEC-MALS) at pH 8.0 and pH 5.0. Unexpectedly, we found that low pH does not trigger sGC trimerization in solution as sGC scatters as a monomer even at pH 5.0 (S3B Fig). Elution of sGC was significantly retarded at pH 5.0 compared to pH 8.0, most likely due to non-specific interaction of the protein with the dextran resin [38]. The same effect was reported also for RVFV Gc ectodomain [25]. Nevertheless, in both PUUV sGc structures, one molecule in the asymmetric unit assembles into a homotrimer around the crystallographic three-fold axis (Fig 1). The protomers adopt the post-fusion domain arrangement, resembling other class II post-fusion structures [14, 20, 21, 33, 34] (S1 Fig). They associate in a parallel arrangement with the fusion loop placed at the same end of a stable elongated molecule. The C-terminal stem region is pointing towards the target membrane (Fig 1).

PUUV Gc and RVFV Gc (Genus: Phlebovirus), both members of the Bunyaviridae family, share some structural features that are different from other class II proteins. Similar to phleboviruses, Gc from hantaviruses has a high cysteine content, with 26 cysteine residues. In our structure we located 24 cysteines involved in 12 disulfide bonds. Electron density for the remaining cysteines (C1094 and C1098), at the C-terminal end of the protein, could not be detected. It was suggested before that the \( ^{787}C-X-X-C^{800} \) motif, mapped to domain II, might be involved in disulfide rearrangement to prevent hantavirus inactivation under conditions of low-pH treatment [39]. In our structure, C787 and C790 are located at the membrane proximal region of domain II and are involved in two different disulfide bonds (with C749 and C913, respectively). From the only other Bunyaviridae fusogen structures (RVFV Gc in its pre-fusion and pre-hairpin conformations, PDB ID 4HJ1 and 4HJC, respectively), the analogous cysteines have a similar arrangement [25] despite the hinge motions between the two conformations. Therefore, from comparing these two structures with the post-fusion structure of PUUV sGc we conclude that in contrast to the fusogen activation in some class I membrane fusion proteins, where disulfide rearrangement is essential for preventing a premature fusion [40], these disulfides do not reorganize. Instead, they are responsible to rigidify the structure and stabilize the orientation of the putative fusion loop.

The putative fusion loop of PUUV sGc displays canonical features of a class II endosomal membrane anchor

Our structure provides a direct view on the putative endosomal membrane anchor of Gc known as the fusion loop and contained between \( \beta \) strands c and b (Fig 2). It was previously demonstrated for Andes virus (ANDV) Gc, a member of the Hantavirus genus, that single mutations in the conserved residues W773, N776 and D779 (W115, N118 and D121 in Gc numbering) located at the fusion loop eliminate cell-cell fusion activity and ANDV pseudotyped particles infectivity [32]. From our structure it is apparent that W773 and P781 form a conserved hydrophobic surface (Fig 2B and 2C), exposed towards the target membrane. The N-H group of the W773 side chain forms a hydrogen bond with the carbonyl oxygen of P781, reducing its hydrophilicity and thereby favors the penetration of the fusion loop into the outer leaflet of the endosomal membrane (Fig 2D). This interaction was reported also for dengue
### Table A

<table>
<thead>
<tr>
<th>Virus</th>
<th>Sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>PUUV Gc</td>
<td>Y E Y E T - G - W G - C N P P D</td>
</tr>
<tr>
<td>RVFV Gc</td>
<td>F E Q C G - G - W G - C G</td>
</tr>
<tr>
<td>TBEV E</td>
<td>D Q S D R - G - W G - N H</td>
</tr>
<tr>
<td>DENV1 E</td>
<td>T F V D R - G - W G - N G</td>
</tr>
<tr>
<td>DENV2 E</td>
<td>S M V D R - G - W G - N G</td>
</tr>
<tr>
<td>DENV3 E</td>
<td>T Y V D R - G - W G - N G</td>
</tr>
<tr>
<td>JEV E</td>
<td>G F T D R - G - W G - N G</td>
</tr>
<tr>
<td>WN V E</td>
<td>G V V D R - G - W G - N G</td>
</tr>
<tr>
<td>SFV E1</td>
<td>Y T G V Y P F - M W G G A Y</td>
</tr>
<tr>
<td>SINV E1</td>
<td>F G G V Y P F - W G G A Q</td>
</tr>
<tr>
<td>CHV E1</td>
<td>F T G V Y P F - M W G G A Y</td>
</tr>
<tr>
<td>EFF-1</td>
<td>F P N Q T P I</td>
</tr>
</tbody>
</table>

### Diagrams B

- **PUUV Gc**
- **RVFV Gc (pre-fusion)**
- **SFV E1**
- **DENV2 E**

### Diagram C

- **Y746**
- **W773**
- **P781**
- **F907**

### Diagram D

- **W773**
- **P781**
- **W773**
- **Y746**
- **N776**

Legend:

