RESEARCH NOTE

Antigenicity of peptides comprising the immunosuppressive domain of the retroviral envelope glycoprotein [version 2; peer review: 2 approved]

Bryony Jenkins¹, Urszula Eksmond¹, George Young¹, George Kassiotis ¹,²

¹The Francis Crick Institute, London, UK  
²Department of Medicine, Faculty of Medicine, Imperial College London, London, UK

Abstract
To achieve persistent infection of the host, viruses often subvert or suppress host immunity through mechanisms that are not entirely understood. The envelope glycoprotein of several retroviruses is thought to possess potent immunosuppressive activity, mapped to a 17-amino acid residue conserved domain. Synthetic peptides corresponding to this immunosuppressive domain can inhibit lymphocyte activation, whereas mutation of key domain residues can increase the lymphocyte response to linked antigenic epitopes. Using three T cell receptors (TCRs) of defined specificity, we examine the effect of the immunosuppressive domain on the T cell response to their respective antigenic peptides. We find that fusion of a T cell epitope to the immunosuppressive domain can greatly modulate its potency. However, the effects heavily depend on the particular combination of TCR and peptide-major histocompatibility complex class II (pMHC II), and are mimicked by sequence-scrambled peptides of similar length, suggesting they operate at the level of pMHC formation or TCR-pMHC interaction. These results offer an alternative explanation for the immunogenicity of T cell epitopes comprising the putative immunosuppressive domain, which is more consistent with an effect on peptide antigenicity than true immunosuppressive activity.

Keywords
Immunosuppressive domain, retroviral envelope, T cell response, T cell receptor, peptide-MHC II complex

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Introduction
Several studies over the last three decades have provided evidence to suggest that the envelope glycoprotein of certain retroviruses is immunosuppressive in vitro and in vivo (Cianciolo et al., 1985; de Parseval et al., 2001; Denner, 2014; Dupressoir et al., 2012; Haraguchi et al., 1997; Kudo-Saito et al., 2014; Mangeney et al., 2007; Schlecht-Louf et al., 2010). Although the precise molecular mechanism remains unresolved, immunosuppressive activity has been pinpointed at a short region of the transmembrane polypeptide that, together with the surface unit (SU), constitutes one part of the trimeric envelope glycoprotein (Cianciolo et al., 1985; Dupressoir et al., 2012; Schlecht-Louf et al., 2010). For example, synthetic peptides corresponding to a region of 17-amino acid residues from the murine leukemia virus (MLV) envelope glycoprotein inhibit immune function in a variety of assays. These assays measure distinct aspects of immune responsiveness. Some measure non-specific lymphocyte or myeloid cell activation in response to mitogens or other generic stimuli (Denner, 2014; Denner et al., 1996; Haraguchi et al., 1993; Haraguchi et al., 1995; Mitani et al., 1987; Tolosa et al., 2012). Others measure antigen-specific T and B cell responses to immunization with synthetic peptides, recombiant envelope domains, and to infection with MLVs (Morozov et al., 2012; Schlecht-Louf et al., 2014; Schlecht-Louf et al., 2010). Use of different assays, many of which are multilayered, has hindered direct comparison of results from different studies, or definition of the specific step in immune function that may be suppressed. Here, we examine the properties of T cell epitopes linked to the immunosuppressive domain and provide an alternative interpretation for the effects.

Materials and methods
Mice
All animal experiments were approved by the Ethical Committee of the Francis Crick Institute, and conducted according to local guidelines and UK Home Office regulations under the Animals Scientific Procedures Act 1986. Inbred C57BL/6J and BALB/cJ mice were originally obtained from The Jackson Laboratory (Bar Harbor, ME, USA) and subsequently maintained at the Francis Crick Institute’s animal facilities, under specific pathogen-free conditions. Male or female mice, between 8 and 12 weeks of age, were used for the isolation of macrophages. T cell receptor (TCR)-transgenic OT-II (Barnden et al., 1998) and DO11.10 (Murphy et al., 1990) mice were kept on the C57BL/6J and BALB/cJ genetic backgrounds, respectively, and were additionally crossed to Rag1−/− mice to prevent rearrangement of endogenous TCR loci.

