Increased epitope complexity correlated with antibody affinity maturation and a novel binding mode revealed by structures of rabbit antibodies against the third variable loop (V3) of HIV-1 gp120

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ABSTRACT

The V3 loop of HIV-1 gp120 is an immunodominant region targeted by neutralizing antibodies (nAbs). Despite limited breadth, better characterization of the structural details of the interactions between these nAbs and their target epitopes would enhance our understanding of the mechanism of neutralization and facilitate designing better immunogens to induce nAbs with greater breadth. Recently, we isolated two anti-V3 neutralizing monoclonal antibodies (mAbs), 10A3 and 10A37, from a rabbit immunized with gp120 of the M group consensus sequence. In this study, crystal structures of these mAbs bound to target epitopes were determined. 10A3 binds to the V3 crown (^{303}TRKSIHIGPGRAF^{317}), using the cradle binding mode similar to human V3 mAbs encoded by IGHV5-51 germline genes and its epitope structure resembles that bound to the human antibodies. In contrast, 10A37, which exhibits greater breadth and potency than 10A3, binds the V3 crown and the succeeding stem region (^{307}IHIGPGRAFYTTGEII^{324}). Unexpectedly, the ^{315}RAFYTT^{320} portion of the epitope existed as helical turns, a V3 structure that has not been observed previously. Its main chain-dominated antigen-antibody interactions not only explain the broad neutralization of 10A37 but also show that its epitope is a potential vaccine target to be further evaluated. In conclusion, our study provides novel insights about neutralization-susceptible epitope structures of the V3 loop of HIV-1 gp120 and demonstrates that, despite low amino acid sequence similarity from human antibody germline genes, rabbits can serve as a useful animal model to evaluate human vaccine candidates.

Importance (150 words)

The apex crown of the third variable loop (V3) of HIV-1 gp120 is the most immunogenic region of the surface glycoprotein and many mAbs targeting this region have been developed. Structural understanding of V3 crown mAbs not only can help understand how antibody responses targeting this unique region, but also contribute to immunogen design for vaccine development. We present here crystal structures of two neutralizing V3 mAbs, 10A3 and 10A37, developed from rabbits immunized with gp120. Our analysis of 10A3 in complex with V3 provided a detailed example of how epitope complexity

can evolve with affinity maturation, while that of 10A37 revealed a novel V3 binding mode targeting the C-terminal side of V3 crown and showed that this region can form a helical structure. Our study provides novel insights about neutralization-susceptible V3 epitope structures and demonstrates that rabbits can serve as a useful animal model to evaluate human vaccine candidates.

INTRODUCTION

The third variable loop (V3) of gp120 plays a critical function in viral entry into host cells. It determines viral tropism by binding coreceptor CCR5 or CXCR4 (1-4). Linked by a disulfide bond between residues 296 and 331 (HXB2 numbering) (5), it is almost always 35 amino acids in length. Structurally, the V3 loop can be divided into 3 regions: the crown (residues 304-318), the stem and the base regions (6). Despite being variable in sequence, the crown region is structurally quite conserved and it often forms a beta hairpin (6-9). The V3 loop is highly immunogenic (10-13) and induces mostly strain-specific neutralizing antibodies (nAbs). High levels of antibodies targeting the V3 loop have also been detected in animals vaccinated with gp120 or V3 peptides (14-18). Many V3 crown-specific monoclonal antibodies (mAbs) have been isolated from HIV-1 infected patients (11, 19) and a number of Fab/epitope complex structures of them have been determined (20-24, 8, 25, 26), setting the foundation for understanding the structural basis of Ab responses against the V3 crown. Sieve analyses of the RV144 clinical trial indicated that the third variable loop (V3) of HIV-1 envelope glycoprotein gp120 specific antibodies correlated with a reduced risk of infection (27, 28), indicating the V3 loop is a potential target for HIV vaccine design.

The antigen binding modes of human V3 crown mAbs have been shown to fall largely into two general categories: cradle or ladle binding modes (24, 8, 25). In the cradle mode, the V3 crown lies along an antigen binding groove resembling a cradle. In the ladle mode, the Ab has a long standing CDR H3 (the handle of the ladle), which interacts with the main chain of the N-terminal beta strand of the V3 crown and a pocket at the base of the CDR H3 (the bowl of the ladle), which interacts with the apex turn of the V3 crown. Data suggested that human V3 crown Abs preferentially use IGHV5-51 germline gene (19), and such Abs (e.*g.* mAb 2557) use the cradle binding mode (8, 25). IGHV3 germline genes are also frequently used and some IGHV3-encoded V3 crown Abs (*e.g.* mAbs 447-52D and 537-10D) use the ladle binding mode (21, 29, 24, 30). In both binding modes, the N-terminal strand of the V3 crown plays a key role in the antibody-antigen interaction. In the cradle binding mode, the N-terminal strand of the V3