- 1: Variable
- 2: Average
- 3: Conserved

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virus E trimer where W101 is interacting in the same way with the carbonyl group of G106 [21]. Notably, the side chain of the charged D779, also located in the fusion loop, is pointing to the opposite direction, away from the purportedly membrane plane. Notably, the essential residue N776 maintains a network of hydrogen bonds principally with the main chain carbonyls of residues C780, G782 and with the amine group of residue G785. Therefore, N776 stabilizes the architecture of the fusion loop, thus explaining its importance for fusion. The fusion loop of PUUV G contains other genus-specific features. It has a three-residue insertion (777 P-X-D 779) conserved among hantaviruses (Figs 2A, S2) where X is typically a proline but can be replaced by serine or glycine (S2 Fig). Unlike post-fusion trimers from the Flavivirus, Alphavirus and Phlebovirus genera, the hydrophobic surface at the tip of domain II is extended by the conserved F907 positioned at the loop connecting strands i and j (Fig 2B). Even though it is less conserved, Y746 located at a third loop contained between strand a and αA helix, might participate in the membrane anchoring as its side chain directing towards the target membrane and is nearly at the same plane of the other hydrophobic side chains of the fusion loop (Fig 2B and 2C).

Interactions between protomers in the PUUV sGC post-fusion trimer

PUUV sGC trimerizes through central interactions in domain I and in the domain-I proximal half of domain II. The total surface buried in trimer interfaces is 5850 Å² (1950 Å² per monomer), 17% larger than in DENV2 E trimer (PDB code 1OK8), but only 3% larger than in the Semliki forest virus (SFV) E1 trimer (PDB code 1RER). In addition to the extensive trimerization interface, there are few elements that are exclusive to the PUUV sGC trimer: unlike other class II members, PUUV G has an N-terminal extension of domain I that donates a strand, Aα, to the Bα-Cα-Hα-Gβ β-sheet from the neighboring protomer, creating an intermolecular continuous beta sheet (Figs 1 and 3A). This N-terminal extension has not been found in structures from the well characterized class II fusion proteins, including that of phlebovirus G [25], and therefore it seems to be a unique feature of hantaviruses. Cross-protomer interactions are not common in class II trimers. Typically, the protomers are packed against one another making interactions between secondary structure elements in adjacent protomers. A cross-protomer swap was reported only in Rubella virus E1 protein where the C-terminal stem region donates two strands to two different β-sheets of a neighboring protomer [34]. Additionally, there are few cross-protomer salt bridges in the PUUV sGC trimer. The most notable one is at the membrane proximal part of domain II, close to the fusion loop, where E770 forms a salt-bridge with R902 from the neighboring molecule (Fig 3B), thereby stabilizing the trimer in the membrane-proximal region. To functionally test the significance of this salt-bridge in a hantavirus

Fig 2. The putative fusion loop of PUUV Gc compared to fusion loops of other viral class II membrane fusion proteins. (A) Structure-based multiple sequence alignment of the fusion loop regions from different class II members. Shading is in the same color scheme as in Fig 1. The PXD insertion in PUUV Gc is highlighted with a black box. Residues of PUUV Gc and RVFV Gc correspond to polyprotein precursor numbering. (B) Clockwise from the top left: PUUV Gc, RVFV Gc, DENV2 E and Semliki forest virus (SFV) E1 fusion loops (PDB codes 5J81, 4HJ1, 1OK8 and 1RER, respectively). The hydrophobic residues that anchor the protein to the cellular membrane are shown in stick representation and the disulfide bonds are shown in ball-and-stick representation. (C) CONSURF analysis [74] of unique hantavirus Gc sequences projected on the surface of PUUV sGc crystal structure. A top view on the fusion loop, down the crystallographic tree-fold axis. The following uniprot (http://www.uniprot.org/) entries were used for the analysis: M9QRJ8, Q9QIZ1, M9QSR6, W5RRK8, Q5MYC0, Q9W3J1, Q2V8Y2, A0A068EN08, A0A07E0Q65, Q66753, M9QY05, A0SSD7, Q2B90Y, Q806Y7, A0A0DSW3U2, F1T2C3, A8RRS6, G0WJH7, P27315, C7AGW1, B1NSM7, Q83867, A0A0751FP0, A0A0K0KIP4, Q9WMK6, A0A0F6T9U0, H8ZXQ0, Q9DXJ5, Q9E158, Q9B1Q0, A0A068ETZ4, A6M375, BSDDK4, V9MFN9, H6WCQ0, Q98BQ0, A0A0T3D4A4, P08668, F6KBK3, A0RZG8, K4MYY7, R4JA1A, USL2G2, O55348, H8ZH6K6, H8ZHL5 (D) Hydrogen bond between W773 and the carbonyl of P781. Yellow dash line represents the distance between P781 carbonyl and W773.