Macrophages
Macrophages were isolated from the peritoneal cavity of naïve euthanized C57BL/6J or BALB/cJ mice (2–6 mice per experiment). Peritoneal cells (containing ~50% macrophages) were plated in flat-bottomed 96 well-plates at 4×10^4 per well the day before their use, in Iscove’s Modified Dulbecco’s Medium (IMDM; Sigma-Aldrich, St. Louis, MO, USA) supplemented with 5% fetal bovine serum (Gibco, Thermo Fisher Scientific, Waltham, MA USA), 2mM L-glutamine, 100U penicillin and 0.1mg/ml streptomycin, and cultured at 37°C in a 5% CO2 atmosphere. Following overnight culture, macrophages were enriched by the removal of non-adherent cells, and were used for the assays.

T cell hybridomas
The envelopes 14-136-reactive H5 and H18 CD4+ T cell hybridomas have been previously described (Young et al., 2012). The ova123-197 reactive OT-II and DO11.10 hybridomas were generated by fusion of ova123-136 stimulated primary splenic CD4+ T cells from single TCR-transgenic OT-II and DO11.10 mice, respectively, with TCRβ-negative BW5147 thymoma cells, using established techniques (Young et al., 2012). In at least two experiments, primary CD4+ T cells from TCR-transgenic mice were also used with comparable results.

Peptides encompassing the immunosuppressive domain
Peptides were synthesized by Insight Biotechnology Ltd., Wembley, UK, at >98% purity. Scrambled sequences represent permutation of the original peptide sequences and were constructed using the peptide manufacturer’s algorithms. All peptides were sufficiently hydrophobic and were dissolved in phosphate-buffered saline prior to use (Table 1).
Table 1. Peptides used in this study. The following peptides were synthesized and used as indicated in the text. The underlined amino acid residues indicate the E561R and A567F double mutation (Schlecht-Louf et al., 2010). Red coloured sequences correspond to the immunosuppressive peptide.

<table>
<thead>
<tr>
<th>Peptide name</th>
<th>Sequence</th>
</tr>
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<tbody>
<tr>
<td>env&lt;sub&gt;124-138&lt;/sub&gt;</td>
<td>PLTSLTPRCNTANNR</td>
</tr>
<tr>
<td>env&lt;sub&gt;548-567&lt;/sub&gt;</td>
<td>LQNRRLDLLLFKEGGLCAA</td>
</tr>
<tr>
<td>env&lt;sub&gt;548-567:E561R/A567F&lt;/sub&gt;</td>
<td>LQNRRLDLLLFKEGGLCAF</td>
</tr>
<tr>
<td>env&lt;sub&gt;124-138&lt;/sub&gt;-env&lt;sub&gt;548-567&lt;/sub&gt;</td>
<td>PLTSLTPRCNTANNRLQNRRGLDLLFLKEGGLCAA</td>
</tr>
<tr>
<td>env&lt;sub&gt;124-138&lt;/sub&gt;-env&lt;sub&gt;548-567&lt;/sub&gt;:SCRAMBLED</td>
<td>PLTSLTPRCNTANNRFSGAKGLRDGLQLNELCLL</td>
</tr>
<tr>
<td>env&lt;sub&gt;124-138&lt;/sub&gt;-env&lt;sub&gt;548-567&lt;/sub&gt;:SCRAMBLED</td>
<td>PLTSLTPRCNTANNRFSGAKGLRDGLQLNELCLL</td>
</tr>
<tr>
<td>env&lt;sub&gt;124-138&lt;/sub&gt;</td>
<td>PLTSLTPRCNTANNRLKLDQVTHKSESFGYVCPGS</td>
</tr>
<tr>
<td>ova&lt;sub&gt;233-339&lt;/sub&gt;</td>
<td>ISQAVHAHAEEINEAGR</td>
</tr>
<tr>
<td>ova&lt;sub&gt;233-339&lt;/sub&gt;-env&lt;sub&gt;548-567&lt;/sub&gt;</td>
<td>ISQAVHAHAEEINEAGRLQNRRGLDLLFLKEGGLCAA</td>
</tr>
<tr>
<td>ova&lt;sub&gt;233-339&lt;/sub&gt;-env&lt;sub&gt;548-567&lt;/sub&gt;:SCRAMBLED</td>
<td>ISQAVHAHAEEINEAGRLQNRRGLDLLFLKEGGLCAA</td>
</tr>
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T cell stimulation