crown is buried deep in the antigen binding groove while the C-terminal residues make additional contacts with the antibody. In the ladle binding mode, the N-terminal strand of the V3 crown interacts with CDR H3 of the antibody and the C-terminal residues are not always observable in the complex structures, indicating there is no or very little contacts with the antibody. MAbs isolated from small animals immunized with V3 peptides or monomeric gp120 have been shown to be able to mimic human mAb binding modes (26). For example, rabbit mAb R56 and mouse mAb 50.1 preferentially recognize the V3 crown similar to the cradle binding mode used by human Abs encoded by IGHV5-51 germline genes (20, 26). However, the epitopes of these mAbs are shorter and less complex than that of human Ab developed from infected patients and their evolution with affinity maturation is not understood.

We have recently isolated a panel of new V3 loop-specific mAbs from a rabbit immunized with gp120 based on the M group consensus sequence (MCON6), and two of them, 10A3 and 10A37, exhibited neutralizing activities (16). They target different regions of the V3 loop: 10A3 recognizes a peptide consisting of residues RKSIRIGPGQAFYAT (a.a.304-320); 10A37 recognizes a peptide consisting of residues RIGPGQAFYATGDII (a.a.308-324), atypical for V3 mAbs. Interestingly, they also competed with PGT121, one of the broadly neutralizing mAbs targeting the V3 base glycan patch (31, 16). To precisely define the epitopes of these two mAbs and characterize their antigen-antibody interactions at atomic level, we determined their Fab/epitope complex structures and compared them with V3 specific rabbit mAb R56 (26), and human V3 specific mAbs derived from the IGHV5-51 germline gene (8, 25). The results showed that mAb 10A3 targets the V3 crown similar to rabbit mAb R56, but makes additional contacts with the C-terminus of the V3 crown region, correlating with additional somatic hypermutations. The cradle antigen-binding mode of 10A3 is similar to those of human V3 specific mAbs derived from the IGHV5-51 gene. In contrast, 10A37 targeted the V3 crown and the succeeding stem region, in a new binding mode not observed previously, and its V3 epitope harbors a helix core. This study provides novel insights about neutralization-susceptible epitope structures of the V3 loop of gp120 and further discerned that rabbit is a useful animal model for the evaluation of the immunogenicity of vaccine candidates.

METHODS

Fab production and purification

MAbs 10A3 and 10A37 were expressed and purified as previously described (16). Briefly, plasmids encoding the heavy and light chains were transfected into 293F cells using 293fectin (Invitrogen). The cell culture supernatant was collected 5 days after transfection and clarified by centrifugation. The mAbs were then purified using protein A column, eluted, and dialyzed in PBS.

The Fab fragments of rabbit mAbs were prepared by papain digestion as described (24). Briefly, the IgG molecule was mixed with papain (Worthington, Lakewood, NJ) at a 20:1 molar ratio in 100 mM Tris (pH 6.8) with 1 mM cysteine hydrochloride and 4 mM EDTA. The mixture was incubated for 1 hour at 37^{o}C and the reaction was stopped by 10 mM iodoacetamide. The Fab fragment was separated from the Fc fragment and the undigested IgG by a protein A column and further purified by size exclusion chromatography. The Fab fragment was then concentrated to about 10 mg/ml for crystallization.

Crystallization, data collection, structure determination and refinement

The $V3_{ConB}$ peptide obtained from NIH AIDS Reagent Program and the $V3_{JR-FL}$ peptide synthesized by Biomatik (Wilmington, DE) were dissolved in water and DMSO, respectively, and mixed with Fabs 10A3 and 10A37-at a 10:1 molar ratio. Crystallizations conditions were screened and optimized using the vapor diffusion hanging drop method. Well-diffracted crystals of 10A3 Fab/$V3_{ConB}$ complex were obtained with a well solution of 32% polyethylene glycol 6000, 1 M LiCL, 0.1 M Tris pH 8.0, whereas those of the 10A37 Fab/$V3_{JR-FL}$ complex were obtained in a well solution of 18% polyethylene glycol 4000, 8.5% Isopropanol, 0.1 M HEPES pH 7.5, 15% glycerol. X-ray diffraction data sets were collected at beam line X6A and X4A, National Synchrotron Light Source (NSLS), Brookhaven National Laboratory. All data sets were processed using the HKL2000 package (32) and XDS (33), and structures determined by molecular replacement using R56 Fab structure (PDB ID 4JO1) as the initial model. Cycles of refinement for each model were carried out in COOT (34) and Phenix (35). Coordinates and

structure factors of 10A3/$V3_{ConB}$ and 10A37/$V3_{JR-FL}$ complexes have been deposited in the Protein Data Bank.