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glycoprotein-mediated cell-cell fusion assay (14, 32) we introduced an alanine substitution of R902 (R244 in Gc numbering) into PUUV GPC. In addition, the same mutation was also introduced to GPC of ANDV to exploit several approaches that have been established for this virus. The Gc sequence of hantaviruses is highly conserved and amounts in the case of PUUV and ANDV to 76% of identity and 89% of similarity (S2 Fig). When cells expressed the wild type and R902A constructs of PUUV and ANDV, Gc localized efficiently at the cell surface (S4A Fig). Upon acid-induced incubation, the PUUV and ANDV Gc R902A mutants induced syncytia as the wild type proteins (S4B Fig), indicating that the inter-protomer salt bridge may have a less crucial role for fusion activity (see discussion below).

Fig 3. Inter-protomer interactions unique to PUUV Gc. (A) Strand A0 at the N-terminus of domain I extends the B0-I0-H0-G0 β-sheet of the adjacent protomer. The donor protomer (protomer 1) is indicated in the same color scheme as in Fig 1 while the neighboring protomer (protomer 2) is shown in faded colors. (B) Inter-trimer salt bridge at the membrane proximal part of domain II. Ionic pairs are in sticks representation. The boundaries of each protomer are highlighted. (C) The glycosylation on N937 mediates interactions between protomers. Right: view of the trimer from the membrane, down the crystallographic three-fold axis. Left: Close-up view on the glycosylation groove between the protomers. N937 and the glycans are in sticks representation. 2F0-Fc electron density map at 1σ is shown in light blue mesh.

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PUUV Gc is predicted to have two glycosylation sites, N898 and N937. In our crystal structure we observed N-linked glycans only on N937 whereas N898 is buried in the trimer interface with no available space to accommodate a glycan chain. We therefore conclude that N898 is not glycosylated. In contrast to other class II post-fusion trimers, where the glycans decorate the perimeter of the trimer assembly, in PUUV Gc the glycans linked to N937 are tightly packed between domain II of one protomer and domain III of the neighboring protomer (Fig 3C). Except one hydrogen bond between N999 (domain III) and the first N-acetylglucosamine residue, all contacts with the glycans are via hydrophobic interactions. Indeed, it was previously reported that eliminating the glycosylation on N928 in Hantaan virus Gc (analogous to PUUV Gc N937) is sufficient to prevent cell fusion [41]. Based on our structure and the previous biochemical data, we conclude that the contribution of the glycans to the PUUV Gc trimer interface is a key element in stabilizing trimer assembly in hantaviruses.

Monoclonal neutralizing antibodies against PUUV Gc target the membrane fusion mechanism

Previous studies on Hantaan virus (HNTV) neutralizing monoclonal antibodies (MAb) against Gc showed sequence dependent reactivity. While the antibodies cross-reacted with other hantaviruses (SEOV, DOBV), they failed to neutralize PUUV [42]. In addition, binding of neutralizing and non-neutralizing MAbs to HNTV Gc was mapped to a region that include most of domain III but no specific epitope was determined [43]. Several neutralizing MAbs against PUUV have been selected [44–46], two of which were shown to recognize Gc (human MAb 1C9 and bank vole MAb 4G2). A peptide scan assay was used to identify the linear epitopes for these MAb [39, 47, 48]. The epitopes for 1C9 and 4G2 Mab map to domain I and II, respectively, and both epitopes contribute to the trimer interface (Fig 4). The Gc-Gc dissociation at pH 6.2–6.4 [39] implies exposure of epitopes in Gc that were previously buried or partially exposed in the assembled virion. However it seems that each antibody targets a different stage in the membrane fusion process. In class II proteins the major conformational change within a protomer during membrane fusion is the relocation of domain III [20, 21, 33]. Our structural overlay analysis shows that PUUV sGc is more structurally related to alphaviruses then to phleboviruses (S5A Fig). Furthermore, previous homology modeling studies used various alphavirus E1 proteins as a template for hantavirus Gc [39]. To generate a pre-fusion model for PUUV sGc monomer, we therefore used SFV E1 protein as our reference model. Interestingly, the 1C9 epitope is exposed in our pre-fusion model while in the post-fusion structure it is protected by domain III (Fig 4). This suggests that binding of MAb 1C9 restricts domain III relocation and thus inhibits the fusion process. However, the multimerization arrangement of Gc on the virus envelope needs to be taken into account as this epitope might be partially or completely buried in the context of the mature virion. In contrast, the epitope of MAb 4G2 maps to domain II in proximity to the fusion loop. It was shown for PUUV that the neutralizing MAb 4G2 binds to Gc at neutral pH, however 4G2 does not recognized Gc that was exposed to low pH [39]. The 4G2 epitope was narrowed down to five residues that are sufficient for the antibody to bind and neutralize (Fig 4, dark yellow surface) [42]. Although this region of the epitope barely makes contacts with the neighboring protomer, the presence of a bound antibody will sterically hinder the formation of the trimer and thereby is expected to prevent fusion. Once a trimer is formed, the 4G2 antibody can no longer bind this epitope and therefore will not be reactive. Taken together, our structural epitope analysis and the disappearance of the 4G2 epitope below pH 6.2 [39] propose that the 4G2 MAb inhibit membrane fusion through interfering in trimer formation.
Hinge-motions in the membrane proximal part of domain II