T cell hybridomas were stimulated by the indicated peptides presented by primary macrophages. T cell clones restricted by H2-A<sup>β</sup>(H5, H18 and OT-II) were stimulated by C57BL/6-derived macrophages, whereas the H2-A<sup>α</sup>-restricted clone (DO11.10) was stimulated by BALB/c/J-derived macrophages. Similar results were also obtained when primary splenic B cells or bone-marrow-derived dendritic cells were used for presentation. Approximately, 1.5×10<sup>5</sup> T cells per well were used in flat-bottomed 96 well-plates in RPMI-1640 medium (Sigma-Aldrich, St. Louis, MO, USA) containing 10% fetal calf serum. At least 50,000 cells were acquired on LSR Fortessa X-20 or FACSCanto II cytometers (BD Biosciences, San Jose, CA, USA) and analyzed with FlowJo v10 (Tree Star Inc., Ashland, OR, USA). Unstimulated hybridoma cells were included as CD69-negative controls, based on which the gating of CD69-positive cells was drawn.

Transcriptional profiling by RNA sequencing

Transcriptional profiles of primary macrophages incubated with the env<sub>124-138</sub>-env<sub>548-567</sub> and env<sub>124-138</sub>-env<sub>548-567:E561R/A567F</sub> peptides were obtained by RNA sequencing. Briefly, duplicate cultures of peritoneal macrophages from C57BL/6 mice were stimulated overnight with 10µM concentration of either peptide or were left unstimulated. RNA was then extracted using the RNeasy Mini QIAcube kit (Qiagen, Hilden, Germany) following the manufacturer’s instructions, and subjected to RNA sequencing (GENEWIZ, Inc., South Plainfield, NJ, USA). Reads were assessed for quality and contamination with FastQC v0.11.2 (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/) and preprocessed with Trimmomatic v0.32 (http://www.usadellab.org/cms/?page=trimmomatic) to remove the identified adapters, low quality read tails and to filter for length, and were then assessed for differential expression with DESeq2 v1.6.3 (http://bioconductor.org/packages/release/bioc/html/DESeq.html) within R v3.1.3. Data for all samples were normalized and log transformed and were then analyzed using GeneSpring v12.1 GX (Agilent, Santa Clara, CA, USA).

Statistical analysis

Statistical comparisons were made using SigmaPlot 13.0 (Systat Software Inc., Germany). Parametric comparisons of normally-distributed values that satisfied the variance criteria were made by unpaired Student’s t-tests. Data that did not pass the variance test were compared with non-parametric two-tailed Mann-Whitney Rank Sum tests. P<0.05 were considered significant.

