ORAL ABSTRACT SESSION 04: UPDATE ON CLINICAL TRIALS

OA04-01

Safety and immunogenicity of LIPO-5, a HIV-1 lipopeptide vaccine: results of ANRS VAC18, a phase 2, randomized, double-blind, placebo-controlled trial

D Salmon-Céron[1], C Durier[2], C Desaint[3], L Cuzin[4], M Surenaud[5], Y Hénin[3], J Lelièvre[6], B Bonnet[7], G Pialoux[8], I Poizot-Martin[9], N Ben Hamouda[5], A Jackson[5], C Flys[5], C Guérin[10], J Aboulker[2], J Choppin[5], and O Launay[11]

[1]Hôpital Cochin, Université Paris Descartes, Paris, France; [2]Inserm, SC10, Villejuif, France; [3]CIC de Vaccinologie Cochin-Pasteur, Paris, France; [4]Hôpital Purpan, Toulouse, France; [5]Institut Cochin,Université Paris Descartes,CNRS (UMR 8104),Inserm U567, Paris, France; [6]Hôpital Henri Mondor, Université Paris 12 , Créteil, France; [7]Hôpital Hôtel-Dieu, Nantes, France; [8]Hôpital Tenon, Paris, France; [9]Hôpital Sainte Marguerite, Marseille, France; [10]Hôpital Cochin, Paris, France; [11]CIC de Vaccinologie Cochin-Pasteur,Hôpital Cochin, Universite Paris Descartes, Paris, France

Background: ANRS HIV-LIPO-5 vaccine includes 5 long peptides, Gag17-35, 253-284, Pol325-355, Nef66-97 and 116-145, containing multiple CD8+ and CD4+ T-cell epitopes, coupled to a palmytoil tail. Phase 1 studies have shown that vaccine dosage at 500µg/lipopeptide elicits cellular immune responses. Whether HIV-LIPO5 immunogenicity varies with the dosage is unknown.

Methods: One hundred and thirty two 21- to 55-year-old HIV negative volunteers, enrolled in 6 HIV-vaccine clinical sites, were randomized to receive either the HIV-LIPO-5 vaccine at 50µg/lipopeptide (N=32;LIPO-5 50), 150µg (N=32;LIPO-5 150), 500µg (N=33;LIPO-5 500) or placebo (N=34). Vaccinations were given IM at weeks 0, 4, 12 and 24. HIV-1 specific CD8+ (IFN-gamma ELISpot on PBMC cultured 12-days) and CD4+ responses (PBMC lymphoproliferation) were assessed at baseline, two weeks after each injection, and at week 48.

Results: No adverse events attributable to vaccine were noted throughout the study. Local reactions appeared dose-dependent; no differences in systemic reactions were observed between groups. Sustained (at least on 2 separate occasions) CD8+ response rates to at least one HIV-1 pool were: 5/32 (16%) for placebo, 22/32 (69%) for LIPO-5 50, 21/33 (64%) for LIPO-5 150 and 21/34 (62%) for LIPO-5 500 groups (P≤.0001 for all comparisons to placebo). Cumulative CD4+ response rates were: placebo: 2/32 (6%), LIPO-5 50: 15/32 (47%), LIPO-5 150: 18/33 (55%) and LIPO-5 500: 15/34 (44%) (P<.0001 for all comparisons to placebo). The majority of CD4+ (75%) and CD8+ (60%) responses were directed towards Gag253-284. CD8+ responses against Nef, Pol were noted in 36% and 33% of vaccinees, respectively. At week 48, CD8+ responses persisted in 47/91 (52%) HIV-LIPO-5 recipients.

Conclusion: ANRS VAC18 shows that low and high doses of HIV-LIPO-5 vaccine elicit sustained CD8+ and CD4+ T-cell responses. According to the good tolerance of the vaccine, the lowest dose of 50 µg appears as the most appropriate to be used in further trials.