Comparative analyses of rabbit and human mAbs

Structural analyses were carried out using ICM (36) and figures were generated using PyMOL (http://pymol.org). The antigen-antibody interactions described in figures are caculated by ICM and PDBePISA (EMBL-EBI). For comparison with rabbit mAbs 10A3 and R56, two V3 human mAbs were chosen that are encoded by IGHV5-51 germline genes: mAbs 2219 and 2557 (PDB IDs: 2B0S and 3MLT). Human antibodies binding to V3 using different binding mode or binding to other parts of the V3 loop, or to V3 loops with highly dissimilar sequences, have been omitted from this analysis.

RESULTS

Determination of the complex structure of 10A3/$V3_{ConB}$

MAb 10A3 is a chimeric antibody with rabbit variable region and human constant region. The peptide used for co-crystallization was selected by screening from a panel of V3 peptides already available by ELISA based on the epitope mapping results (16). 10A3 Fab was co-crystallized with a 15-mer clade B consensus V3 peptide ($V3_{ConB}$, NNTRKSIHIGPGRAF), which differs from MCON6 gp120 immunogen at only residue 315 (NNTRKSIHIGPG**Q**AF), which does not play a key role in the antibody binding (see below). The crystal of the complex belongs to orthorhombic space group $P2_122_1$, and the complex structure was determined by molecular replacement and refined to 1.9Å resolution (Fig. 1; Table 1). As there is only one complex in the asymmetry unit, we assigned the chain identities (IDs) of the light and heavy chains and the peptide epitope as L, H, and P, respectively. Amino acid residues on the light and heavy chains were numbered following the Kabat and Wu convention (37), and V3 residues were numbered based on HXB2 scheme. A residue is referred to by its number preceded by its chain ID, for example, Arg^{P315} refers to arginine residue 315 of the peptide epitope. Thirteen V3 residues

(^{303}TRKSIHIGPGRAF^{317}) were observed in the electron density and have been built into the final structure.

The complex structure of 10A3/V3$_{ConB}$ shows that 10A3 binds the V3 crown by using the cradle-binding mode. The antigen-binding pocket is deep and shaped like a cradle with the third complementarity determining regions (CDRs) of the light and heavy chains (L3 and H3) situated at each end of the cradle (Figs. 1 and 2), and CDRs H1 and H2 forming a wall on one side of the peptide while CDRs L1 and L2 on the other side. The periphery of the cradle is negatively charged, contributed by Glu^{L50} (L2) and Asp^{L93} (L3) of the light chain on one side, and Asp^{H53} (H2) of the heavy chain on the other side (Fig. 1D, Fig. 2A). The bottom of the cradle is hydrophobic, contributed by Ala^{L91}, Leu^{L89} ~~and~~ Phe^{L94}, Phe^{H96} and a disulfide bond between Cys^{H35} and Cys^{H50} near CDR H2. Such CDR loop disulfide bonds are rarely observed in human Abs but quite frequently in rabbit ones (26, 38).

Detailed antigen-antibody interactions of 10A3/V3$_{ConB}$

The antigen-antibody interactions of 10A3 buried a total of 969Å^2 surface area with 475Å^2 from the antibody and 494Å^2 from the antigen, involving both hydrophilic and hydrophobic ones. (1) The hydrophilic interactions. The side chains of epitope residues, Arg^{P304} and His^{P308}, interact directly with negatively charge residues of 10A3 at the periphery of the cradle. Specifically, the N-terminal Arg^{P304} forms a salt bridge with Asp^{H53} (from CDR H2) and its side chain also stacks with the benzyl group of Phe^{P317} that can stabilize its orientation. His^{P308} forms also a potential salt bridge with Glu^{L50} (L2). Additionally, Ser^{P306} can form hydrogen bonds with the side chain of Asn^{L32} (L1) and the carbonyl group of Tyr^{L28} (L1). The side chain of Asn^{H95} forms a hydrogen bond with the carbonyl oxygen of His^{P308}, and it has the biggest contact area (~ 50Å^2) with the epitope among residues of the heavy chain or the whole antibody. (2) The hydrophobic interactions. Several highly conserved residues, including Ile^{P307}, Ile^{P309} and Pro^{P313}, of the V3 crown play key roles on the hydrophobic interactions. Ile^{P307} and Ile^{P309} are buried into a hydrophobic pocket and the residues of 10A3 that contribute these hydrophobic interactions are Ala^{H33} (H1), Cys^{H50} and Ala^{H52} (H2) and Leu^{L89}, Ala^{L91} and Phe^{L94} (L3). Pro^{P313} stacks with two aromatic