Results and discussion

We used synthetic peptides corresponding to the conserved env<sub>548-567</sub> region of the Friend MLV envelope precursor gPr80 (LQNRRGLDLLLFKEGGLCAA), which contains the originally described 17-amino acid residue immunosuppressive peptide (Cianciolo et al., 1985). As controls, we introduced two amino acid substitutions (E561R and A567F), previously shown to abrogate the immunosuppressive activity of this region (Schlecht-Louf et al., 2010), and also used scrambled sequences for both peptides (Figure 1). These peptides were tested for their effects on the antigenicity of the H2-A<sup>α</sup>-restricted env<sub>124-138</sub> CD4<sup>+</sup> T cell epitope in the SU of F-MLV (PLTSLTPRCNTAWNR). As immunosuppressive peptides have generally been found active only as part of larger polypeptides (Denner, 2014), we used peptide fusion of the T cell epitope and the immunosuppressive peptide into a single molecule (env<sub>124-138</sub>-env<sub>548-567</sub>). Fusion with the immunosuppressive peptide env<sub>548-567</sub> had no measurable effect on the ability of the env<sub>124-138</sub> epitope to stimulate two env<sub>124-138</sub>-specific CD4<sup>+</sup> T cell
clones (Figure 1A and F) that differ in functional avidity (Young et al., 2012). CD4+ T cell responses to env124–138 were similarly unaffected by the addition in the cultures of the immunosuppressive peptide env548–567, either as a separate entity or fused with the unrelated H2-Ab-restricted ovalbumin (ISQA VHAAHAEI) (Supplementary Figure 1). In contrast, fusion with either the doubly point-mutated (Figure 1B and G; p=0.003 and p<0.001 for clones H5 and H18, respectively) or sequence-scrambled immunosuppressive peptide (Figure 1C and H; p=0.005 and p=0.021 for clones H5 and H18, respectively) significantly increased the antigenicity of the env124–138 epitope for both clones by ~10-fold. Increased antigenicity of the env124–138 epitope as a result of mutations at the two residues or sequence scrambling of the fused immunosuppressive peptide could be interpreted as reversal of immunosuppression due to these modifications. However, comparison with the env124–138 epitope on its own revealed that fusion with the index immunosuppressive peptide was in fact neutral (Figure 1A and F), whereas fusion with the modified immunosuppressive peptides improved antigenicity.

Peptide length is an important contributor to the antigenicity of MHC II-restricted epitopes. Indeed, N-terminal extensions of the env124–138 epitope have been shown to increase antigenicity (Young et al., 2012), in line with findings in other systems (Carson et al., 1997; Holland et al., 2013). The open structure of the MHC II groove allows presentation of peptides that extend at either end of the core epitope, and these epitope-flanking residues can contribute to T cell stimulation (Holland et al., 2013). Importantly, the involvement of epitope-flanking residues critically depends on the particular pair of TCR and peptide-MHC II (pMHC) complex, as contact between particular epitope-flanking residues and residues in the TCR is necessary (Holland et al., 2013). To examine whether the observed effect of the index or modified immunosuppressive peptides was TCR- and peptide sequence-dependent, we used

Figure 1. In vitro responses of Ab-restricted env124–138-reactive CD4+ T cell hybridomas H5 (top row) and H18 (bottom row), to stimulation with the indicated peptides. Plotted are the frequencies of T cells that express CD69 following overnight stimulation. Data are the mean (±SEM) of 2–5 individual experiments.
additional fusion peptides. Notably, a peptide that carried the E561R/A567F substitutions and was additionally sequenced-scrambled enhanced antigenicity of the env<sub>124-138</sub> epitope for the H5 clone (p=0.004), but not the H18 clone (Figure 1D and 1I). Moreover, extending the length of the env<sub>124-138</sub> epitope with the sequence that naturally occurs in the F-MLV SU (env<sub>548-567</sub>) enhanced activation of the H18 clone (p=0.007), but not of the H5 clone (Figure 1E and 1J). These two clones share the same TCRβ chain, but use different TCRα chains, which are responsible for the difference in functional avidity (Young et al., 2012). The disparate behaviour of the two clones in response to the last two fusion peptides demonstrate that changes in antigenicity depend on the particular TCR. This finding argues against general immunosuppression caused by the env<sub>548-567</sub> peptide.

Also arguing against immunosuppressive ability, env<sub>124-138</sub> fusion peptides containing the index immunosuppressive peptide or the E561R/A567F mutant induced comparable transcriptional changes to the APCs used in these assays (Figure 2A). Incubation of primary macrophages with either of the two env<sub>124-138</sub> fusion peptides altered their transcriptional signature in comparison with the absence of peptide, with Tnfsf14 (also known as HVEM-L or LIGHT) most strongly induced (between 3-and 4-fold) (Figure 2A). However, the transcriptional signatures induced by the two peptides were effectively identical (Figure 2A).