It has been shown that in class II membrane fusion proteins there is a hinge motion between domain I and II [reviewed in [19]], and mutations at that region affect the pH threshold for fusion. However, it seems that in phlebovirus G this region is more rigid [25]. As mentioned before, we also obtained crystals of PUUV sG at pH 8.0 (sGXF2, see Table 1). Intriguingly, despite the slightly basic pH of the crystallization condition, sG still adopted the post-fusion conformation and assembles as trimers around the crystallographic 3-fold axis, however in a different space group lattice (Table 1). Although individual domains superposition did not reveal significant differences (Fig 5A) we still observed some noteworthy differences in the post-fusion structure of PUUV sGXF2, particularly in the membrane proximal part of domain II including the fusion loop. In sGXF2 this region has higher B-factor values than in the crystal form obtained at pH 6.0 (Fig 5B and 5C). Domain II undergoes a hinge motion of 4.5° away from the three-fold axis in the Ca backbone with respect to the sGXF1 structure, increasing the distances between the fusion loops by approximately 35% (Fig 5D). Intriguingly, in sGXF2, E770 and R902 adopt different rotamers that do not allow the salt bridge to form that is in contrast to the β-barrel at the domain I-II interface which limits the hinge motion at that region, unlike other class II membrane fusion proteins, but similar to RVFV G (Fig 5A) [25]. The absence of this inter-protomer salt-bridge plausibly contributes to the flexibility of the trimer at domain II membrane proximal region in the sGXF2 structure (Fig 5E). However the unaffected fusion activity of the R902A in our functional assay suggests that it is not mandatory for fusion activity (S4B Fig). Indeed it was suggested before that there is no preferred distance between fusion loops of class II proteins required for fusion activity [49]. Finally, it was postulated that histidine residues function as pH sensors in class II membrane fusion proteins from
flaviviruses [50–53]. We did not observe any significant differences in rotamers of histidine residues between the low and high pH crystal form. Furthermore, the poor sequence similarity between PUUV GC (post fusion) and RVFV GC (pre-fusion) shows no conserved histidines neither in sequence nor in three-dimension position (S5B Fig) implying that pH-sensing mechanism might be different in these two viruses.

The stem region stabilizes the PUUV GC post-fusion trimer

The total length of the stem region connecting between domain III and the TM domain is 46 residues (1069–1114) (S2 Fig). To maximize solubility we included in our expression construct just the first 38 residues of the stem. However, in both our crystal structures (sGC_XF1 and...
sGC<sup>XP2</sup>) only the first eight residues of the stem (1069–1076) are visible in the electron density map, indicating either major flexibility or proteolytic cleavage at the C-terminus of sGC during preparation. Unlike flaviviruses, in which the stem has an α-helical structure [54], or rubella virus in which the stem has a mixed α/β secondary structure content [34], secondary structure prediction of the stem region from PUUV GC shows mostly random coil structure with a few residues predicted to be in β-strand conformation towards the TM domain (S2 Fig, pink/gray arrow). This might resemble the rubella E1 C-terminal β-strand ‘n’ as it joins the i-j β-sheet of a neighboring protomer [34]. It is possible that the C-terminal part of the stem region of PUUV GC might extend the i-j β-sheet from domain II of the adjacent protomer and thereby might enhance the stability of the trimer.

Most of the inter- and intramolecular contacts at that region of the stem of PUUV sGC are either main-chain/main-chain or main-chain/side-chain interactions (Fig 6A). Interestingly, R1074 side chain at the N-terminal of the stem is inserted into a negatively charged cavity at the same protomer (Fig 6A). The main-chain carbonyls of G883, D884, K893 and C894 create the cavity’s negative charge and lead the stem to a canyon formed by two adjacent protomers (Fig 6A). In flaviviruses the domain III-proximal part of the stem participates in both, intramolecular contacts with domain II and intermolecular interactions with the adjacent protomer, in what that appears to be a late-stage fusion intermediate [55]. The resemblance of our stem region orientation to flavivirus E stem implies the same for PUUV GC.

