Surface plasmon resonance (SPR) reveals direct binding of HSV glycoproteins gH/gL to gD and locates a gH/gL binding site on gD

Tina M. Cairns[1*], Noah T. Ditto[3], Doina Atanasiu[1], Huan Lou[1], Benjamin D. Brooks[3], Wan Ting Saw[1], Roselyn J. Eisenberg[2], and Gary H. Cohen[1]

[1] Department of Microbiology, School of Dental Medicine, University of Pennsylvania, Philadelphia, PA, USA

[2] Department of Pathobiology, School of Veterinary Medicine, University of Pennsylvania, Philadelphia, PA, USA

[3] Carterra Inc., Salt Lake City, UT, USA

*Corresponding author

E-mail: tmcairns@upenn.edu (TMC)

Abstract

Herpes simplex virus (HSV) requires fusion between the viral envelope and host membrane. Four glycoproteins, gD, gH/gL, and gB, are essential for this process. To initiate fusion, gD binds its receptor and undergoes a conformational change that hypothetically leads to activation of gH/gL, which in turn triggers the fusion protein gB to undergo rearrangements leading to membrane fusion. Our model predicts that gD must interact with both its receptor and gH/gL to promote fusion. In support, we have shown that gD is structurally divided into two "faces:" one for binding receptor and the other for its presumed interaction with gH/gL. However, until now, we have been unable to demonstrate a direct interaction between gD and gH/gL. Here, we used surface plasmon resonance to show that the ectodomain of gH/gL binds directly to the ectodomain of gD when: 1) gD is captured by certain anti-gD monoclonal antibodies (MAbs) that are bound to a biosensor chip; 2) gD is bound to either one of its receptors on a chip; and 3) gD is covalently bound to the chip surface. To localize the gH/gL binding site on gD, we used multiple anti-gD MAbs from six antigenic communities and determined which ones interfered with this interaction. MAbs from three separate communities block gD-gH/gL binding and their epitopes encircle a geographical area on gD that we propose comprises the gH/gL binding domain. Together, our results show that gH/gL interacts directly with gD, supporting a role for this step in HSV entry.

Importance

HSV entry is a multi-step process that requires the actions of four glycoproteins, gD, gH/gL, and gB. Our current model predicts that gD must interact with both its receptor and gH/gL to promote viral entry. Although we know a great deal about how gD binds its receptors, we have

43 been heretofore unable to demonstrate a direct interaction between gD and gH/gL. Here, we
44 used a highly sensitive, surface plasmon resonance technique to clearly demonstrate that gD and
45 gH/gL interact. Furthermore, using multiple MAbs with defined epitopes, we have delineated a
46 domain on gD that is independent of that used for receptor binding and which likely represents
47 the gH/gL interaction domain. Targeting this interaction to prevent fusion may enhance both
48 therapeutic and vaccine strategies.

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Introduction

HSV entry into a cell requires four glycoproteins, gD, gH/gL, and gB, to promote fusion between the viral envelope and host membrane (1-4). In our ongoing studies to determine the mechanistic role for these proteins in viral entry, we have developed a model that posits that fusion is driven by a cascade of protein-protein interactions, initiated by the binding of gD to one of its receptors, HVEM or nectin-1 (5-7). Such binding induces a conformational change in gD (8) that somehow allows it to communicate with gH/gL (9-11), thereby activating gH/gL into a form that in turn triggers the fusogenic activity of gB (12-14).

Crystal structures of gD with and without the cellular receptors HVEM and nectin-1 (8, 15-18) show that the C-terminus of the gD ectodomain "tail" must vacate the receptor binding site before the interaction with receptor can occur, demonstrating that there is a necessary structural change in gD required to initiate fusion. We postulated that this conformational change in gD structure and/or the subsequent exposure of the underlying residues render gD capable of interacting with and activating the gH/gL heterodimer (9-11). In support, we have shown that gD is structurally divided into two "faces:" one for receptor binding and the other for its presumed interaction with gH/gL. However, despite numerous studies, both from our lab and others (19-25), that indirectly support the ability of gD to interact with gH/gL, we have heretofore been unable to show that gD and gH/gL bind to each other directly.

The critical requirement for an interaction between gD and gH/gL in viral fusion is supported by several studies. First, in Epstein-Barr virus (EBV), cryo-electron microscopy (EM) and crystallography have revealed the structure of a gp42-gH/gL complex (26, 27). Like gD, gp42 is a receptor binding protein for EBV and is considered a functional (albeit not

structural) homologue of gD. Second, complexes of gH/gL with other viral proteins have been visualized for human cytomegalovirus (28, 29). Third, when gB, gD, and gH/gL were swapped between HSV-1 and the closely related saimiriine herpesvirus 1 (SaHV-1), cell-cell fusion was observed only when gD and gH/gL were both from the same virus, suggesting that the two proteins interact with each other in a species-specific manner (19, 20). Fourth, gH/gL and gD were co-immunoprecipitated from transfected and HSV-infected cells, as well as from virions (21, 25), suggesting, but not directly demonstrating, that such interactions took place during fusion.

Our laboratory has tried several ways to examine this issue. First, we found that gD and gH are sufficiently close together in HSV virions to be cross-linked to each other (24). Second, we used a bimolecular complementation assay, in which complementary halves of the yellow fluorescent protein (YFP) were engineered onto the C-termini of the genes of gD and gH, respectively (30). We found that when cells were transfected with plasmids expressing half-YFP tagged gD and half-YFP tagged gH/gL, YFP fluorescence was restored (22, 30), indicating an interaction between gD and gH. However, when co-expressed with gB and a gD receptor, this YFP-tagged complex was not functional for fusion (30). We proposed that the two half-YFP tags stabilized a normally transient interaction between gD and gH/gL but that cell-cell fusion was blocked because gH/gL was not released from gD for the next step in the pathway (presumably its interaction with and activation of gB).

In this study, we readdressed this issue using surface plasmon resonance (SPR) as the most sensitive way to determine if there is even a transient interaction between gD and gH/gL. We bound anti-gD MAbs to a biosensor chip to capture soluble gD, then added soluble gH/gL. We used forms of each protein that would maximize even a modest interaction, i.e. gD2(285t)

and gH2t/gL2 (12, 31). We looked for three things: 1) direct evidence of a gD-gH/gL interaction; 2) evidence that this interaction has functional consequences; and 3) data that would reveal portions of gD that constitute the site of interaction. To address points 2 and 3, we used our panel of virus-neutralizing and fusion-blocking anti-gD monoclonal antibodies (MAbs) with known epitopes to observe which ones might prevent the interaction. Using this strategy, we found that gH/gL binds directly to gD. This binding is specific, as we found no interactions between gD and gB or between gB and gH/gL. Furthermore, this interaction is blocked by certain anti-gD MAbs that mapped to defined epitopes. These epitopes outlined a potential gH/gL binding region on gD that spanned a face adjacent to, but distinct from, the receptor binding site. Thus, our results show that gH/gL does indeed interact physically with gD, defining a critical role for this step in HSV entry.

Results

gH/gL binds to gD when gD is immobilized via certain anti-gD MAbs

Since we could only detect a direct interaction between gD and gH/gL by either cross-linking the proteins on the virion surface (24) or by stabilizing the endodomains of gD and gH/gL through bimolecular complementation (30), we postulated that the gD-gH/gL interaction was transient, as suggested by Heldwein (32). Therefore, we decided to use SPR, which monitors binding of proteins in real-time and is sensitive enough to detect weak or transient interactions. To maximize our ability to detect such interactions, we chose the HSV-2 forms of gD and gH/gL, as we previously showed that type-2 forms are more than twice as efficient at activating gB than HSV-1 forms (12), potentially due to a tighter interaction between these

proteins. In addition, we used the truncated form of the gD ectodomain [gD2(285t)], as the C-terminal ectodomain tail (amino acids 286-306) of the longer form [gD2(306t)] can obstruct receptor binding (8, 10, 31) and may also interfere with gD's interaction with gH/gL (9). For gH/gL, we used a construct consisting of the gH2 ectodomain truncated just before the transmembrane region, co-expressed with full-length gL2 (gH2t/gL2). We examined each soluble glycoprotein as both a ligand (i.e., first protein added to the chip containing a coupled MAb) and as an analyte (i.e., second protein added).

In our initial experiments, we used the Carterra CFM/Ibis SPR system (33-35) to print a large panel of previously characterized gD MAbs (33) onto an SPR chip (Fig. 1A). Then gD2(285t) was flowed across this array, followed by gH2t/gL2. Our working hypothesis was that if a particular MAb captured gD and allowed gH/gL binding, it meant that the site for gD-gH/gL binding was not blocked by the MAb. Conversely, if there was no gH/gL binding, it might mean that the gH/gL binding site on gD was blocked. This system allowed us to evaluate 31 MAbs in one experiment.

The gD2(285t) community map (Fig.1B) (33) illustrates the competitive relationships between the MAbs; those that reside in the same color community have epitopes that are located near one another. Real-time binding of gD2(285t) to a fixed MAb is illustrated in Fig. 1A by the initial increase in response units (RU). When we flow gH2t/gL2 across the gD-MAb complex, binding of gH/gL would be seen as a second increase in RU (Fig.1A). The actual binding curves for gD-gH/gL as captured via each MAb are arranged by community color in Figs. 1D-G.