side chains of Tyr^{H97} and Tyr^{L49} (Fig. 2C). Although 10A3 has a very short four residue CDR H3 (NFYL, Kabat definition), it plays several important roles in antigen binding. In addition, Phe^{H96} contributes to the hydrophobic pocket burying the two conserved isoleucines, Ile^{P307} and Ile^{P309}, of V3 and Tyr^{H97} stacks with Pro^{P313} in the arch region of V3. Notably, the backbone of the epitope also involves extensively in binding the antibody, and there are six contacts between the backbone of V3 and 10A3 (Figs. 2B and 2C). Another point to note is that the side chain of the signature residue Arg^{P315} (would be Gln in non-clade B strains) point away from the antigen binding site, even though it can form a salt bridge with Glu^{L50} (3.6Å).

Determination of the complex structure of 10A37/$V3_{JR-FL}$

The Fab of rabbit mAb 10A37, which has a better potency and breadth of neutralizing activity than 10A3 does (16), was co-crystallized with a 23-mer JR-FL V3 peptide, NNTRKSIHIGPGRAFYTTGEIIG ($V3_{JR-FL}$; 301-324); its sequence differs from that of MCON6 immunogen at two positions (NNTRKSIHIGPG**Q**AFY**A**TGEIIG). The complex structure was also determined by molecular replacement and refined to 2.3Å resolution (Fig. 3; Table 1). The crystal of the complex belongs to monoclinic space group $P2_1$, and there are two essentially identical Fab/V3 complexes in the asymmetry unit (V3 epitope Cα RMSD = 0.3Å). For simplicity, only one complex is used here and the residues are numbered the same way as mentioned above for the 10A3/$V3_{ConB}$ complex using L, H, and P for denoting light chain, heavy chain, and V3, respectively. Sixteen residues of V3, from 307 to 324 with sequence IHIGPGRAFYTTGEII, were observed in the electron densities and have been built into the final structures (Figs. 3 & 4). It is clear that 10A37 has a new mode of binding V3 crown, different from what have described previously (39, 24, 8, 25). Surprisingly, the epitope of 10A37 has a helix core (^{315}RAFYTT^{320}), with the N-terminus of the epitope extending straight out on one side of the helix core and the C-terminus bent back on the other side. A circular dichroism experiment using a full-length cyclic V3 (JR-FL sequence) revealed that it has weakly helical conformation (not shown), suggested that some region of V3 may have intrinsic propensity for a helical conformation. Interestingly,

the heavy chains of 10A3 and 10A37 are derived from the same rabbit germline gene IGHV1S45*01 (15), but their CDR H3 lengths are very different: 4 vs 12 residues (Kabat definition), respectively.

Detailed Antigen-antibody interaction of 10A37/V3$_{JR-FL}$

The antigen-antibody interactions buried a total of 918Å^2 surface area, contributed equally from the antibody and the V3 epitope. There are two pockets on the surface of 10A37 antigen binding site (Fig. 3D): one is ~10Å deep, burying the side chains of Phe^{P317} and Tyr^{P318} from the helix core and another shallow one, accommodating Pro^{P313} before the helix. The side chain of Ile^{P323} is also half buried at the edge of the deep pocket. Again, we can divide the antigen-antibody interactions into hydrophilic and hydrophobic ones. (1) Hydrophilic interactions between the side chains of V3 residues and 10A37 (Fig. 4A). At the bottom of the deep pocket, Asp^{H95} (of CDR H3) is buried by the side chain of Tyr^{P318}; the OH group of Tyr^{P318} located between an OD atom of Asp^{H95} (2.63Å) on one side and the OH of Tyr^{L93} (L3; 2.65Å) on the other side. The side chain of His^{P308} at the N-terminal end of the epitope can also form a hydrogen bond with the OH group of Tyr^{H100A} (H3). (2) Hydrophobic interactions. As aforementioned, Phe^{P317} and Ile^{P323}, in addition to Tyr^{P318}, are buried in a hydrophobic pocket, formed by Phe^{H34} (H1), Tyr^{H58} (H2), Try^{L93} and Ile^{L95D} (L3). The aromatic plane of Phe^{P317} is on the top of Phe^{H34} and Try^{L93}, while the side chain of Ile^{P323} is on the top of Tyr^{H58} and Ile^{L95D}. The V3 arch residue Pro^{P313} is buried in a smaller hydrophobic pocket formed by residues Gln^{L30} (L1), Tyr^{L93} (L3), and Tyr^{H100A} (H3). Additional contacts between Tyr^{P318} and Try^{L93} (L3), together with intra-chain interactions between Phe^{P317}, Ile^{P323} and Tyr^{P318}, strengthen overall hydrophobic interactions. Interestingly, Gln^{P315} and Ala^{P319} of V3 $_{JR-FL}$, the two residues different from the gp120 used as the immunogen to elicit 10A37, only use their backbone to contact with antibody. There are eleven main chain interactions between the backbones of V3 and 10A37 making a notable contribution to the way 10A37 grasps its V3 epitope (Fig. 4B).