The stem region’s sequence is conserved among hantaviruses (S2 Fig). A recently published work exploring the stem region characteristics in ANDV showed inhibition of fusion activity for stem peptides derived from the C-terminal half of the stem region but not for peptides that were derived from the N-terminal half (domain III-proximal) [56]. The nature of the stem interactions with domain II observed in our structure might explain a weak binding of such exogenous peptides. Nevertheless, the zipper-like contact that we observed for residues 1069–1076 is evidently strong enough to immobilize a covalently attached stem segment but apparently not to bind a soluble peptide. In Semliki forest virus (genus: Alphavirus) it was shown that no specific sequence of the stem region was required for membrane fusion [57]. R1074 (R417 in Gc numbering) is the only residue at the base of PUUV sGC stem that maintains side chain intramolecular contacts with domain II and it is highly conserved among hantaviruses (except HNTV and SEOV where it is substituted with lysine of similar properties, S2 Fig). To investigate the role of R1074 in membrane fusion, we introduced an alanine substitution of R1074 in both, PUUV and ANDV GPC in order to test their activity in the available in vitro systems established mostly for ANDV [17, 58]. The R1074A mutants of ANDV and PUUV GC were expressed as the wild type proteins, localized on the cell surface and assembled into virus like particles (VLPs) (S4A Fig). However, despite being present on the cell surface, we found that the fusion index of the R1074 mutants from PUUV and ANDV dropped below 0.2, indicating a strong impairment of the acid pH-triggered syncytia formation activity (Fig 6B and 6C). The fact that the mutation of a conserved residue such as R1074 in hantavirus Gc from PUUV and ANDV led to equivalent fusion activity results provides a direct proof for its high conservation among hantaviruses in both, structure and function. Therefore, this data imply that the PUUV GC structure can be used for rational design and characterization of mutations in different hantaviruses. In this context, and to further assess mechanistically the stage in which the R1074A mutant was arrested in the fusion process, we used the ANDV system to test acid-induced trimerization. Therefore, the wild type or R1074A mutant GC from ANDV was incorporated together with wild type GC into VLPs, that were collected and concentrated from the supernatants of cells expressing ANDV wild type or R1074A mutant GPC (S4 Fig). The concentrated VLPs were then treated at pH 7.4 or pH 5.5 and the glycoproteins subsequently extracted by non-ionic detergent. Their sedimentation on sucrose gradients revealed
that the R1074A mutant underwent trimerization at pH 5.5 as efficient as the wild type control (Fig 6D). However, when the resistance of the trimer was tested for its stability by trypsin digestion, not only the neutral pH form, but also the acid-treated R1074A mutant was readily degraded by trypsin, in contrast to the low pH form of wild type Gc (Fig 6E). From these data it can be concluded that the R1074A mutant underwent acid-induced trimerization, but this trimer did not reach a stable post-fusion conformation. This difference in stability may be related to an incomplete fold-back of the stem region against the trimeric core. Combining our structural and functional data we conclude that the ‘base’ of the stem region in hantaviruses is essential for fusion through the formation of a stable post-fusion trimer.

It was shown previously for class II membrane fusion proteins that the activity of small molecule inhibitors in an assay for infectivity correlates well with their capacity to compete with stem-derived peptides [59]. Schmidt and co-workers suggested that the conformational transition from a pre-fusion arrangement to a post-fusion trimer will require removal of the ligand, imposing a barrier to completion of the fusion process. For this reason, in silico screens found potential pocket-binding compounds, that in some cases yielded active inhibitors [60–63]. Thus the electrostatic interaction of R1074 in a well-defined cavity at the base of the stem region and our functional data showing its role in trimer stabilization and membrane fusion activity suggest that this cavity might be a target for small molecule fusion inhibitors.

**Evolutionary implications of the PUUV sGc structure**

The existence of a class II fold in a virus family other than Flaviviridae and Togaviridae was already suggested to diverge either from a viral or a common cellular class II ancestor [25, 35, 64, 65]. What are the driving forces that shaped the evolution of class II membrane fusion proteins? To address this question we computed structure-based sequence alignment based on both, the full-length ectodomains and the individual domains of various class II membrane fusion protein structures and calculated the corresponding cladograms (Fig 7). As expected, cladograms based on the structures of the individual domains do not show significant difference in topology compared to the full-length-based cladogram. Despite the structural similarities of phlebovirus Gc to flavivirus E proteins [25], PUUV Gc seems to be more structurally related to alphavirus E1 proteins (S5A Fig). On the other hand, rubella virus (RV) E1 and PUUV Gc appear to be more related in terms of the particle arrangement. Both assemble into pleomorphic virions with a non-continuous protein envelope with local symmetry properties in contrast to other viral class II membrane fusion proteins that are part of an icosahedral
envelope arrangement [12, 34]. Furthermore, while the viruses containing class II membrane fusion proteins assembled into icosahedral symmetry are all arthropod-borne, hantaviruses and RV are transmitted among mammals (rodent-to-human and human-to-human, respectively). As suggested before for RV, a human-restricted infection cycle forced the virus to evolve unique structural features for its fusogen [34]. It is possible that hantaviruses followed a similar evolutionary path in mammals and further diverged to an additional branch separated from arboviruses containing class II membrane fusion proteins (Fig 7). Nonetheless, other evolutionary mechanisms such as convergent evolution, cannot be ruled out for this observation.
Hopefully with the determination of more fusogens structures from the Bunyaviridae family the molecular basis for these proteins evolution will be more comprehensively studied.