From previous work, we knew that all members of the red community strongly compete with each other for binding to gD, and each MAb has potent neutralizing activity (11, 33, 36,

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37). This community is subdivided into red and pink sub-communities based on properties such as receptor blocking (nectin-1 only for red, both nectin-1 and HVEM for pink) (33). Here, we observed that when gD was presented via any one of the six pink sub-community MAbs, there was a significant increase in RU upon addition of gH/gL, providing the first evidence that gD can directly bind gH/gL (Fig. 1D). In contrast, when gD was presented by any one of the four red sub-community MAbs, there was no increase in RU upon injection of gH/gL (Fig. 1D), suggesting that these MAbs blocked gH/gL binding. Since red sub-community MAbs block both gH/gL binding and receptor binding (11), it suggests that these MAbs bind to residues at the interface of these two interaction sites. Alternatively, red sub-community MAbs could induce a conformational change, preventing gH/gL binding.

The green community was also divided into sub-communities (yellow and green) based on epitope mapping and competition data (11, 33, 38). We detected a gD-gH/gL interaction when gD was captured by any of the members of the green/yellow communities (Fig. 1E). In contrast, when gD was captured via the four MAbs within the blue community (Fig. 1F) or nine of the eleven MAbs within the brown community (Fig. 1G), gH/gL failed to bind. The two exceptions within the brown community were MAbs 4E3E and 4G4D, both of which showed an increase in RUs upon gH/gL injection (Fig. 1G). These two MAbs are located on the periphery of the brown community that borders the green community (Fig. 1B), likely explaining why they behave more like green MAbs than brown MAbs in terms of gH/gL binding. However, their gH/gL binding curves exhibited a different pattern of gH/gL binding than what was seen with other MAbs (Fig. 1G). Instead of a rapid increase in RUs that quickly levels off [e.g., pink community MAbs (Fig. 1D)], there is a slow, steady rise in RUs that continues throughout the

entire injection (Fig. 1G). We propose that 4E3E and 4G4D may partially block the gH/gL binding site on gD (Table 1).

As yellow sub-community MAbs bind to linear epitopes spanning residues 1-23 at the N-terminus of gD (33, 39, 40), their ability to bind gH/gL binding suggests that the N-terminus of gD is not involved in this interaction. At least one MAb within the green sub-community (MC2) binds a discontinuous epitope located on the face of the gD structure adjacent to that of yellow MAb epitopes (11, 41), identifying another region that is not involved with gH/gL binding. By overlaying all the data onto the gD2(285t) MAb community map, we observed a striking picture of the localization of positive (black) and negative (white) gH/gL binding among the MAb communities (Fig. 1C). As gH/gL binding is allowed by all members of the green and pink communities, we conclude that these regions are not part of the interface between gD and gH/gL. Since these two groups of MAbs include ones that either block HVEM or nectin-1 binding (or both), these data suggest that gH/gL binds a different face of gD than that used to bind receptors.

Complex formation is specific for gD and gH/gL, but only when gD is the ligand

To test for the specificity of the gD-gH/gL interaction, we once again used the Carterra SPR system to analyze possible binding between different combinations of purified, soluble forms of gD, gH/gL, and the HSV fusion protein, gB (Fig. 2). Each glycoprotein was tested as both a ligand and an analyte. For each MAb used for capture, we show two curves: the control (glycoprotein 1 only) and the experimental (glycoproteins 1 + 2). We then stacked the curves for each MAb onto one graph, with the name of the MAbs used to capture glycoprotein 1 listed to

the right. In the case of the control curve, we flowed buffer in lieu of a second glycoprotein in order to observe any decrease in binding of glycoprotein 1 to the capture MAb.

As shown in Fig. 2A, gH/gL bound to gD when gD was captured by certain MAbs (e.g., 77S and D10G12) but not by others (e.g., BD80 and MC5). Next, we reversed the orientation by capturing gH/gL via an anti-gH/gL MAb (making it the ligand) and then flowing gD across the chip surface (making gD the analyte). For this experiment, we used multiple MAbs against gH/gL that bound to distinct, non-overlapping epitopes across the protein (11, 33, 42-47). Interestingly, gH/gL was unable to bind to gD regardless of which anti-gH/gL MAb was used for capture (Fig. 2B). Therefore, we conclude that the binding between gD and gH/gL as detected via SPR is unidirectional, i.e. it occurs when gD is the ligand and gH/gL is the analyte (Fig. 2A), but not the reverse (Fig. 2B). Such results may imply that gH/gL requires a conformational change to accommodate gD binding, and this cannot happen when gH/gL is immobilized by the capturing MAbs. Another possible explanation is that all of the anti-gH/gL MAbs tested could block gD binding. However, we find this explanation unlikely since the MAbs bind to several different regions of gH/gL.

Next, we examined gH/gL and gB for binding. For gB capture, we used multiple MAbs that bind to distinct epitopes (42, 44). We were unable to detect any interaction between gH/gL and gB regardless of which protein was presented as the analyte or the ligand or which MAb was used for capture (Fig. 2C, D). Likewise, we detected no binding between gD and gB (Fig. 2E, F). One caveat here is that the gB used here [gB2(727t)] is in its post-fusion form (48, 49), and this might account for its inability to bind to the other HSV core glycoproteins.

Our overall conclusion is that gD and gH/gL can interact when gD is captured and presented by a subset of anti-gD MAbs; conversely, gD and gH/gL do not bind when gD is captured by another subset of MAbs, giving us some sense of where the interface might be. Furthermore, gH/gL may require a conformational change to accommodate gD binding, as capturing MAbs prevented binding when gH/gL was presented as a ligand. Finally, we failed to detect any direct interaction between gH/gL and gB or between gD and gB.

gH/gL can bind directly to gD

While we have posited that anti-gD MAbs that allow for gH/gL binding do so by presenting (and not blocking) an available binding site on gD, it remained possible that capture by these anti-gD MAbs induced a conformational change in gD which enabled it to bind gH/gL. To distinguish between these possibilities, we next asked whether gD could bind gH/gL when gD was directly coupled to the biosensor chip (Fig. 3A). In this case, we used the BIAcore 3000 biosensor system as we were studying a limited set of interactions. gD2(285t) was amine coupled to the CM5 SPR chip and then gH2t/gL2 was flowed across the chip surface as an analyte (Fig. 3A). As with the Carterra system, gH/gL binding would be indicated by an increase in RU. We found that gD2(285t) directly coupled to the chip surface was capable of binding to gH2t/gL2 (Fig. 3B, black curve). This interaction was specific, as gD did not bind to itself (Fig. 3B, grey line) or other non-HSV control proteins (data not shown). These data indicate that MAbs are not required to induce conformational changes to allow gD-gH/gL binding and that the interaction site on gD2(285t) is open.

In contrast, when gH/gL was coupled to the chip (Fig. 3C) with gD as the analyte, no interaction was observed between the two glycoproteins (Fig. 3D). Thus, in two different formats (Figs. 2, 3) gD-gH/gL binding was unidirectional, occurring only when gD was presented as the ligand and when gH/gL was presented as the analyte. Such results suggest that gH/gL requires a conformational change to accommodate gD binding and this cannot happen when gH/gL is immobilized on a biosensor chip, either directly (Fig. 3D) or by capture with MAbs (Fig. 2B).

In summary, we have shown that gH/gL does bind gD. This interaction can be observed in at least two ways: when gD is directly coupled to the biosensor chip, or when gD is first captured by certain anti-gD MAbs. Our next goal was to carry out a more detailed study of the nature of the interaction.

Analysis of the gD-gH/gL interaction

When gD was directly coupled to the BIAcore CM5 sensor chip, regeneration proved to be difficult, possibly due to inactivation of gD (see Materials and Methods for details). Therefore, the next experiments were performed using the MAb capture method (Fig. 4A). To ensure that there were no significant differences between the MAb capture results using the Carterra and BIAcore systems of SPR, we chose one representative MAb that allowed gH/gL binding via Carterra (1D3, yellow sub-community) and one that did not (MC5, blue community) and tested gD-gH/gL binding using the BIAcore for SPR. First, the two MAbs were coupled to separate flow cells of a CM5 chip. Next, gD2(285t) was injected across the chip surface and captured via MAb 1D3 (Fig.4B) or MAb MC5 (Fig. 4C). Then, we injected gH/gL and

247 monitored for binding. As in the Carterra SPR system, we found that gH/gL bound to gD when
248 it was captured by 1D3 (Fig. 4B) but not when it was captured by MC5 (Fig. 4C). This result
249 gave us confidence that the two SPR systems were interchangeable.

250 To determine if the binding of gH/gL to gD was dose-dependent and to begin to look at
251 the kinetics of the interaction, we flowed serial dilutions of soluble gH/gL over a fixed
252 concentration of gD2(285t), which had been captured by MAb 1D3, and binding was recorded
253 (Fig. 4D). We observed that binding was dose-responsive, i.e. the higher the concentration of
254 gH/gL that was flowed across gD the greater was its binding. However, we were unable to
255 calculate an affinity constant for gH/gL binding to gD because the data did not fit any of the
256 models in the BIAevaluation software package. This may be due to either the nature of the
257 binding interaction or the inclusion of the 1D3-gD binding step prior to gD-gH/gL binding.
258 However, the shape of the binding curves suggests that gH/gL not only binds to gD rapidly (fast
259 on-rate), but also rapidly dissociates from it (fast off-rate). We estimate that binding of gH/gL to
260 gD is in the nM range.