We next examined if our findings with env<sub>124-138</sub>-specific CD4<sup>+</sup> T cell clones extended to other combinations of TCR and pMHC. To this end, we used the OT-II and DO11.10 clones, which react with the same ova<sub>323-339</sub> epitope presented by H2-A<sup>b</sup> and H2-A<sup>d</sup>, respectively. Fusion of the ova<sub>323-339</sub> epitope with the env<sub>548-567</sub> E561R/A567F mutant, but not the index immunosuppressive peptide enhanced the response of the OT-II clone (Figure 2B) (p=0.04). In contrast, neither peptide fusion affected the response of the DO11.10 clone (Figure 2B), indicating that effects of the immunosuppressive peptides can be observed in some pMHC combinations or TCR-pMHC pairs, but not others. Thus, this pattern of changes in T cell activation, depending on the particular TCR-pMHC pair, is more consistent with an effect mediated by epitope-flanking residues than genuine immunosuppression. The potential of the immunosuppressive peptide, and modifications thereof, to alter TCR or BCR recognition of linked epitopes should, therefore, be considered when interpreting the antigenicity or immunogenicity of the retroviral envelope glycoprotein.

**Figure 2.** *In vitro* responses of peritoneal macrophages or hybridomas OT-II and DO11.10 to stimulation with the indicated peptides. (A) Transcriptional comparison of primary macrophages incubated overnight in the absence of peptide or in the presence of 10 µM of the indicated peptide. Each dot represents the normalized counts for individual transcripts and green diagonal lines enclose changes in relative transcript abundance of <2-fold in each comparison. (B) *In vitro* responses of A<sup>b</sup>-restricted and A<sup>d</sup>-restricted ova<sub>323-339</sub>-reactive CD4<sup>+</sup> T cell hybridomas OT-II and DO11.10, respectively, to stimulation with the indicated peptides. Data are the mean (±SEM) of 2–3 individual experiments.
Data availability
RNA-sequencing data reported in this paper are available at: www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-5260 (accession number, E-MTAB-5260).

Raw values for T cell responses shown in Figure 1, Figure 2B and Supplementary Figure 1 are available from the Open Science Framework: https://osf.io/8y8h4/; doi, 10.17605/OSF.IO/8Y8H4 (Kassiotis, 2016).

Author contributions
GK conceived the study. GK, BJ, UE and GY designed the experiments. BJ, UE and GY carried out the research. GK, BJ, UE and GY contributed to the preparation of the manuscript. All authors were involved in the revision of the draft manuscript and have agreed to the final content.

Competing interests
No competing interests were disclosed.

Grant information
This work was supported by the Wellcome Trust [102898/B/13/Z]; and the Francis Crick Institute, which receives its core funding from Cancer Research UK, the UK Medical Research Council, and the Wellcome Trust [all under grant number FC001099].

The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Acknowledgments
We are grateful for assistance from the Biological Research and Flow Cytometry Facilities at the Francis Crick Institute.

Supplementary material
Supplementary Figure 1: In vitro responses of Ab-restricted env124-138-reactive CD4+ T cell hybridoma H18, to stimulation with the indicated combination of peptides. The X-axis denotes the concentration of the env124–138 peptide. All other peptides were given at constant 10–6 M concentration. Plotted are the frequencies of T cells that express CD69 following overnight stimulation. Data re the mean (±SEM) of 1–6 individual experiments.

Click here to access the data.

References


Kassiotis G: Antigenicity of peptides comprising the immunosuppressive domain of the retroviral envelope glycoprotein. Open Science Framework. 2016. Data Source


Open Peer Review

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Stephanie Gras
Infection and Immunity Program and Department of Biochemistry and Molecular Biology, Biomedicine Discovery Institute, Monash University, Clayton, VIC, Australia

Emma Grant
Monash University

Carine Farenc
Monash University, Australia

This work gives insights into the immunosuppressive role of the envelope glycoprotein of certain retrovirus. They present the T cell response of 3 TCRs stimulated with different peptides encompassing both the T cell epitope and the immunosuppressive domain. The research note is of interest, clear and well written, and the final conclusion seems appropriate.