Comparison of the antigen-antibody interactions of rabbit V3 mAbs 10A3 and R56

The binding mode of 10A3 is very similar to that of another rabbit V3 mAb R56; they both recognize the crown of V3, mimicking the cradle-binding mode of human V3 mAbs derived from the IGHV5-51 germline gene (Fig. 5) (26). Interestingly, the light chains of 10A3 and R56 are derived from the same rabbit light chain germline gene (IGKV1S15*01), although their heavy chains are derived from different germlines gene (IGHV1S45*01 and IGHV1S40*01, respectively; Fig. 5C) (15). The light chain backbone structures of the two antibodies superimposed remarkably well (Cα RMSD = 0.5 Å) (Fig. 5A). In terms of CDRs, 10A3 and R56 are similar to each other with respect to CDRs H3, L1, L2 and L3. Both mAbs have a short 4-residue (Kabat definition) CDR H3 with similar sequence: NFYL (10A3) and NFDL (R56). Sequence alignment analyses show the parallel evolution of 10A3 and R56 during affinity maturation (Fig. 5C). Within the VL gene, there were six identical mutations on both 10A3 and R56 that diverged from the germline sequence (Gly to Val^{L3}, Pro to Leu^{L4}, Thr to Ser^{L25}, Glu to Gln^{L27}, Phe to Val^{L27B} and Ile to Asn^{L32}; numbering based on 10A3). Within CDR L3, two residues had identical mutations (Gln to Leu^{L89} and His to Asp^{L93}). Within the VH gene, four sites had identical mutations (Lys to Gln^{H13}, Thr to Lys^{H23}, Ala to Gly^{H49}, and Ala to Thr^{H52A}) and one convergent mutation (Ile to Met^{H34}). There were many other mutations in the VL gene, however, most of which were not for residues that make direct contacts with antigens, suggesting their indirect role in shaping the overall paratope conformation.

Not surprisingly, 10A3 and R56 share many common antigen-antibody interactions using identical/similar amino acid residues (Fig. 5C). For the light chain, four of eight positions are conserved, including Tyr^{L28}, Asn^{L32}, Tyr^{L49}, and Leu^{L89}. For the heavy chain, three of six residues are identical (Cys^{H50}, Asn^{H95}, and Phe^{H96}). 10A3 and R56 share the N-terminus and the arch of V3 crown as the common epitope region. Two hydrophobic epitope residues Ile^{P307} and Ile^{P309} are buried into hydrophobic pockets on the antigen binding sites comprised of Cys^{H50}, Leu^{L89}, Phe^{H96}, while Pro^{P313} stacks against the aromatic plane of Tyr^{L49}. In the case of 10A3, the latter interaction is strengthened by Tyr^{H97} that stacks against Pro^{P313} on the opposite side of Tyr^{L49}. Two main chain interactions are also conserved, including Ile^{P307}_O and Asn^{L32}_ND2, Gly^{P312}_N and Asn^{H95}_O. Overall, the antigen-antibody interactions are more

conserved for the light chain, which play a dominant role in antigen binding for both 10A3 and R56, most likely due to their light chains derived from the same germline gene.