261 We next tested MAbs for their ability to block gD-gH/gL binding (Fig. 5A). Thus far, we
262 showed that when gD is presented by MAbs from the blue, brown, or red sub-communities,
263 gH/gL is unable to bind. However, we wondered if these MAbs would block gH/gL binding to
264 pre-existing MAb/gD complexes such as 1D3/gD, which can bind gH/gL. To answer this
265 question, we captured gD with 1D3 (yellow sub-community) and then flowed a second non-
266 competing MAb, thus "sandwiching" the gD molecule between the two MAbs. We then flowed
267 gH/gL across this sandwich (Fig. 5A). We defined blocking as at least a 50% reduction in
268 gH/gL binding. For clarity, only gH/gL binding curves are shown in Figs. 5B and 5C. We chose
269 MAbs MC5 (blue), MC23 (red), and MC14 (brown) to represent the three communities that

blocked gH/gL binding (Fig. 1). Likewise, we chose MAbs 77S (pink), and D10G12 and MC2 (green), to represent the communities that failed to block gH/gL binding.

We found that MAbs MC5 (blue curve), MC23 (red curve), and MC14 (brown curve) all inhibited the binding of gH/gL to the 1D3/gD complex as compared to that of 1D3/gD alone (black curves) (Fig. 5B). We postulate that the blocking MAb prevents the interaction between gD and gH/gL. In concordance with the results in Fig. 1D-E, MAbs D10G12 (green) and 77S (pink) did not interfere with gH/gL binding (Fig. 5C). Green community MAb MC2 caused a modest reduction in gH/gL binding (28% that of the no MAb control) that was still above our 50% cutoff for blocking (Fig. 5C). Thus, gH/gL binding can be blocked in two ways: 1) when gD is captured to the sensor chip via an inhibitory MAb (Fig. 1); and 2) when an inhibitory MAb is added to a pre-existing, binding-competent MAb/gD complex (Fig. 5B).

Since the anti-gD MAbs that allow gH/gL binding map to three distinct antigenic communities (green, yellow, and pink), we wondered whether we could sequentially bind MAbs from these three communities and still be able to detect gH/gL binding. We used 1D3 (yellow) to capture gD and then flowed MAb 77S (pink), followed by MAb MC2 (green). Each of these MAbs bound to gD and did not interfere with each other (Fig. 5D). Finally, we flowed gH/gL across this multi-MAb/gD complex and remarkably, it bound (Fig. 5D). We conclude that the site on gD for gH/gL binding excludes the residues in the epitopes of each of these MAbs.

gH/gL can bind to a gD/receptor complex

Our hypothesis that the gH/gL binding site occupies a face of gD that differs from the face that is used for binding nectin-1 and HVEM (10, 11) is supported by our finding that MAbs

292 from the pink sub-community block nectin-1 and HVEM binding yet do not interfere with gH/gL
293 binding (Fig. 1). A direct prediction from these findings is that gD should be able to bind both
294 receptor and gH/gL simultaneously. To formally test this concept, we used the Carterra SPR
295 system (Fig. 1A) to screen a panel of MAb/gD complexes for their ability to bind both nectin and
296 gH/gL (Fig. 6). We first printed our panel of anti-gD MAbs and then captured gD. Next, we
297 flowed either nectin-1 (top curve) or buffer (bottom curve, control) across the chip surface,
298 followed by gH/gL. We observed four outcomes that depended on which MAb was used for gD
299 capture: 1) gD presented by MAbs in the yellow and green sub-communities bound both nectin
300 and gH/gL (Fig. 6A), demonstrating that nectin and gH/gL occupy distinct binding sites; 2) gD
301 presented by pink sub-community MAbs did not bind nectin, but did bind gH/gL (Fig. 6B),
302 demonstrating that these MAbs interfere only with receptor binding; 3) gD presented by blue and
303 brown community MAbs bound nectin but not gH/gL (Fig. 6C), demonstrating that these MAbs
304 occupied the site(s) needed for gH/gL binding; and 4) gD presented by red sub-community
305 MAbs were unable to bind either nectin or gH/gL (Fig. 6D). In this last case, the data indicate
306 that there is a subset of residues involved in both receptor and gH/gL binding. These amino
307 acids may define an "edge" between the two functional faces of gD. Alternatively, MAbs that
308 simultaneously interfere with receptor binding and gH/gL binding may preclude access to
309 different residues required for nectin-1 and gH/gL binding, respectively.To probe this question
310 further, we tested gH/gL binding conditions where gD is first bound to and presented by a
311 receptor (Fig. 7A). This format of three proteins (receptor-gD-gH/gL) should more closely
312 reflect the complex that forms prior to fusion. In Figs. 7C,D,F,G only the gH/gL binding curves
313 are shown for clarity. The full set of binding curves, showing all three injections (receptor, gD,

314 and gH/gL), are shown in Fig. 7B,E. We used this format to examine gH/gL binding to gD when
315 the latter was bound to truncated, purified forms of both HVEM and nectin-1.

316 First, we coupled the anti-HVEM MAb CW10, which does not block receptor binding
317 (50), to the biosensor chip and used it to capture HVEM (Fig. 7A). Next, we flowed gD, which
318 was captured by HVEM, and then flowed gH/gL across the CW10/HVEM/gD complex and
319 monitored binding. The complex bound gH/gL in a stable fashion (Fig. 7B). Moreover, in
320 agreement with what was seen in Fig. 5B, gH/gL binding to gD was blocked by MAb MC14
321 (brown community) (Fig. 7C). In contrast, MAb MC2 (green sub-community) did not block gD-
322 gH/gL binding (Fig. 7D). Because neither MC14 nor MC2 interfere with the binding of gD to
323 HVEM (11), we conclude that MC14 but not MC2 blocks the site of the gD-gH/gL interaction.
324 Since MC14 recognizes a linear epitope (Table 1), we presume that some or all of these gD
325 residues are involved in binding to gH/gL.

326 To examine binding of gH/gL to a complex of gD and nectin-1, we used the anti-nectin
327 MAb CK31 (51) to capture the receptor. Next, gD was flowed across the chip surface, followed
328 by gH/gL. As expected from previous results (Fig.7), the CK31/nectin/gD complex bound
329 gH/gL (Fig. 7E). The steep slope of the gH/gL curve is reflective of the rapid dissociation of
330 gD/nectin from MAb CK31 (Fig. 7E). As we found with gD/HVEM (Fig. 7C), MAb MC14
331 blocked gH/gL binding (Fig. 7F), but MAb 1D3 did not (Fig. 7G). Neither MC14 nor 1D3
332 interfere with the binding of nectin to gD (7, 11) (Fig. 7A,C).

333 We conclude that the gH/gL binding site occupies a portion of gD that differs from either
334 of the receptor binding domains (i.e., nectin-1 and HVEM) (17, 18, 52, 53). The residues that
335 constitute the binding interfaces between both receptors and gD are known from crystallographic

studies (17, 18). Hence, these amino acids can be excluded from those that interact with gH/gL. Likewise, MAbs that block gD-gH/gL binding (Table 1) have enabled us to determine a possible gH/gL binding region on gD (Fig. 8, see Discussion).

Discussion

gH/gL binds directly to gD

Based on multiple studies (9-11, 13, 23, 30), we proposed that HSV entry and cell-cell fusion occurs in a cascade of events involving the four essential glycoproteins: gD (the receptor binding protein), gH/gL (the key regulator of fusion), and gB (the fusogen). One of the two gD receptors, HVEM or nectin-1, is also required. As stressed by Heldwein (32), "Determining how the triggering signal reaches the fusogen gB represents the next frontier in structural biology of herpesvirus entry."

In thinking about the fusion cascade and the role of gD in it, we proposed that gD would have distinct sides (11), one of which would bind HVEM/nectin-1 and the other would bind gH/gL. We have extensively studied side one (receptor binding) using epitope mapping and mutational analysis (7, 11, 37, 38, 45, 50, 52-54). Crystallographic studies illuminated the sites of receptor binding (16-18) as well as the amino acids recognized by the HSV neutralizing MAb E317(15) which is a member of the pink sub-community and blocks gD-receptor binding (Fig. 1B).

However, until now, we had no direct evidence that gD physically interacts with gH/gL in a functionally relevant fashion. The major accomplishment of the work reported in this paper

357 is the demonstration of a physical interaction between HSV gD and gH/gL, in real time, that can
358 be blocked by neutralizing and fusion-blocking MAbs. We showed that the interaction between
359 gD and gH/gL is specific and that certain anti-gD MAbs can block it while others cannot.
360 Furthermore, we found that gD can be presented to gH/gL for binding in several different ways:
361 when captured by an anti-gD MAb, when coupled directly to a biosensor chip, or when first
362 captured by one of its receptors. We also found that the interaction between gD and gH/gL is
363 unidirectional, i.e. gH/gL binds to gD when gD is presented as a ligand, but there is no
364 interaction when gH/gL is the ligand and gD is the analyte. Such results suggest the gH/gL may
365 require a conformational change to accommodate gD binding and this cannot happen when
366 gH/gL is immobilized to a biosensor chip.
367

368 **Defining the site on gD to which gH/gL binds**

369 By mapping the epitopes of anti-gD MAbs that either allowed or blocked gD-gH/gL
370 binding, we identified the potential interaction site on gD (Fig. 8). We found that gH/gL can
371 bind gD simultaneously with MAbs in the pink, yellow, and green sub-communities (Fig. 1). It
372 is noteworthy that the epitopes for pink and yellow sub-community MAbs overlap the receptor
373 binding sites, as we also found that receptor and gH/gL can bind to gD simultaneously (Fig. 5).
374 Since the gD-nectin-1 and gD-HVEM interfaces are known from crystallographic studies (16-
375 18), none of these residues are part of the gH/gL binding site. Together, we excluded multiple
376 sites from being involved in gH/gL binding (Fig. 8, grey).