OA04-02

Strong HIV-specific CD4 and CD8 T-lymphocyte proliferation in HIV-1 DNA prime/ modified vaccinia virus Ankara (MVA) heterologous boost vaccinees

C Nilsson[1], S Aboud[2], K Karlén[3], M Marovich[4], B Wahren[1], E Sandström[5], H Gaines[1], G Biberfeld[1], and K Godoy-Ramirez[3]

[1]Swedish Institute for Infectious Disease Control, Karolinska Institute, Solna, Sweden; [2]Muhimbili University of Health and Allied Sciences, Dar es Salaam, Tanzania, United Republic of; [3]Swedish Institute for Infectious Disease Control, Solna, Sweden; [4]Walther Reed Army Institute for Research, Rockville, Maryland, USA; [5]Venhälsan and Karolinska Institutet, Stockholm, Sweden

Background: We determined HIV-1-vaccine-induced lymphoproliferative responses in vaccinees immunized with a multigene, multiclade HIV-1 plasmid DNA vaccine boosted with heterologous HIV-1 recombinant MVA in a phase I HIV safety and immunogenicity study (HIVIS01/02).

Methods: Healthy volunteers were immunized intradermally or intramuscularly (with or without adjuvant GM-CSF protein) with DNA expressing HIV-1 gag, env, rev and rt at months 0, 1 and 3 using a Biojector and were boosted at nine months with an MVA expressing heterologous inserts of HIV-1 gag, env and pol genes. Lymphoproliferative responses to AT-2 inactivated HIV-1 antigen were tested by a 3H-thymidine uptake assay and a flow-cytometric assay of specific Cell-mediated immune-response in Activated whole blood (FASCIA-WB) two weeks after HIV-1 MVA boost (n=38). A FASCIA using peripheral blood mononuclear cells (FASCIA-PBMC) was also employed during the later part of the study (n=14).

Results: Thirty-five of 38 (92%) vaccinees were reactive by the 3H-thymidine-uptake assay (SI >8). Thirty-two of 38 (84%) vaccinees were reactive by the CD3+CD4+ T-cell FASCIA-WB (%Stimulation >1.2), seven (18%) also exhibited CD8+ (CD3+ CD4-) T-cell responses. Of the 14 vaccinees analyzed using all three assays, ten (71%) and eleven (79%) demonstrated CD4+ T-cell responses in FASCIA-WB and FASCIA-PBMC, respectively. CD8+ T-cell reactivity was observed in 3 of 14 (21%) and 7 of 14 (50%) using the FASCIA-WB and FASCIA-PBMC, respectively. There was strong correlation between the proliferative responses measured by the 3H-thymidine uptake assay and the CD4+ T-cell FASCIA-WB (r=0.68; p<0.01).

Conclusion: HIV-1 specific T-lymphocyte proliferative responses were detected in a high proportion (37/38) of volunteers following HIV-1 DNA/MVA immunization. The FASCIA revealed both CD4+ and CD8+ T-cell proliferation in response to HIV-1 antigen stimulation. A standardized FASCIA-PBMC, which allows simultaneous phenotyping may be an option to the conventional 3H-thymidine uptake assay for assessment of vaccine-induced T-cell proliferation, especially in isotope-restricted settings.

OA04-03

Characterization of cell-mediated immune responses generated by recombinant modified vaccinia Ankara (rMVA)-HIV-1 in a phase I vaccine trial

JR Currier[1], M De Souza[2], S Ratto-Kim[1], R Paris[2], V Nguay[1], J Cox[3], P Earl[4], B Moss[4], S Sriplienchan[2], P Thongcharoen[2], J Kim[1], M Robb[1], N Michael[1], and M Marovich[1]

[1]Military HIV Research Program, Rockville, Maryland, USA; [2]AFRIMS, Bangkok, Thailand; [3]IAVI, Rockville, Maryland, USA; [4]NIAID, Besthesda, Maryland, USA

Background: Potency of the cell-mediated immune response is now the critical metric for down-selection of candidate HIV-1 vaccines. Here we characterize the potency (magnitude and quality) of cell-mediated immunity generated in response to a multigenic rMVA-based HIV-1 (CRF01_AE-derived) vaccine.

Methods: 49 healthy, vaccinia-naïve volunteers were enrolled in a Phase I randomized, double-blind, dose-escalation, route-comparison, placebo-controlled trial to assess the safety and immunogenicity of MVA-CMDR HIV-1 vaccine. The study was divided into Part A: low-dose 10^6/pfu ID versus 10^7 pfu/IM and Part B: high-dose 10^7 pfu/ID vs 10^8 pfu/IM. Vaccinations were given at months 0, 1 and 3 with an active:placebo ratio of 10:2. Chromium-release CTL, IFNg Elispot, and polyfunctional flow cytometry (IL-2/IFNg/TNFa/MIP-1b/CD107a), were performed on all volunteers. Synthetic peptide pools and GLP-grade MVA were used to assess insert (Gag/Pol/Env) and vector immunogenicity respectively.