Some section could be developed or clarify:

1. Abstract: “The effects heavily depend on the particular combination of TCR and peptide-major histocompatibility complex class II, and are mimicked by sequence-scrambled peptides of similar length, suggesting they operate at the level of TCR-pMHC interaction”. The addition/substitution within the peptides could also influence the peptide stability within the MHC-II, or half-life of the pMHC-II complex, and therefore change the T cell stimulation, this should probably be discuss, or acknowledge that the TCR-pMHC-II interactions might not explain everything.

2. Methods. A brief explanation about “scrambled” peptides would be helpful, as would a sentence explaining why peptides were reconstituted in PBS rather then DMSO.

3. Conclusion. I would like a bit more explanation for the unexpected results. As well as maybe considering taking into account the comment from the abstract to re-word the strong conclusion “In contrast, neither peptide fusion affected the response of the DO11.10 clone, indicating that effects of the immunosuppressive peptides can be observed in some TCR-pMHC pairs, but not others”.

Minor comments:
1. Title: I would suggest changing “comprising” by “within”.

2. Table 1: the shade section is not visible, either the colour needs to be darker or maybe bold the section.

3. The peptides env548-567 and env548-567-E561R-A567F are in Table 1 but don’t seem to be used in the exp? Were they used as control?

4. The env124-138 + ova323-339-env548-567 used in the supplemental figure are not listed in this table.

**Competing Interests:** No competing interests were disclosed.

We have read this submission. We believe that we have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Author Response 14 Feb 2017

George Kassiotis, The Francis Crick Institute, London, UK

We wish to thank the Reviewers for their astute and constructive comments. Below is a point-by-point reply and a list of changes we have made to the manuscript in response to these comments:

**Major comments:**

1. We agree with the Reviewer that peptide alterations could affect the peptide-MHC-II complex (pMHC) itself, not only TCR binding to it. Our definition of TCR-pMHC interaction was meant to be broad enough to include effects on pMHC formation. Obviously, anything that affects pMHC formation or stability will also affect TCR-pMHC interaction, by reducing ligand availability. All these alternatives are on the same side of the argument, the other side being biological activity of the immunosuppressive domain. We have modified this sentence to read: “…at the level of pMHC formation or TCR-pMHC interaction.”

2. “Scrambled” peptides are permutation of the original peptide sequence. The rationale for using them is that they would retain the physico-chemical characteristics (molecular mass, polarity, acidity, etc), but not any sequence-dependent domain, structure or recognition motif. Practically, these were constructed using the peptide manufacturer’s (GeneScript) algorithms. The peptides were all sufficiently hydrophobic to dissolve in PBS. This was chosen in order to avoid any effect of organic solvents.

3. Again we agree with the Reviewer and rephrased this sentence to read: “…in some pMHC combinations or TCR-pMHC pairs, but not others”. Given what is known about peptide-flanking residues and their effect on pMHC formation and stability and TCR binding, the results might not be unexpected. In fact, we believe this is the most parsimonious explanation for the effects of the putative immunosuppressive domain, one that needs not invoke any new biological activity or mechanism.

**Minor comments:**
1. The word “comprising” in this context was meant to be synonymous with “including” or “containing”. The word “within” would have the opposite meaning. The immunosuppressive domain is within the antigenic peptides, not the reverse.

2. The shading has been replaced with red colour text for enhanced contrast.

3. These peptides were used for the experiments described in Supplementary figure 1.

4. The env124-138 and ova323-339-env548-567 peptides were used as separate entities, not as a fusion. They are listed in rows 1 and 10 of Table 1, respectively.

**Competing Interests:** No competing interests were disclosed.

Reviewer Report 08 December 2016

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Jean-Marie Saint-Remy
Center for Molecular and Vascular Biology, University of Leuven, Leuven, Belgium

I think this paper addresses a major issue with consequences for basic research and for the design of new forms of immunotherapy. The concept of “reversal of immunosuppression” is fundamental and stands, luckily enough, in contrast with the overwhelming view that every bit of immunological studies should be considered as eliciting “active immunosuppression”.

This paper is therefore novel and susceptible to shed new light in the field.

Experiments are neatly planned and well described.

The discussion is well equilibrated.

I therefore strongly recommend the indexing of these new findings.

**Competing Interests:** No competing interests were disclosed.

I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.