377 Conversely, MAbs in three other communities (red, blue, and brown) all blocked gD-
378 gH/gL binding (Fig. 1). The epitopes for these three communities are distinct and non-
379 competing and encircle a large area of gD (Fig. 8, orange), which is separate from the receptor-

binding face. Since binding by any one of these MAbs blocks gH/gL binding, we suggest that the gH/gL interface on gD spans a large region encompassing these epitopes and the area between them (Fig. 8D, triangle). Our inability to fit the dose response data to a 1:1 binding model remains an issue. Perhaps it means that there is more than one site for gH/gL to bind to gD, although the MAb blocking data argues that this is likely not the case. It could also be due, at least in part, to the configuration of the experiment, i.e. that gD is held by a MAb prior to testing gH/gL binding. The best way to resolve this issue relies on structural data obtained by cryo-eletronmicroscopy or crystallography and that is a consideration for future studies.

The Properties of MC2 (green) and MC5 (blue) are distinct

Both MC2 (green community) and MC5 (blue community) are potent virus neutralizing MAbs (11). They do not block receptor binding but do block membrane fusion (41, 55) (Table 1). Our initial hypothesis was that MC2 and MC5 neutralize virus by occluding gD residues needed to trigger later events, presumably the interaction of gD with gH/gL (9, 11). In support, we show that the binding of gD to MC5 prevents the binding of gH/gL to gD (Figs. 1F and 4C; Table 2). To our surprise, binding of MC2 to gD does not prevent gH/gL from binding (Fig. 1E and 7D). Therefore, MAb MC2 must neutralize virus and block membrane fusion in another, as yet undefined, way. We know that the binding of MC2 induces the C-terminus of gD2(306) to assume an "open" conformation similar to that caused by receptor (11). One possibility is that MC2 neutralizes virus by triggering this conformation too soon, starting the fusion cascade prematurely (Table 2).

Brown community MAbs that block gH/gL binding but do not neutralize virus

We know from earlier studies (11, 56) that the linear epitopes of brown community MAbs overlap a region of gD within the C-terminal tail previously termed the "profusion domain" (57, 58). This domain was defined as a region of gD discrete from the receptor binding sites that is required for HSV entry (57). The profusion domain is located near the C-terminus of the gD ectodomain (residues 260-285). It was suggested that the profusion domain might include a binding site for either gB or gH/gL, or both (25, 57). Here, we show that these MAbs block gD-gH/gL binding (Fig. 1G). However, MAbs mapped to epitopes outside the profusion domain (e.g., MC5 and MC23) also block gH/gL binding (Fig. 1D,F), suggesting either a large gD-gH/gL interface on gD or multiple gH/gL binding sites. Interestingly, MAbs whose epitopes overlap the profusion domain, such as MC4, do not neutralize virus but do inhibit glycoprotein-mediated cell-cell fusion (11, 41) (Table 1), which is perplexing since gH/gL binding is required for both processes. One explanation for this unique phenotype may be the differential accessibility of these gD epitopes in virions versus when gD is presented on the cell membrane.

Ultimately, the question as to where gD physically binds to gH/gL will be determined by structural studies. Based on data presented in this paper, we now identify three regions on gD (Fig. 8): 1) the region colored dark grey, which is not part of the gD-gH/gL contact site and includes the nectin-1 and HVEM binding sites, and the epitopes for MAbs from the green, yellow, and pink communities; 2) the region colored orange, which may be part of the gD-gH/gL contact site and is defined by the epitopes for MAbs from the brown, blue, and red communities that block gD-gH/gL binding; 3) the regions colored white, containing the rest of the gD

molecule for which no data are available. Our challenge now is to develop methods to stabilize the gD-gH/gL interaction for crystallography or cryo-EM studies so that this interaction site can be directly visualized. In addition, targeting the precise site of the gD-gH/gL interaction to prevent virus entry may enhance both therapeutic and vaccine strategies.

Materials and Methods

Cells and soluble proteins. All soluble proteins used in this study were purified from baculovirus-infected insect (Sf9) cells. HSV type-2 gD(285t) was purified using a DL6 immunosorbent column as described previously (11, 31, 59). HSV-2 gB(727t) was purified by use of a DL16 immunosorbent column (60). The hexahistidine -tagged protein gH2t/gL2 (containing the full-length gH2 ectodomain) was purified via nickel affinity chromatography (13, 61). Soluble nectin-1(346t) and HVEM(200t) were purified as described earlier (7, 62).

Antibodies. The following anti-gD MAbs were used in this study: 1D3 (11, 63, 64); DL6, DL11, DL15 (11, 37, 46, 56, 65); MC1, MC2, MC4, MC5, MC8, MC9, MC10, MC14, MC15, MC23 (11, 54); LP2 (kindly provided by A. Minson and H. Browne) (36); HD1, HD2, HD3, H162, H170, H193 (66, 67); 11S, 12S, 45S, 77S, 97S, 106S, 108S, 110S (63, 68); BD78, BD80 (kindly supplied by Becton Dickinson Co.) (11, 56); 4E3E, 4G4D, 11B3AG (gifts of R. N. Lausch) (33); E317 (15); and D10G12 (from Chiron Corporation, now Novartis) (33). For gB: MAbs C226 (provided by Becton Dickinson Co.) (44); DL16, DL21, SS55, SS63, and SS144 (69). For gH/gL: MAbs 53S (61, 68); CHL2, CHL4, CHL5, CHL17, CHL18, CHL21, CHL37

(43); and CΔ48L3 (13). MAbs CK31 (51) and CW10 (50) were generated against nectin-1 and HVEM, respectively.

Screening for protein-protein binding using the continuous flow microspotter (CFM)/ surface plasmon resonance imaging (SPRi). Glycoprotein binding experiments were performed using the Carterra Inc. CFM/SPRi system. We used a method described previously(33-35) with the following modifications. A CFM 2 was used to create a 48-spot microarray of amine-coupled anti-HSV glycoprotein MAbs on a CDM200M sensor chip (Xantec GmbH). Upon docking the printer chip into the SPR imager (IBIS MX96), the chip was blocked with ethanolamine and the system primed with a running buffer of PBS-0.01% Tween 20. Protein binding was performed in a classical sandwich assay format using 100 nM soluble gD, gB, or gH/gL as antigen, followed by 100 nM soluble gD or gB or 400 nM soluble gH/gL as analyte, and 1M glycine pH 2.0 for regeneration. Sensorgrams showing the gD, gB, or gH/gL capture followed by a buffer analyte instead of a glycoprotein analyte were included as negative controls. All experiments were done at room temperature.

Glycoprotein binding using the BIACORE 3000. Experiments were carried out on a BIACORE 3000 optical biosensor at 25°C following previous guidelines (11, 70, 71). All injections were performed at a flow rate of 5 μL/min using HBS-EP buffer (10 mM HEPES, pH 7.4, 150 mM NaCl, 3 mM EDTA, 0.005% surfactant P20). After each experiment, the chip surface was treated with brief pulses of 0.2 M Na_2CO_3 (pH 10) until the RU signal returned to baseline (regeneration).

First, soluble, purified gD2(285t) was amine-coupled directly to a CM5 sensor chip (GE Healthcare Bio-Sciences, Pittsburgh, PA). Purified gH2t/gL2 (0.4 mg/ml) was then injected for 240 s (analyte) and the binding was recorded. The experiment was also performed in the reverse orientation, with soluble gH2t/gL2 amine-coupled to the chip (ligand) and gD2(285t) injected across the surface (analyte). To regenerate the chip surface, 0.2 M Na_2CO_3 (pH 10) was injected until the RU signal returned to baseline. We found that the gD-coupled surface could only be regenerated a limited number of times before a new chip became necessary. Therefore, additional experiments were performed by first capturing soluble gD to the chip surface via the amine-coupled anti-gD MAb 1D3.

For kinetic analysis of gD-gH/gL binding, gD2(285t) was first captured via immobilized 1D3. Next, serial 2-fold dilutions of gH2t/gL2 in HBS-EP were flowed across the chip surface for 240 s, with an additional 240 s allowed for disassociation. Sensorgrams were corrected for nonspecific binding by subtracting the signal achieved on Fc2 (gH/gL injection only) from that on Fc1 (gD injection, followed by gH/gL). The signal obtained when buffer alone was injected was then subtracted from the total signal. Sensorgrams were analyzed using BIAEvaluation software version 4.1.

To test for blocking of gD-gH/gL binding via anti-gD MAbs, a gH/gL binding-permissive (1D3) or non-permissive (MC5) anti-gD IgG was amine-coupled to a CM5 sensor chip. Next, 0.05 mg/mL of purified gD2(285t) was injected across the chip until approximately 300 response units (RU) was captured by the coupled anti-gD MAb. Purified anti-gD IgG (0.1 mg/mL) was then injected for 120 s, followed by soluble gH2t/gL2 (0.2 mg/mL) for 120 s.