Results: Vector-specific responses were robust (>80% response rate at high-dose), durable (maintained at least 6 months), and exhibited a dose-dependent increase in both magnitude and response rate among the 4 arms of the trial. HIV-insert-specific responses were detected using all assay platforms, but were lower than the vector-specific responses in both magnitude and response rate in all arms of the trial (~60% at high-dose by CTL, Elispot and ICS assays). Specifically, polyfunctional analysis revealed a TNFa/IL-2/IFNg bias in CD4+ T cells and a MIP-1b/CD107a/IFNg bias in CD8+ T cells, with CD4+ T cell responses more frequent than CD8+ T cell responses to the HIV inserts. Vector-specific immune responses showed a boosting effect from the 2nd to the 3rd immunization.

Conclusion: rMVA vaccination induces a dose-dependent, robust and durable polyfunctional cellular immune response as measured by IFNg Elispot, CTL and intracellular cytokine stimulation assays. Although vector-specific responses tend to dominate over insert-specific responses, the data supports further exploration of MVA as a vector modality in prime-boost vaccination strategies.

OA04-04

Perceived parental willingness for their adolescents to participate in future HIV prevention trials: a survey conducted amongst adolescents in Soweto

K Otwombe[1], J Dietrich[1], K Sikkema[2], G de Bruyn[1], M van der Watt[1], and G Gray[1]

[1]Perinatal HIV Research Unit, Johannesburg, South Africa; [2]Duke University, Durham, North Carolina, USA

Background: Following the high HIV prevalence rates in Sub-Saharan Africa, several target specific interventions have been put in place with varying degrees of success. In implementing these interventions, adolescents have become a crucial target group. This study specifically examines perceived parental willingness for their adolescent to participate in HIV prevention trials by taking parent-adolescent communication into account.

Methods: The willingness to participate in future HIV prevention trials questionnaire and the Parent-Adolescent Communication Scale (PACS) formed part of a larger adolescent survey conducted among 16-18 year olds living in Soweto, an urban setting in Johannesburg, South Africa. Adolescent participants were interviewed about communication with parents or guardians regarding their sexual health. The questionnaires were interviewer administered.

Results: In total, 303 questionnaires were administered with a sample of 176 (58.1%) females and 127 (41.9%) males (median age = 17). 184 (60.7%) participants had both parents alive, 78 (25.7%) only the mother alive and 20 (6.6%) only the father alive. Only 33 (10.9%), 24 (7.9%) and 7 (2.3%) participants indicated their mothers, fathers and guardians had post school training respectively. The PACS had a reliability of 0.77 with scores ranging between 7 and 28 with a median of 16. A score greater than 14 was categorized as representing good communication skills. 266 (88%) of the participants indicated their parents would be willing to allow them to participate in a future HIV vaccine trial. There was an association between parental willingness to participate and PACS scores ($p < 0.05$, OR=0.4085, CI 0.2-0.8) in which univariate analysis showed that willingness was dependent on good communication scores (OR=2.4, CI 1.2-5.0). The effect was particularly strong for females (OR=8.3, CI 2.2-30.7).

Conclusion: Perceived parental willingness for their adolescents to participate in future HIV vaccine trials is high and appears to be strengthened by good parent-adolescent communication.

OA04-05

Safety and viral load changes in HIV-1 infected subjects treated with autologous dendritic immune therapy following ART discontinuation (CTN#239)

J Routy[1], M Boulassel[2], L Mona[3], V Sylvie[4], T Cécile[5], A Jonathan[6], G John[7], B Jean-Guy[8], S Fiona[9], J Renu[10], H Don[10], T Irina[10], N Charles[10], and S Rafick-Pierre[11]

[1]McGill University and INSERM Unit 743, Montréal, Québec, Canada; [2]McGill University health Centre, Montréal, Québec, Canada; [3]Maple Leaf Clinic, Toronto, Ontario, Canada; [4]Clinique Médicale l'Actuel, Montréal, Québec, Canada; [5]Centre de recherche du centre Hospitalier de l'Université de Montréal, Montréal, Québec, Canada; [6]Ottawa General Hospital, Ottawa, Ontario, Canada; [7]Southern Alberta Clinic, Calgary, Alberta, Canada; [8]Medical du Quartier Latin, Montréal, Québec, Canada; [9]Hamilton Health Sciences, McMaster University Medical Center, Hamilton, Ontario, Canada; [10]Argos Therapeutics Inc, Durham, NC, USA; [11]University of Montreal Research Centre, and INSERM Unit 743, Montreal, Quebec, Canada