Materials and Methods

Protein expression and purification

The open reading frame encoding the ectodomain of Gc (sGc) from PUUV (M segment residues 659–1106) were amplified from the M segment cDNA of Puumala virus P360 strain (GenBank accession code P41266.1) and subcloned into the pAcGP67 vector (BD Biosciences) in frame with the baculovirus gp67 signal sequence and a C-terminal eight-histidine purification tag. Sf9 insect cells (Expression Systems) were co-transfected with sGc expression constructs and linearized baculovirus genomic DNA (Expression Systems) to produce recombinant baculoviruses expressing sGc. Virus stocks were amplified with three sequential infections of Sf9 cells. For sGc expression, Thi insect cells (Expression Systems) grown at 27°C were infected at a density of 2 × 10⁶ cells/ml with 1% (v/v) of third-passage (P3) baculovirus stock. After culture in suspension for 96–108 h at 20°C the culture media was collected and its pH was adjusted with addition of Tris pH 8.0 to final concentration of 20 mM. Following medium concentration, secreted sGc was purified by nickel affinity chromatography (Ni-NTA agarose, QIAGen). A subsequent anion-exchange chromatography purification step (monoQ, GE Healthcare) resulted in two populations of sGc eluting in different salt concentrations. From this point on the two populations (termed sGc XF1 and sGc XF2) were separated and further went through the same steps. The His-tag was subsequently removed with carboxypeptidase A (CPA) treatment at 4°C for 16 h (1 mU CPA per microgram of sGc). CPA was then inhibited with 1 mM EDTA and 1 mM 1,10-phenanthroline and separated from sGc by size-exclusion chromatography (Superdex 200 10/300 GL, GE Healthcare). Protein samples were concentrated to 2.5–3.5 g/l, frozen in liquid nitrogen and stored at -80°C in 10 mM Tris pH 8, 0.1 M NaCl.

Crystallization and structure determination of sGc

Crystals of sGc XF1 (eluted from the mono-Q at low salt concentration) were grown by hanging drop vapor diffusion at 16°C. sGc XF1 at 2.4 g/l in 10 mM Tris pH 8.0, 0.1 M NaCl was mixed in 2:1 protein to reservoir containing 12% (w/v) polyethylene glycol 2000 mono-methyl ether (PEG 2000 MME), 0.1 M MES pH 6.0 and 0.2 M ammonium sulfate. Multi-crystals clusters appeared after 3–5 weeks and very few single crystals were observed after 6–8 weeks. A single crystal was then crushed and used as microseeds in drops pre-equilibrated for 24 h prior to seeding. Rhombohedron shaped crystals reached a size of 150 × 70 × 70 μm 7–10 days post-seeding and belonged to space group R3₂. Crystals were frozen in liquid nitrogen in reservoir solution supplemented with 30% PEG 400 as a cryoprotectant. Derivative sGc XF1 crystals were obtained by soaking in reservoir solution plus 1 mM methyl mercury phosphate (Hampton Research) for one week. sGc XF2 crystals appeared in 40% (w/v) polyethylene glycol 400 (PEG 400), 0.1 M Tris pH 8.0, 0.2 M lithium sulfate (1:1 protein to reservoir ratio). After 12 weeks sharp-edges cubic crystals were observed and reached a size of 60 × 60 × 60 μm. Upon optimization, crystals with cubic morphology at the size of 75 × 75 × 75 μm appeared after 4–6 weeks and belonged to space group I₂₁. Data were collected at 100 K on a PILATUS detector (Dectris) and processed with XDS [66]. The structure of sGc XF1 was determined by single isomorphous replacement with anomalous signal (SIRAS) with PHENIX [67]. Initial atomic coordinates for sGc XF1 built with PHENIX were used as starting model in refinement and building cycles with the highest resolution (1.84 Å) native data set. The atomic model was completed with COOT [68] and refined to an R_free of 21% with PHENIX and REFMAC [69]. The structure of sGc XF2 was determined by molecular replacement using domains I+III and domain II...
of sG\textsubscript{C}\textsuperscript{XP1} as separate search models. Atomic coordinates and structure factors for sG\textsubscript{C}\textsuperscript{XP1} and sG\textsubscript{C}\textsuperscript{XF2} have been deposited in the Protein Data Bank (ID codes 5J81 and 5J9H, respectively). See Table 1 for data collection and refinement statistics. All molecular graphics were produced using PyMol (PyMOL Molecular Graphics System, Version 1.8 Schrödinger, LLC). Molecular surface calculations were performed using UCSF Chimera [70]. Surface electrostatic potential was calculated with APBS [71]. B-factor analysis was calculated using baverage module in the CCP4 suite [72]. Surface conservation was calculated using CONSURF server (http://consurf.tau.ac.il/) [73].

**PUUV sG\textsubscript{C} pre-fusion conformation modeling**

PUUV sG\textsubscript{C} structure was superimposed on the crystal structure of Semliki forest virus E1 in its pre-fusion state (PDB ID codes 2ALA) using domains I+II and domain III as two separate rigid bodies. The flexible linker between domain I and domain III was eliminated from the model.