To test for receptor-gD-gH/gL binding, anti-receptor MAbs CW10 (HVEM) or CK31 (nectin-1) were amine-coupled to a CM5 sensor chip. Next, 0.1 mg/mL of soluble receptor was injected for 120s, followed by 0.05 mg/mL of purified gD2(285t) for 120 s, then 0.2 mg/mL gH2t/gL2 for 120s.

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Conflict of Interest

Benjamin D. Brooks and Noah T. Ditto are employed by Carterra, Inc.

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Figure Legends

Fig. 1. gD2(285t) binds gH2t/gL2 when gD is captured via certain anti-gD MAbs. (A) Graphical representation of the Carterra CFM/SPR protocol. A panel of anti-gD MAbs was printed to a CDM200M sensor chip. Next, soluble gD (light grey) was flowed across the chip surface and captured by the MAbs. This can be seen on the binding curve as an increase in RU upon gD injection. Then, soluble gH/gL (orange and blue) was flowed across the surface; some MAbs (e.g., black) allowed for the binding of gH/gL, while others (e.g., blue) did not. If gH/gL bound to gD, it generated a further increase in RU (black curve). If gH/gL did not bind, only a decrease in RU would be observed, representing the off-rate of the first glycoprotein-MAb complex (blue curve). Theoretical binding curves are shown to the right. (B) The gD2(285t) MAb community plot, as first illustrated in Cairns et al. (33). gD2(285t) was separated into four MAb communities: blue, brown, green, and red. The red community is subdivided into red and pink. The pink spheres within the red community highlight the group Ib MAbs. Likewise, the green community is subdivided into green and yellow. The yellow spheres/squares within the green community highlight group VII MAbs (N-terminal, linear epitopes). Spheres indicate that competition was measured as both a ligand and an analyte; squares indicate that competition was measured as either a ligand or an analyte only. Solid connecting lines specify that competition between the two MAbs was measured in both directions (each as a ligand and analyte). However, dashed connecting lines identify that the competition between MAbs was measured in one direction only. (C) Lensed view of the community map. Black, MAbs that do not permit gD-gH/gL binding. White, MAbs that permit gD-gH/gL binding. Gray, MAbs that exhibit partial gH/gL binding (see curves below). Two MAbs, MC1 (yellow) and HD1 (red), did not yield binding data (MC1 exhibited poor binding to gD, while HD1 was sensitive to the acidic

766 regeneration solution (33)). (D-G) gD and gH/gL binding curves. MAbs from each community/
767 sub-community are indicated by color. MAb E317 has been assigned to the pink sub-community
768 based on MAb competition, epitope mapping, and functional data (Table 1). The start of the
769 gH/gL injection (arrow) is indicated on each curve. An asterisks indicates gH/gL binding
770 (increase in RU upon gH/gL injection). This experiment was performed across the anti-gD MAb
771 panel three times, with a single representative experiment shown for each MAb. X-axis, time
772 (seconds). Y-axis, resonance units (RU).

773

774 **Fig. 2. Screening soluble HSV-2 glycoproteins for binding using CFM/SPR (IBIS MX96).**

775 Experiments were performed using the Carterra Inc. CFM/SPRi system. (A,E) gD as the ligand.
776 A panel of anti-gD MAbs was printed to a CDM200M sensor chip. Next, soluble gD was flowed
777 across the chip surface and captured by the MAbs. Then, soluble gH/gL (A) or soluble gB (E) or
778 buffer (negative control curve for each printed MAb) was flowed across the chip surface. The
779 printed MAbs are listed to the right of each set of binding curves. Time of gD, gH/gL, gB, and
780 buffer injections are indicated on the X-axis by arrows. (B,C) Same protocol as above, but with
781 anti-gH/gL MAbs printed and gH/gL as the ligand (first injection). (D,F) Same protocol as
782 above, but with anti-gB MAbs printed and gB as the ligand. Each set of MAbs was tested a
783 minimum of two times. X-axis, time (seconds). Y-axis, RU.

784

785 **Fig. 3. gD2(285t) directly coupled to a biosensor chip can bind gH2t/gL2.** (A) Schematic of
786 the BIACORE 3000 protocol for analyzing gD-gH/gL binding. gD2(285t) was attached directly
787 to the biosensor chip via amine coupling. Then either soluble gH/gL (top) or gD itself (bottom)

was injected across the chip surface. The chip was monitored for protein-protein binding, which would result in an increase in RU. Binding curves are shown in (B). Black curve, response after gH/gL injection; gray curve, response after gD injection. X-axis, time (seconds). Y-axis, RU. (C) Schematic of the BIACORE 3000 protocol for analyzing gD-gH/gL binding, reverse orientation. Soluble gH/gL was attached directly to the biosensor chip via amine coupling. Then either soluble gH/gL itself (top) or gD (bottom) was injected across the chip surface. Binding curves are shown in (D). Binding was tested a minimum of three times. Black curve, response after gH/gL injection; gray curve, response after gD injection.

Fig. 4. gD-gH/gL binding can be recapitulated on the BIAcore 3000 biosensor. (A) Diagram outlining the BIACORE 3000 protocol. Anti-gD MAbs 1D3, which is permissive for gH/gL binding, or MC5, which is non-permissive, were coupled to a CM5 biosensor chip on separate flow cells (Fc1-2 for 1D3, Fc3-4 for MC5). Sequential injections of soluble gD and soluble gH/gL were performed. An increase in RU after the gH/gL injection indicated gD-gH/gL binding (red box). Theoretical binding curves are shown to the right. Experimental data for gD captured via 1D3 or MC5 are shown in (B) and (C), respectively. The RU from a control Fc where only gH/gL was injected was subtracted from each. The gD-gH/gL binding resulting from gD capture via MAb 1D3 was observed many times, and is used as a control in follow-up experiments (see Fig. 5). Inhibition of the gD-gH/gL interaction by MAb MC5 was performed three times. (D) The binding of gH/gL to gD is dose-dependent. Serial dilutions of soluble gH/gL were injected across a CM5 chip where gD was captured via 1D3. Only the gH/gL binding curve is shown. The curves were stacked from highest concentration of gH/gL (250 nM,

black curve) to the lowest (15.6 nM, light gray curve). This experiment was repeated twice, and a representative experiment is shown. X-axis, time (seconds). Y-axis, RU.

Fig. 5. Certain anti-gD MAbs block gD-gH/gL binding. (A) Diagram outlining the BIACORE 3000 protocol. Anti-gD MAb 1D3, which is permissive for gH/gL binding, was coupled to a CM5 biosensor chip. Sequential injections of soluble gD, anti-gD MAb, and soluble gH/gL were performed. An increase in RU after the gH/gL injection indicated gD-gH/gL binding. (B-C) gH/gL binding curves. If the anti-gD MAb blocked the gD-gH/gL interaction, a decrease in RUs upon gH/gL injection, as compared to when no MAb was injected (black curve, control) was observed (B). If the gH/gL binding curve mirrored that of the control, then no blocking was observed (C). Each MAb was tested a minimum of two times and is colored according to their MAb community as shown in Fig. 1. (D) Multiple anti-gD MAbs can bind to gD simultaneously with gH/gL. The protocol was performed as outlined in (A), with multiple injections of non-competing, gH/gL-permissive anti-gD MAbs. Injection points for glycoproteins and MAbs are highlighted with arrows. X-axis, time (seconds). Y-axis, RU.

Fig. 6. Screening gD for both nectin-1 and gH/gL binding using the Carterra CFM/SPR protocol. A panel of anti-gD MAbs was printed to a CDM200M sensor chip as explained in Fig. 2. Two curves are shown for each printed MAb. In both cases, soluble gD2(285t) is first injected across the chip surface and bound by the printed MAb (as seen by the initial increase in RU). The top curve shows protein binding after an injection of soluble nectin-1 (thin arrow) followed by an injection of soluble gH2t/gL2 (thick arrow). The bottom curve (control) shows

protein binding after an injection of buffer (no increase in RU) followed by an injection of soluble gH2t/gL2 (thick arrow). In cases where no nectin-1 binding was observed, the two curves overlapped. MAbs are designated by the color of their antibody community as shown in Fig. 1. (A) MAbs that allow both nectin-1 and gH/gL binding. (B) MAbs that allow gH/gL binding but not nectin-1. (C) MAbs that allow nectin-1 binding but not gH/gL. (D) MAbs that do not permit either nectin-1 or gH/gL binding. X-axis, time (seconds). Y-axis, RU.

Fig. 7. Receptor-bound gD is capable of binding gH/gL. (A) Diagram outlining the BIACORE 3000 protocol. An anti-receptor MAb (CW10 for HVEM or CK31 for nectin-1) was coupled to a CM5 biosensor chip. Sequential injections of soluble receptor, gD or gD pre-incubated with an anti-gD MAb, and soluble gH/gL were performed a minimum of two times. An increase in RU after the gH/gL injection indicated gD-gH/gL binding. (B-D) gH/gL binding curves for when gD was captured via its receptor HVEM. (B, E) Sequential injections of soluble receptor, soluble gD, and soluble gH/gL were performed.. Each injection start is demarked by a thin arrow under the binding curve, while each injection stop is demarked by a thick arrow above the curve. (C) Anti-gD MAb MC14, which blocks gH/gL binding, was pre-bound to gD. Only the gH/gL binding curve is shown. (D) Anti-gD MAb MC2, which does not block gH/gL binding, was pre-bound to gD. Only the gH/gL binding curve is shown. Neither MC14 nor MC2 block the binding of gD to HVEM. (E-G) gH/gL binding curves for when gD was captured via its receptor nectin-1. (F) Anti-gD MAb MC14 was pre-bound to gD. (D) Anti-gD MAb 1D3, which does not block gH/gL binding, was pre-bound to gD. 1D3 does not block the binding of gD to HVEM. X-axis, time (seconds). Y-axis, RU.