Moreover, the epitope structures of V3 co-crystallized with 10A3 and R56 are very similar (Cα RMSD = 0.9 Å) (Fig. 5B), especially at the N-terminus and the arch of V3 crown, shared epitope region of the two mAbs. The side chains also align very well, except for Arg^{P304} and Lys^{P305}. However, 10A3 has a longer V3 epitope; it recognizes 13 residues (^{303}TRKSIHIGPGRAF^{317}), while R56 recognizes only 10 residues (^{303}TRKSIHIGPG^{314}), i.e., 10A3 epitope has an extension of three more C-terminal residues than that of R56. Two major factors may have allowed 10A3 to bind the additional three residues: Asp to Glu^{L50} and Ser to Asp^{H53} mutations (Figs. 5A and 5C). Glu^{L50} can potentially form an extra salt bridge with Arg^{P315} (distance = 3.6Å) in addition to the close interaction with His^{P308} (2.7Å), but the side chain of the unmutated germline Asp^{L50} of R56 is too short to interact with Arg^{P315} (likely > 4Å away). Mutation of Ser to Asp^{H53} allows its side chain to form a salt bridge with Arg^{P304}, positioned its guanidinium group to stack with the aromatic plane of Phe^{P317}, further stabilizing the C-terminal end of the V3 crown. In contrast, this is impossible for Arg^{P304} of V3 forms a buried salt bridge with Asp^{H34} on the surface of R56 (26). Thus, additional mutations in affinity maturation have introduced V3 contacts in 10A3 that are lacking in R56, further stabilized the C-terminal V3 crown region.

Comparison of the antigen-antibody interactions of rabbit 10A3 with human IGHV5-51 encoded V3 mAbs

Crystal structures of several human V3 mAbs derived from IGHV5-51 germline gene have been determined, including the mAb 2557, a typical human IGHV5-51 encoded V3 mAb (19, 8, 25). They all use the cradle binding mode to bind the V3 crown. The overall conformations of the V3 peptides bound to 10A3 and 2557 are similar, although the V3 epitope recognized by 2557 is one amino acid longer at the C-terminus and forms a rather regular two-stranded anti-parallel beta sheet, whereas the peptide bound to 10A3 exists as a hairpin coil (Fig. 6A). However, the V3 epitopes of the two antibodies orient nearly perpendicular to each other in relationship to their antigen binding sites. The apex arch of V3 crown is

laid on top of the CDR H3 when complexed with 10A3, while it points towards the CDR L1 when complexed with human mAb 2557. Another difference between the rabbit 10A3 and R56 from that of human IGHV5-51 V3 mAb is the extreme short CDR H3; the CHR H3 in the rabbit mAbs is buried under the epitope, while the CDR H3 in the human ones forms the wall on one side of the cradle. Nevertheless, the epitope structures of V3 co-crystallized with 10A3 and 2557 are similar (Cα RMSD = 1.58 Å) (Fig. 6B), especially at the N-terminus and the arch of V3 crown, the common epitope region for both of antibodies. The C-terminus of the mAb bound V3 crown was more variable than the N-terminus, which is the case of all the human V3 mAbs derived from IGHV5-51 germline gene.

Structural analyses show the high similarities between rabbit and human V3 mAbs using the cradle binding mode in general. There is considerable overlap in the distribution and number of contacts formed with the V3 loop by different mAbs (Fig. 6C). A detailed comparison of contact area between the epitopes of rabbit mAbs 10A3 and R56 with those of selected human V3 mAbs 2219 and 2557 shows their similar recognizing pattern. First, they all focus on the N-terminus of V3 crown and have very few contacts with the C-terminus. Second, positively charged residues at the N-terminus of V3 crown play key roles on the antigen-antibody interaction. Third, Pro^{P313} in the arch region always stacks against aromatic planes. Fourth, V3 residue 315 (often Arg^{P315} and Gln^{P315} for clade B and non-clade B strains, respectively) does not play a significant role in antibody binding. This also explained that we could crystallize 10A3 with Arg^{P315} while the antibody was induced by a gp120 with Gln^{P315}. In spite of the mAb sequence and underlying germline differences, it is clear that the rabbit mAbs can recognize the V3 crown in similar binding modes as those of the human mAbs.

DISCUSSION

In this study, we determined and analyzed Fab/peptide complex structures of two recently isolated rabbit anti-V3 neutralizing mAbs 10A3 and 10A37, and defined their epitopes at the atomic level. Our results showed that 10A3 recognizes the V3 crown region (^{303}TRKSIHIGPGRAF^{317}), and 10A37 targets the V3 crown and the succeeding stem region (^{307}IHIGPGRAFYTTGEII^{324}). By and large, 10A3 is

similar to previously reported rabbit mAb R56, except that its epitope is longer than that of R56 by three amino acids at its C-terminal end, resulting in a hairpin structure. In contrast and unlike most of vaccine-induced V3 specific mAbs, 10A37 targets primarily the C-terminal end of the V3 crown as well as the succeeding stem region, a newly observed V3 binding mode. Moreover, its epitope has an α-helix core that has not been previously observed. Early theoretic prediction suggested that V3 can contain a short helix near the C-terminal region of V3 (40), and some NMR studies also reported that C-terminal portions of the V3 loop could assume an alpha helical structure in trifluoroethanol/water mixture (^{324}IGTIRQAHC^{332} (41) and ^{320}TGEIIGDIR^{328} (42)). But these helical conformations were observed in unusual buffer conditions and are at downstream of the helical region observed in our crystal structure: ^{315}RAFYTT^{320}.