Background: We demonstrated in a phase 1 trial that an immunotherapy (AGS-004) consisting of a monocyte-derived dendritic cells (DC) and RNA encoding autologous HIV antigens (Gag, Nef, Rev, Vpr) derived from the patient's own pre-ART plasma induced immunogenicity in most patients. Based on these results a multicenter phase 2 trial was implemented to assess the safety and proportion of patients demonstrating viral load (VL) < 1000, <5000 and <10,000 copies/mL during the 12 week ART structured treatment interruption (STI).

Methods: Subjects on their initial ART regimen with VL < 50 copies/ml, CD4 > 450 cells/uL, CD4 nadir > 200 cells/uL and a pre-ART VL >10,000 to 500,000 copies/mL were eligible. The treatment consists of 4 intradermal AGS-004 doses administered monthly in combination with ART followed by two more doses during the 12 week STI. Subjects who participated in the phase 1 study were included and received a second cycle of AGS-004. Subjects may continue AGS-004 booster administration if VL remains < 10,000 copies/mL.

Results: 33 subjects were enrolled from 11 Canadian sites, and AGS-004 successfully manufactured and administered to 21 subjects. 9 subjects have successfully completed 12 weeks of STI. The immunotherapy related AEs were Grade 1 or 2 flu-like, GI symptoms, fatigue, and injection site reactions. During the STI, no reports of autoimmunity or AIDS defining events were observed. After an initial viral rebound, 4 out of 9 subjects had >2 instances of VL measures <1000 copies/mL when assessed every 2 weeks during the STI. At Week 12 of STI 5 subjects had viral loads <10,000 copies/mL with CD4 >350 cells/µL including 4 subjects with viral loads <5000 copies/mL.

Conclusion: Results from this phase 2 autologous immunotherapy trial demonstrated that this therapy is safe and induced partial control of VL when compared to pre-ART VL during the 12-week STI.

OA04-06 LB

Post-infection cellular immune responses in recipients following ALVAC-HIV® + AIDSVAX® B/E prime-boost vaccination in the Thai phase III trial.

JH Kim[1], C Karnasuta[2], R Trichavaroj[2], J Kaewkungwal[3], S Chantakulkij[2], S Ratto-Kim[1], C Eamsila[2], S Sukwit[2], S Nitayaphan[2], P Pitisuttithum[3], NL Michael[1], J Chiu[2], S Rerks-Ngarm[4], MS de Souza[2], RM Paris[2]

[1]U. S. Military HIV Research Program, Rockville, Maryland, USA; [2]U. S. Military HIV Research Program/AFRIMS, Bangkok, Thailand; [3]Vaccine Trial Centre, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand; [4]Ministry of Public Health, Nonthaburi, Thailand

Background: The phase III prime-boost trial of ALVAC-HIV® (vCP1521) and AIDSVAX® B/E spanned 2003 to 2009 in Thailand. Both candidates express HIV CRF 01_AE and subtype B antigens, the predominant circulating HIV-1 subtypes in Thailand. This preliminary study assessed cell-mediated immune (CMI) responses, viral load and CD4 counts in a subset (N=47) of anti-retroviral naïve incident infections (< 270 days after estimated infection) that occurred during the trial.

Methods: Study participants were randomized 1:1, vaccine:placebo. The immunization regimen was 0, 1, 3 and 6 months for ALVAC-HIV®, with AIDSVAX® being administered at 3 and 6 months. Cytotoxic T lymphocyte (CTL) assays were conducted on freshly isolated peripheral blood mononuclear cells (PBMC) in a standard chromium release assay using autologous EBV-transformed B cells as targets (N=47). Interferon-gamma (IFN-γ) ELISpot assays were performed using cryopreserved PBMC (N=43). Target antigens for both CMI assays matched those of the vaccine candidates. Concurrent viral load and CD4 counts were measured using commercial assays. HIV genotyping was performed using the multiregion hybridization assay.