**Hydrodynamic and multiangle scattering analysis**

Analytical size-exclusion chromatography and multiangle light scattering (MALS) experiments were performed in 20 mM sodium acetate pH 5.0, or Tris-HCl pH 8.0 and 0.1 M NaCl. A total of 0.2 mL sG\textsubscript{C} at 2.5 g/L was loaded onto a Superdex 200 (10/300) column coupled to mini DAWN TREOS spectrometer and Optilab T-rEX (Wyatt technology) refractometer at a flow rate of 0.7 mL/min. PUUV sG\textsubscript{C} was detected as it eluted from the column with a UV detector at 280 nm, a light scattering detector at 690 nm, and a refractive index detector. The molar mass of PUUV sG\textsubscript{C} was determined from the Debye plot of light scattering intensity versus scattering angle. Data processing was performed with ASTRA software (Wyatt Technology).

**Expression, cell surface localization of mutant Gc and assembly into VLPs**

Mutations were introduced into the expression vectors pI.18/ANDV-GPC [74] and pWRG/PUUV-M(s2) (kindly provided by Jay Hooper, USAMRIID, USA) [75] coding for GPC from ANDV strain Chi-7913 and PUUV strain K27 (GenBank accession numbers AAO86638 and L08754), respectively, by using DNA synthesis and sub-cloning into the corresponding expression vectors (Genscript). For expression and localization analysis, 8 μg of plasmids were calcium-transfected into 293FT cells (Invitrogen) grown on 100 mm plates and 48 hrs later, proteins located on the cell surface were biotinylated using a cell-surface protein isolation kit (Pierce), and the fractions corresponding to intracellular and surface proteins separated on a neutravidin resin. The presence of Gc and β-actin in each fraction were analyzed by western blot using anti-Gc 2H4/F6 [76] and anti-β-actin (Sigma) MAb at a 1:2,500 dilution. Primary antibodies were detected by chemiluminescence using anti-mouse immunoglobulin horseradish peroxidase conjugate (Thermo Fisher Scientific). To prepare VLPs, a previously established protocol was used [17]. Briefly, 48 hrs post-transfection the supernatant of 293FT cells transfected with wild type or mutant pI.18/ANDV-GPC or pWRG/PUUV-M(s2) constructs was collected and VLPs concentrated by ultracentrifugation for 1 hr at 135,000 g. The presence of VLPs was assayed by western blot analysis as described above.

**Cell-cell fusion activity of mutant Gc**

A fluorescence-based syncytia assay was performed as reported before (32). Vero E6 cells (ATTC) seeded in 16-well chamber slides were transfected with 0.5 μg of wild type or mutant pI.18/ANDV-GPC or pWRG/PUUV-M(s2) constructs using lipofectamin 2000 (Invitrogen).
48 hrs later, the cells were incubated for 5 min at 37°C with MEM culture media adjusted to the corresponding pH. Next, incubation of cells was continued for 3 hrs at 37°C in neutral pH MEM culture media. To label the cell cytoplasm, cells were subsequently incubated for one hr with 1 μM 5-chloromethylfluorescein diacetate (Cell Tracker CMFDA, Molecular Probes). Subsequently, cells were fixed with 4% (w/v) paraformaldehyde, permeabilized with 0.1% (v/v) Triton X-100 and Gc detected with anti-Gc 2H4/F6 MAb and anti-mouse immunoglobulin MAb Alexa555 conjugate (Invitrogen). Cell nuclei were stained with DAPI 1 ng/μl in PBS. To visualize syncytia samples were examined under a fluorescence microscope (BMAX51; Olympus) and pictures taken for quantification (ProgRes C3; Jenoptics). The fusion index of Gc-expressing cells was calculated using the formula: 1 - [number of cells/number of nuclei]. For each sample approximately 200 nuclei per field were counted (200 x magnification) and the mean fusion index of five fields calculated from at least two independent experiments.

Multimerization analysis of mutant Gc

Acid-induced Gc trimerization was tested by sucrose sedimentation using a previous protocol [17]. Briefly, VLPs were incubated for 30 min at the indicated pH to allow for Gc conformational changes. The pH back-neutralized, and Triton X-100 (0.5%; v/v)-extracted glycoproteins were subsequently loaded to the top of a sucrose step gradient (7–15%, w/v). After 16 hrs of centrifugation at 150,000 g, fractions were collected and the presence of Gc in each fractions tested by western blot analysis.

Trypsin resistance of mutant Gc

The stability of neutral pH and acid pH conformation of a Gc mutant was assayed by its resistance to trypsin as shown for wild type Gc previously [17]. In brief, VLPs including wild type or mutant Gc were incubated at the indicated pH and presence of Gc assessed by western blot as described above.