The epitope of 10A3 and its interaction with the V3 crown is an example demonstrating the increased complexity of an antibody's epitope correlating with its affinity maturation (26). In the case of rabbit mAb R56, which has a V3 binding mode very similar to 10A3 (Fig. 5), only the first half the V3 crown was observed when it is in complexed with R56. Since the V3 crown has the propensity to form a beta hairpin (6, 43, 9), the C-terminal half of the crown is likely located spatially next to the N-terminal half. But R56 has not developed contact that can stabilize the C-terminal half of the V3 crown, it therefore could not be observed in the R56/V3 structure. However, in the case of 10A3, contacts have been developed through additional somatic hypermutations, and these contacts further stabilize the C-terminal half of the V3 crown, allowing it to be observed in 10A3/V3 complex structure. We have only speculated previously about this relationship between affinity maturation and the complexity of an antibody's epitope (26), but here we have demonstrated that, by the complex structure of rabbit mAb 10A3, 10A3 has a binding mode essentially identical to that of R56 but with additional somatic hypermutations. Together with R56, our results of 10A3 further support the notion that rabbit antibodies can mimic the binding modes of human antibodies, at least against the V3 crown. This similarity is likely predetermined by the structure of the V3 crown and its immunogenicity. Human antibodies encoded by IGHV5-51 have an antigen binding site that can best accommodate the beta hairpin structure of V3 crown, burying the N-

terminal half of the V3 crown in the cradle-like binding site. The immunodominance of the V3 crown and the ideal shape for the cradle-binding site can then explain the preferential gene usage of IGHV5-51 (19). It is then not surprising that rabbit can mount immune responses against the V3 crown and produce antibodies with a binding mode similar to those of human antibodies.

Our structure of the 10A37 complex demonstrate that the C-terminal end of the V3 crown can have a helical conformation, different from the commonly observed beta strand. In all the currently available Env trimer structures, including the high resolution cryoEM structure of the JR-FL trimer, this region has a beta strand conformation, suggesting that the beta strand is the preferred structure in the prefusion trimer. However, V3 loop tend to flick out easily (44, 45), and this region may become accessible for antibody binding; it can be a vulnerable site for immune responses because the C-terminal end of the V3 crown is quite conserved in sequence (8), and possibility of multiple structural conformations can be a mechanism for masking this region (46). Our structural data also explain the breath of 10A37 in neutralization (Table 2) (16). Although 10A37 has a deep pocket for binding the side chains of Phe^{P317} and Tyr^{P318} and is thus side chain specific, these two residues are highly conserved in HIV strains (8). In addition, the rest of the antibody/V3 interactions are largely backbone contacts, which are not influenced much by sequence variations. Interestingly, 10A3 and 10A37 have similar binding affinities (not shown), and we speculate the difference in the breadth is due to the difference in the target epitopes.

In conclusion, our study provides novel insights about neutralization-susceptible epitope structures of the V3 loop of gp120 and more evidences that, despite low amino acid sequence similarity from human antibody germline genes, rabbits can serve as a useful animal model to evaluate human vaccine candidates.

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FIGURE LEGENDS

FIG 1. Structure of Fab 10A3 in complex with $V3_{ConB}$. (A) and (B) Ribbon representations of the Fab 10A3 in complex with $V3_{ConB}$ from two different perspectives. The light and heavy chains are colored cyan and green, respectively, while the epitope is colored magenta (The coloring scheme is kept the same for all the figures, except where indicated otherwise). (C) The antigen binding site of 10A3 with the CDR loops labeled and colored differently from the rest of Fab. (D) Electrostatic potential surface of the antigen binding site of 10A3, with the red color indicating negative charged while the blue positively charged. Inset: The sequence of the peptide used for crystallization is shown, and residues observed in the electron density map are shown in magenta.

FIG 2. Antigen-antibody interactions of 10A3/$V3_{ConB}$. (A) Hydrophilic interactions between the side chains of the epitope and residues of 10A3. (B) Hydrophilic interactions between the main chain of the epitope and residues of 10A3. (C) Schematic illustration of antigen-antibody interactions. Hydrogen-binding interactions are indicated by dashed lines between the residues, while van der Waals contacts are indicated by eyelashes. Residues in solid ovals contribute to the interactions by their main chain atoms, and those in dashed ovals contribute by their side chain atoms.