855 **Fig. 8. Epitope mapping of gD reveals a potential gH/gL binding face**. Surface
856 representation of the gD crystal structure is shown in white (PDB 2C36). Antibody-resistant
857 mutations (Table 1) were used to position MAb epitopes onto the structure. We chose three
858 "sentinel" MAbs, MC5, MC14, and MC23, to represent each of the three MAb communities that
859 contain antibodies that block the gD-gH/gL interaction; these MAb footprints are colored orange.
860 Dark gray residues denote areas that, when bound by receptor or MAbs, do not block gH/gL
861 binding. White residues denote areas for which we have no binding or blocking information.
862 The gD structure is rotated 90^{o} from (A) to (B), (B) to (C), and (C) to (D). We define the gH/gL
863 binding face as the point when the epitopes for all three blocking MAbs (MC5, MC23, MC14)
864 are visible on the same face, and have marked this area with a dashed purple triangle (D).

865

866 **Table 1.** Properties of anti-gD MAbs.

MAb	Epitope (gD residues) [a,b,c,d,e]	Neutralizes HSV-2 [a,d]	Blocks gD2-receptor binding [c,d]	Blocks cell-cell fusion or spread [b,f]	Blocks gD2-gH2/gL2 binding
1D3	10-20	+	HVEM	ND	-
110S	1-29	+	HVEM	ND	-
H170	1-23	+	HVEM	ND	-
MC2	64,67,243,245,246,248	+	-	+	-
D10G12	ND	-	ND	ND	-
HD3	ND	+	- (for nectin) ND (for HVEM)	ND	-
LP2	216	+	Nectin	ND	+
MC23	213	+	Nectin	+	+
DL15	ND	-	Nectin	ND	+
E317	27, 38, 132, 139, 140, 215, 222-224, 227, 231, 235, 238	+	Both	ND	-
DL11	38, 132, 140, 222-224	+	Both	+	-
77S	38, 222-224	+	Both	ND	-
97S	38, 222-224	+	Both	ND	-
106S	38, 222-224	+	Both	ND	-
108S	38, 222-224	+	Both	ND	-
MC5	54, 75-79	+	-	+	+
H162	54, 75-79	+	-	+	+
VID	54	+	-	ND	+
11S	ND	-	-	ND	+
H193	ND	+	ND	ND	+
MC4	262-272	-	-	+	+
MC8	262-272	-	-	ND	+
MC9	262-272	-	-	ND	+
MC10	262-272	-	-	ND	+
MC14	262-272	-	-	ND	+
MC15	262-272	-	-	ND	+
BD78	262-272	+	-	ND	+
BD80	262-272	+	-	ND	+
DL6	272-279	-	-	+	+
4E3E	ND	+	ND	ND	+/-
4G4D	ND	+	ND	ND	+/-

867 [a] Cairns et al. (33)

[b] Atanasiu et al. (41)

[c] Lee et al. (15)

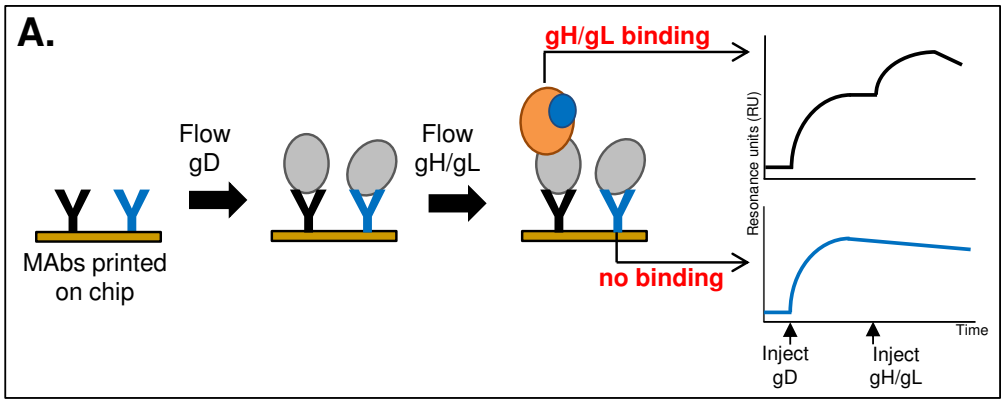
[d] Lazear et al. (11)

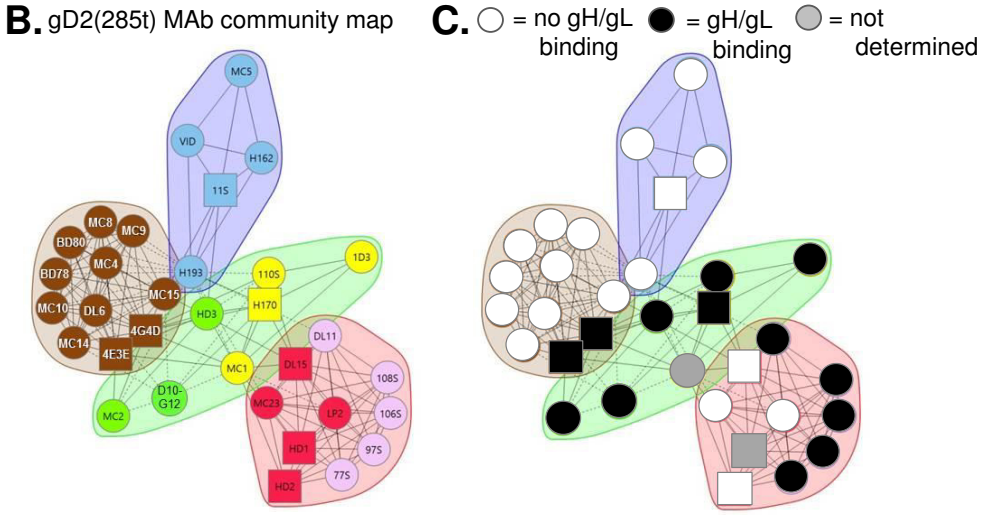
[e] Minson et al. (36)

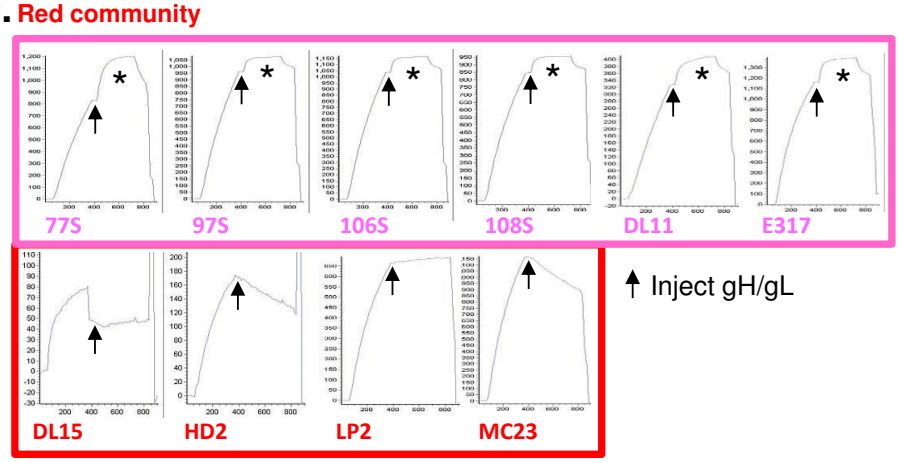
[f] Saw et al. (55)

Table 2. Mechanism of action of inhibitory anti-gD MAbs.

MAb	Mechanism of neutralization/ inhibiting fusion
Pink sub-community	Blocks receptor binding (HVEM and nectin)
Red sub-community	Blocks receptor binding (nectin) and gH/gL binding
Yellow sub-community	Blocks receptor binding (HVEM)
Green sub-community	Induces a gD conformational change
Blue community	Blocks gH/gL binding
Brown community	Blocks gH/gL binding