Class II membrane fusion protein cladogram construction

A set of structures of class II fusion proteins in their post fusion conformation was obtained from the DALI server [77] with the atomic coordinates of PUUV sGc as the query. Structures of viral class II fusion proteins and of C.elegans EFF-1 were aligned with the MUSTANG server [78]. The resulting structure-based sequence alignment was used for the estimation of the cladogram by the neighbor-joining method with the BLOSUM62 substitution matrix using Jalview [79, 80]. The same process was further executed on individual domains.

Supporting Information

S1 Fig. Comparison of PUUV sGc with other class II proteins in their post-fusion conformation. From left: crystal structures of PUUV sGc, Semliki forest virus E1 (PDB entry 1RER), Rubella virus E1 (PDB entry 4ADI) and Dengue virus glycoprotein E (PDB entry 1OK8) in their post-fusion conformation. To simplify, only one protomer from each trimer is shown. (TIF)

S2 Fig. Multiple sequence alignment (MSA) of human pathogenic hantviruses. Amino acid sequence alignment of Gc from selected hantviruses. Conserved residues were replaced with periods. Domain colors are as in Fig 1. Arrows denote β-strands and cylinders represent α-helices. Glycans are represented by cyan hexagons and disulfide bonds are indicated in green. The unoccupied glycosylation site is represented with single grey hexagon. Light pink and gray shading regions corresponds the unmodeled stem and transmembrane regions,
respectively. Cytoplasmic C-terminal tail presented with no shading. Secondary structure prediction of the C-terminal β-strand is represented by a pink/grey arrow. Numbered green circles represent cysteine residues, where cysteine residues with the same numbering are disulfide linked. Black bars indicate neutralizing epitopes. Database sequence accession codes are per legend and correspond to the Uniprot database (http://www.uniprot.org).

**S3 Fig. PUUV sGc is a monomer in solution.** (A) A total of 0.2 mL of sGc (1 g/L) was loaded onto a Superdex 200 (30/100) size-exclusion column pre-equilibrated with 20 mM Tris buffer pH 8.0 and 100 mM NaCl. The eluate was analyzed for absorbance at 280 nm. Inset: Standard curve obtained with proteins of known masses. The position of Gc on the curve is indicated with an arrow. The corresponding MW of sGc was calculated using the line equations of a standard curve. The MW of sGc calculated from the sequence is 49.3 KDa excluding glycosylations. On the right, a Coomassie stained SDS-PAGE analysis of the two preparations. (B) SEC-MALS analysis of PUUV Gc in different pHSs. 0.2 mL at 2.5 g/L were loaded onto Superdex 200 column at pH 8.0 and pH 5.0. The elution was analyzed for absorbance at 280 nm (right y axis) and for multiangle light scattering, which was converted to molecular mass (left y axis; material and methods). Gray rectangle represents the Mw range between 50–60 KDa. Colors are as per legend.

**S4 Fig. Cellular localization and cell-cell fusion activity of wild type and mutant Gc from PUUV and ANDV.** (A) Western blot analysis of the presence of Gc in different cellular fractions and the supernatant of 293 FT cells expressing wild type or mutant GPC from PUUV and ANDV. Fractions correspond to non-biotinylated intracellular fraction, biotinylated cell surface fraction and the concentrated supernatant of cells. (B) Representative fluorescence micrographs of Vero E6 cells expressing wild type or R902A mutant GPC from PUUV or ANDV, and treated at different pHs. The cell cytoplasm was labelled with 5-chloromethylfluorescein diacetate (CMFDA; green fluorescence), nuclei with DAPI (blue fluorescence) and Gc was detected with anti-Gc MAb (Alexa555; red fluorescence). Cells from a partial microscopy field are shown from a representative experiment. Mock indicates cells transfected with an empty expression plasmid. Arrows indicate syncytia. (200 X magnification). Quantitative analysis of these cell-cell fusion assays is presented also in Fig 6C.

**S5 Fig. Structural alignment and comparison of PUUV with other class II membrane fusion proteins** (A) PUUV Gc shows more structural similarity to alphaviruses then to other class II proteins. Table represents the DALI server (http://ekhidna.biocenter.helsinki.fi/dali_server/start) scores with PUUV Gc as the query. Z-score describe the statistical significance of a pairwise comparison score (higher score represents higher similarity), n/nt is the ratio between the number of aligned residues (n) and total residues in the structure (nt), σ is the Root mean square deviation (RMSD) for the aligned residues and % represents sequence identity. Bunyaviridae are in greens, Togaviridae in reds, Flaviviridae in blues and eukaryotes are in grey. (B) Sequence alignment of PUUV and RVFV Gc proteins. Alignment was obtained using MAFFT [81] the secondary structure assignment for RVFV was based on PDB entry 4HJ1. Colors scheme is as in Fig 1.

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Author Contributions

Conceived and designed the experiments: MD HBR NDT EAB.

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Contributed reagents/materials/analysis tools: MD YM NDT.

Wrote the paper: MD.

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