FIG 3. Structure of Fab 10A37 in complex with $V3_{JR-FL}$. (A) and (B) Ribbon representations of the Fab 10A37 in complex with $V3_{JR-FL}$ from two different perspectives. (C) The antigen binding site of 10A37 with the CDR loops labeled and colored differently from the rest of Fab. (D) Electrostatic potential surface of the antigen binding site of 10A37. Inset: The sequence of the peptide used for crystallization is shown, and residues observed in the electron density are shown in magenta.

FIG 4. Antigen-antibody interactions of 10A37/$V3_{JR-FL}$. (A) Hydrophilic interactions between the side chains of epitope and residues of 10A37. (B) Hydrophilic interactions between the main chains of the

epitope and residues of 10A37. (C) Schematic illustration of antigen-antibody interactions. The helix in the epitope is indicated by a pink shed.

FIG 5. Structural comparison of rabbit V3 mAb complexes 10A3/$V3_{ConB}$ with R56/$V3_{JR-FL}$. (A) Superimposition of the light chain variable domain structures of 10A3/$V3_{ConB}$ and R56/$V3_{JR-FL}$ (Cα RMSD = 0.32Å). 10A3 and its epitope are colored the same way as in Fig. 1. The light and heavy chains of R56 are colored in grey and its epitope is colored in orange. (B) Superimposition of the backbone structures of V3 epitopes bound to antibodies 10A3 and R56 with the side chains shown in sticks (Cα RMSD=0.92 Å). (C) Sequence alignment of the heavy (top) and light (bottom) chains of 10A3, R56 and their germlines. CDR1, 2, and 3 are indicated. Critical residues are indicated as shown in the legend.

FIG 6. Structural comparison of rabbit V3 mAb complex 10A3/$V3_{ConB}$ with human V3 mAb complex and others encoded by IGHV5-51 germline genes. (A) Superimposition of the backbone structures of 10A3/$V3_{ConB}$ and 2557/$V3_{NY5}$ (Cα RMSD=0.94 Å). $V3_{ConB}$ and $V3_{NY5}$ peptides are shown in magenta and red, respectively. 10A3 VL and VH are colored in cyan and green, while those of 2557 are colored in grey. Note that the V3 epitope bound in different orientations relative to the mAbs. (B) Superimposition of the peptides bound to 10A3 and 2557 with the side chains shown in sticks (Cα RMSD=1.58 Å). (C) Comparison of the V3 epitopes of rabbit and human mAbs. Plot showing the distribution and number of contact formed with the V3 loop by different mAbs. Squares containing letters indicate peptide differences from that complexed with 10A3, the sequence of which is shown above the grid.

Table 1. Crystallographic data collection and refinement statistics.

	Fab 10A3/V3$_{ConB}$	**Fab 10A37/V3$_{JR-FL}$**
Data collection		
Space group	$P2_122_1$	$P2_1$
Cell dimensions		
a, b, c (Å)	62.85, 83.87, 90.61	43.23, 173.90, 70.9142.16, 170.38, 70.33
α, β, γ	90.00, 90.00, 90.00	90.00, 99.9798, 90.00
Resolution (Å)	1.90 (2.01-1.90)	2.30 55 (2.4470-2.3055)
CC (1/2)	100.0 (94.1)	99.8 6 (91.983.0)
R_{sym}	6.5 (46.8)	7.610.0 (49.754.6)
$I/\sigma I$	31.1 (5.1)	15.611.9 (3.83.0)
Completeness (%)	99.8 (98.8)	99.2 (98.6)99.6 (99.5)
Redundancy	13.3 (10.4)	5.14.3 (5.14.3)
Refinement		
Resolution (Å)	39.86-1.90	43.9244.61-2.5530
Unique reflections	38,386	43,18833,251
R_{work} / R_{free}	17.85/22.43	20.3761/26.5025.21
No. atoms		
Protein	3,312	6,6256,622
Solvent	668	223227
Average B factors (Å^2)	28.0	48.045.2
r.m.s. deviations		
Bond lengths (Å)	0.006	0.008
Bond angles (°)	0.855	0.9701.049
PDB Code	5V6M	5V6L

Statistics in parentheses refer to the outer resolution shell.

Table 2. Neutralizing activities of mAbs in a TZM-bl assay: IC50 (ug/ml)

	SF162	Ss1196	QH0692	Bx08.16	W61D-TCLA.71	BaL.26	MW965.26	92BR025.9
R56	0.1	7.18	8.6	3.18	ND	2.07	<0.02	ND
10A3	0.05	5.51	ND	1.9	<0.01	1.06	<0.02	39.2

ND: not determined.
Adapted from Refs (15, 16).

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