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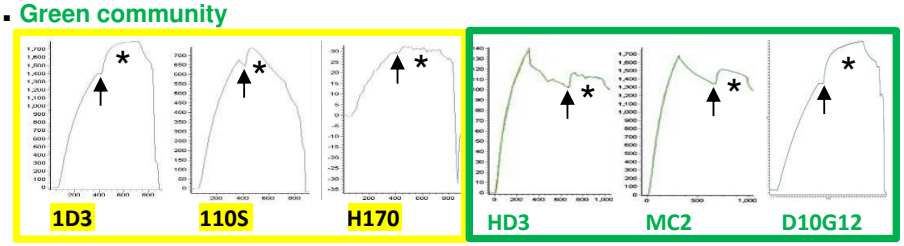
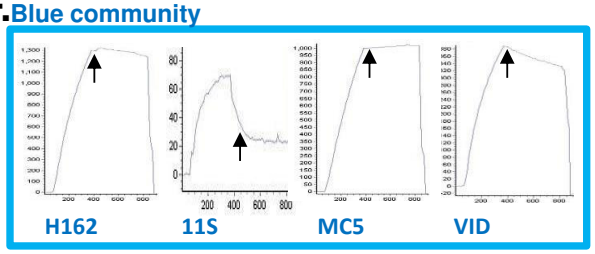
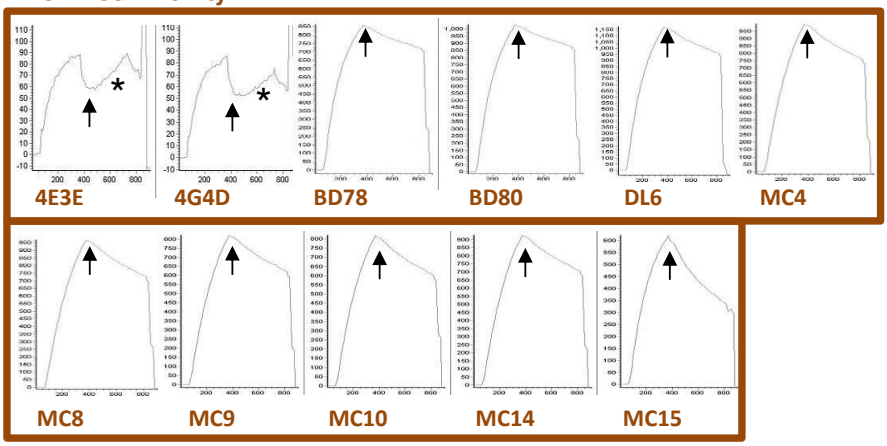
E. Green community

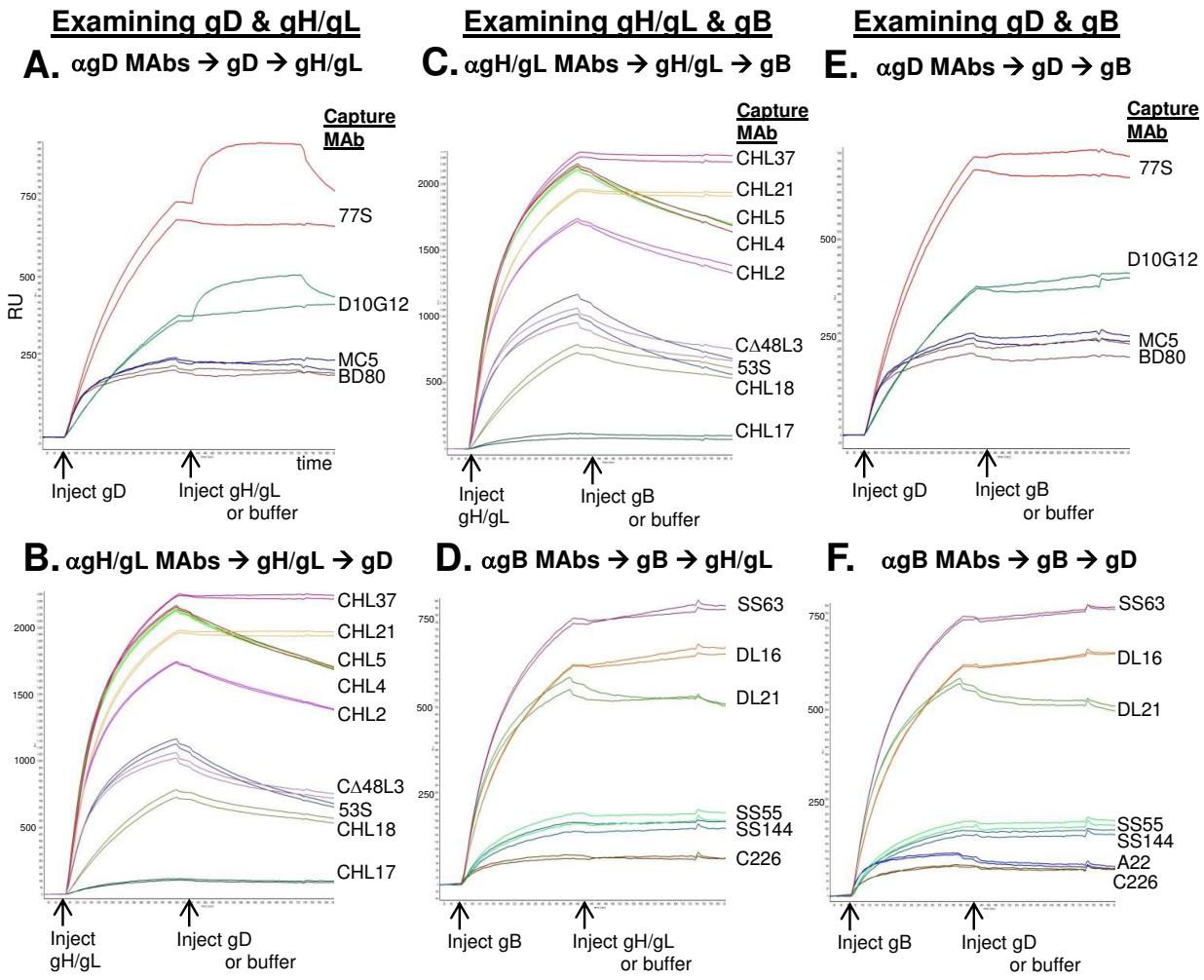


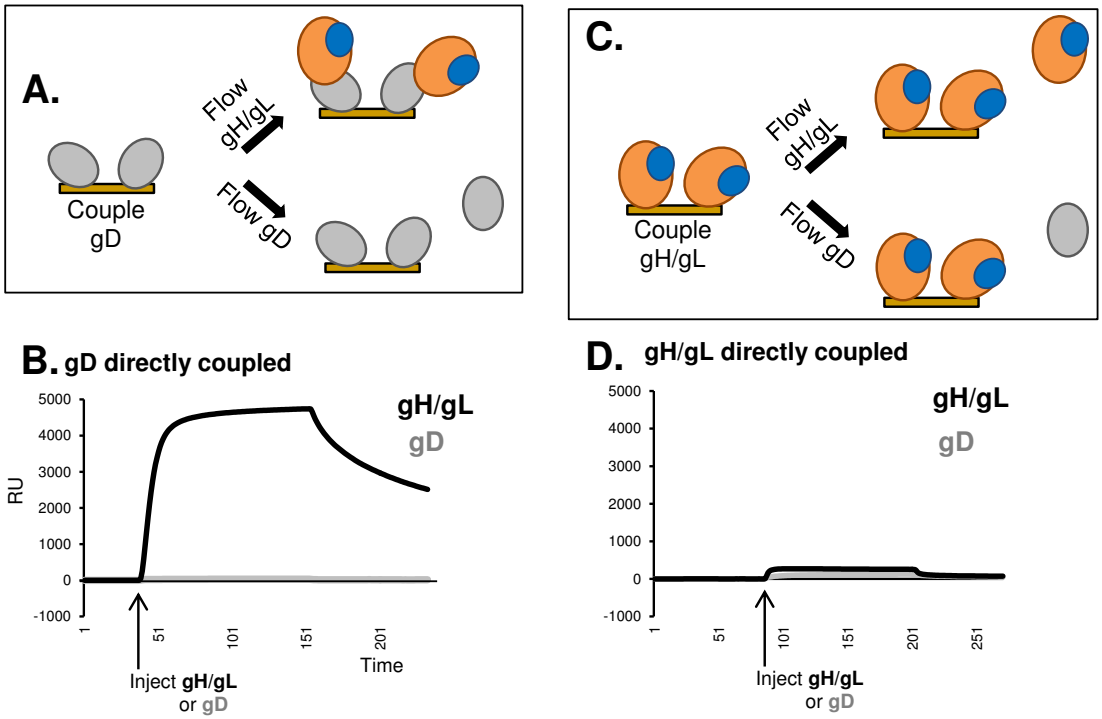
F. Blue community

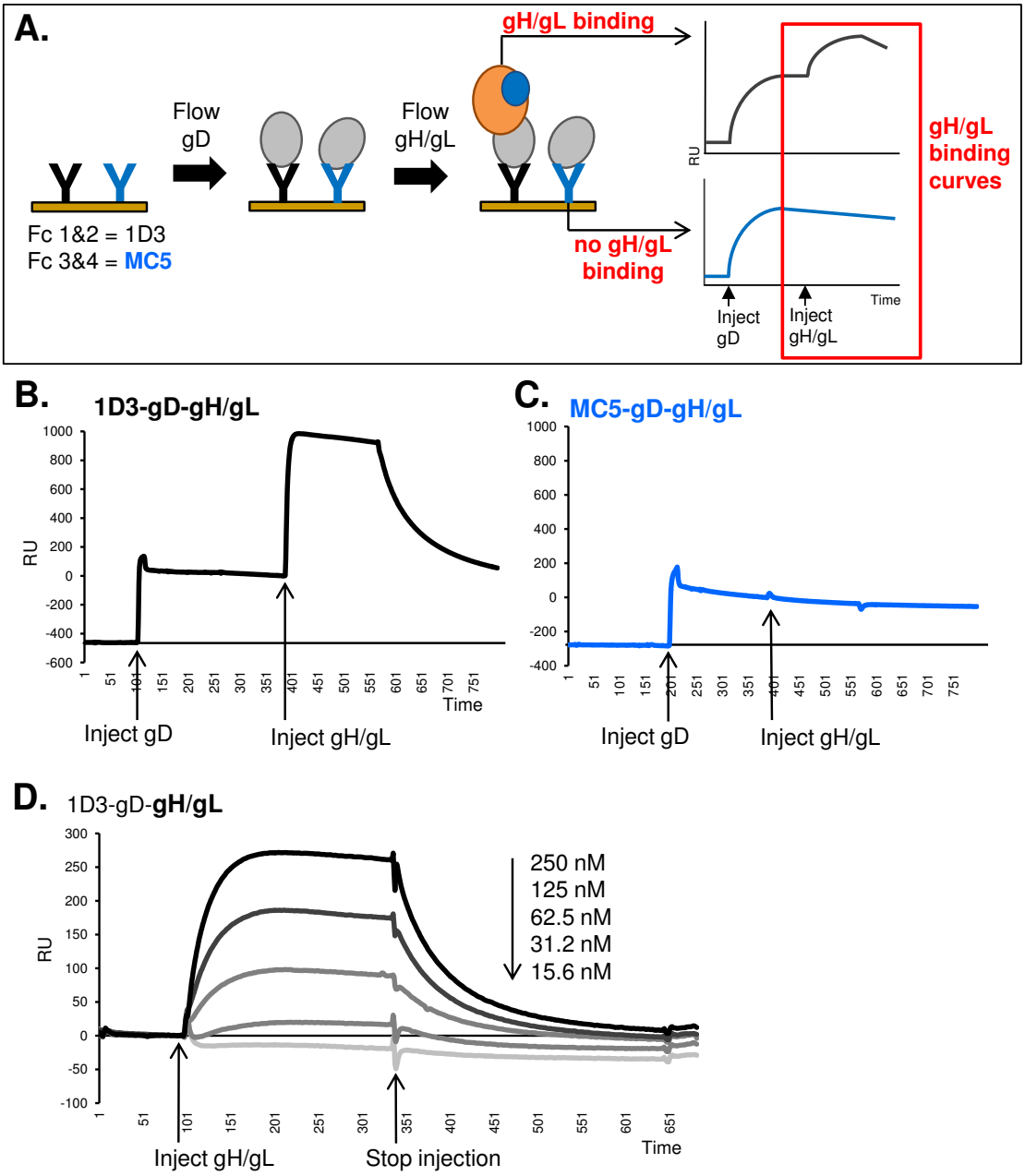


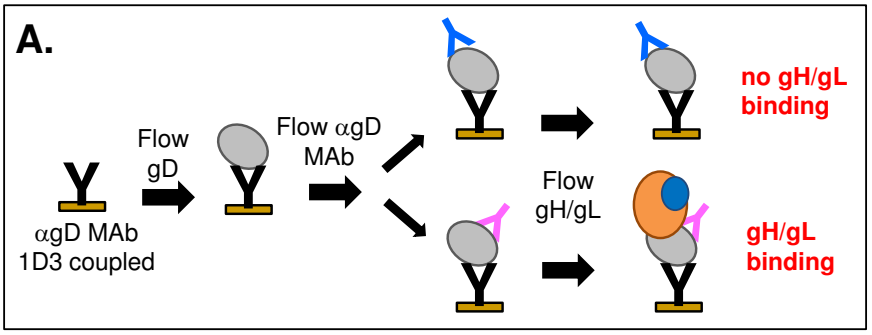
G. Brown community

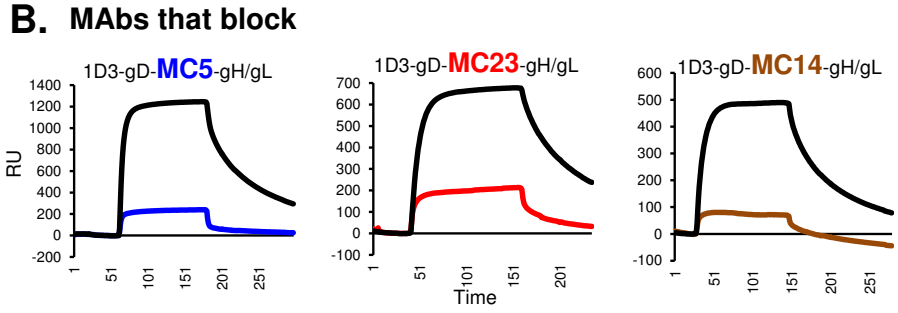


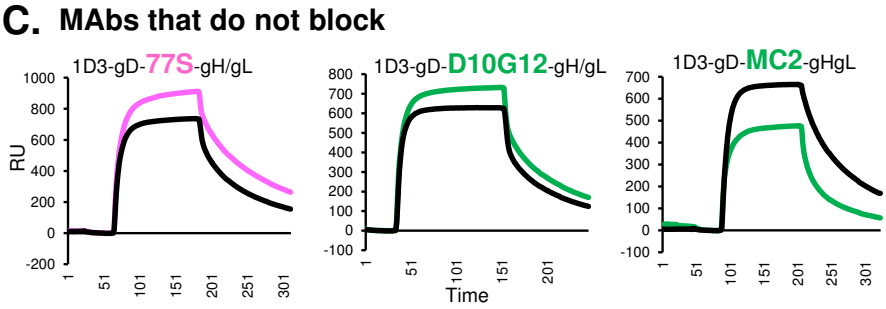


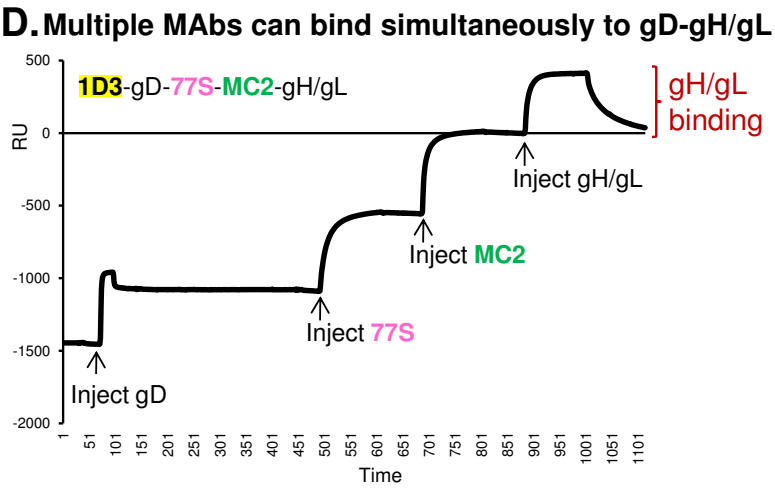




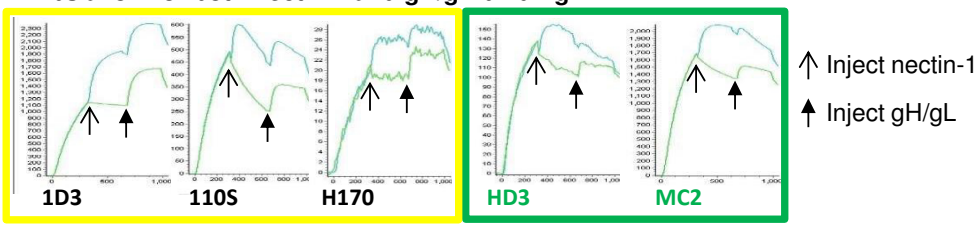




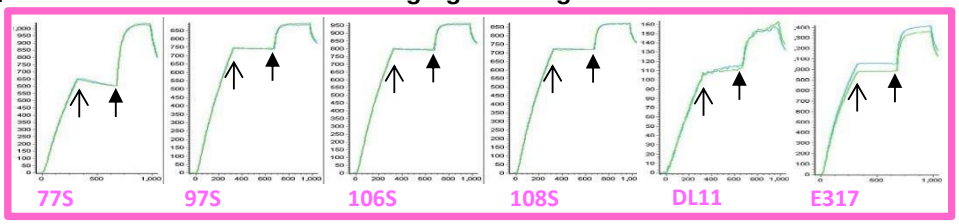




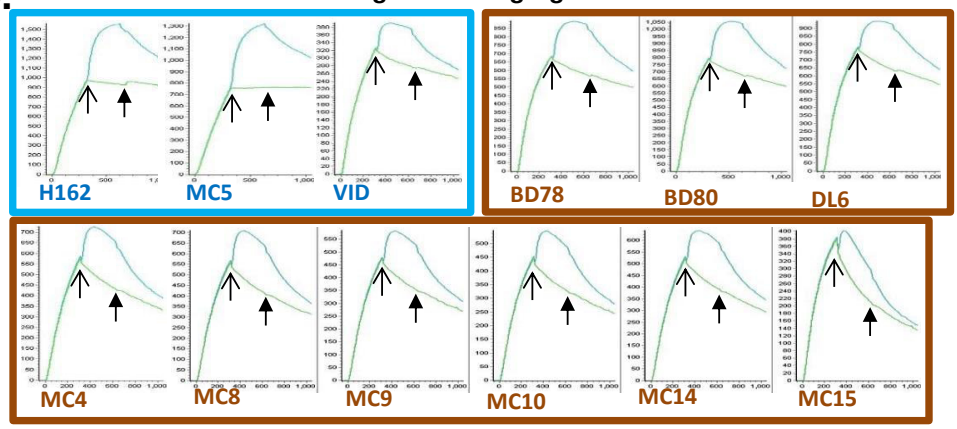
A. MAbs allow for both nectin-1 and gH/gL binding



B. MAbs block nectin-1 but allow for gH/gL binding



C. MAbs allow for nectin-1 binding but block gH/gL



D. MAbs block both nectin-1 and gH/gL binding