Results: Data are still blinded with respect to immunization status. The median time from infection to CMI assessment was 164 days (range: 113-265). The frequency of HIV-specific CD8+ CTL activity was 64%, with equivalent responses to Env (19/47) and Gag/Pol (18/47) antigens. HIV-specific IFN-γ ELISpot responses were measured in 47% of subjects, but the response was predominantly to Gag – 37% versus 19% for Env. Median viral load and CD4 counts were 25338 copies/ml (range: <50-272509) and 571 cells/µl (range: 220-1067), respectively. CRF01_AE was the predominant infecting subtype (82%; 37/45).

Conclusion: Robust CD8+ mediated CTL responses to HIV antigens expressed by the ALVAC-HIV® immunogen were observed in participants who became infected during the trial. Determining the relevance of these responses to viral control and/or CD4 T cell counts following un-blinding (October, 2009) constitutes a high priority.

ORAL ABSTRACT SESSION 05: NEW VACCINAL APPROACHES

OA05-01

In vivo electroporation enhances the immunogenicity of ADVAX, a DNA-based HIV-1 vaccine Candidate, in healthy volunteers

S Vasan[1], A Hurley[1], SJ Schlesinger[1], D Hannaman[2], DF Gardiner[3], DP Dugin[3], MM Boente-Carrera[3], RM Vittorino[3], M Caskey[4], J Andersen[4], Y Huang[3], J Cox[5], T Tarragona[6], DK Gill[6], H Cheeseman[6], L Clark[6], L Dally[7], C Smith[7], C Schmidt[5], H Park[5], E Sayeed[5], J Gilmour[6], P Fast[5], R Bernard[2], and DD Ho[1]

[1]Aaron Diamond AIDS Research Center, Rockefeller University, New York, USA; [2]ICHOR Medical Systems, San Diego, CA, USA; [3]Aaron Diamond AIDS Research Center, New York, NY, USA; [4]Rockefeller University, New York, NY, USA; [5]International AIDS Vaccine Initiative, New York, NY, USA; [6]International AIDS Vaccine Initiative, London, United Kingdom (Great Britain); [7]The EMMES Corporation, Rockville, MD, USA

Background: In healthy volunteers, we sought to determine the safety, tolerability, and immunogenicity of ADVAX, a subtype B'/C, DNA-based, multigenic, HIV-1 vaccine candidate, when injected intramuscularly immediately followed by in vivo electroporation (EP) using the TriGrid™ Delivery System.

Methods: Forty healthy volunteers aged 18-60 were enrolled in a double blind randomized phase-I trial. Eight volunteers each received either low dose (LD, 0.2 mg); mid dose (MD, 1.0 mg); or high dose (HD, 4.0 mg) ADVAX or saline placebo via EP. Another eight volunteers received 4.0mg ADVAX intramuscularly (IM). Vaccinations were given at weeks 0 and 8. The protocol was subsequently amended to administer a third dose of HD EP/placebo at week 36 to volunteers receiving either HD ADVAX via EP (n=8) or placebo via EP (n=3). Total study follow-up is 14 months.

Results: There have been no vaccine or device related serious adverse events to date. After two vaccinations in all subjects, the IFNg ELISPOT response rates were IM: 1/8 (13%), LD-EP: 3/8 (38%) MD-EP: 7/8 (88%) and HD-EP: 6/8 (75%). In the same order, the mean (range) response to peptide pools spanning all antigens was 72, 120 (70-193), 151 (53-440), and 141 (59-336) SFC/million PBMCs. The breadth of the response improved with EP and increasing dosage, with responses to 1, 1, 3, and 4 of the 4 ADVAX gene products. ICCS analysis of ELISPOT responders revealed a balanced CD4+/CD8+ response. There were no responses to placebo, by definition. An analysis of responses after the third vaccination in the high dosage group is ongoing.

Conclusion: This study is the first demonstration in healthy volunteers that EP in vivo is safe, tolerable, and effective in improving the magnitude and breadth of cellular immune responses to a DNA-based vaccine.

OA05-02

Analysis of DNA compared to Ad5 vaccination, as single and mixed modalities, demonstrates robust induction of cellular immune responses in macaques

LA Hirao[1], L Wu[1], A Satishchandran[1], AS Khan[2], A Finnefrock[3], D Casimiro[3], J Shiver[3], MR Betts[1], NY Sardesai[2], and DB Weiner[1]

[1]University of Pennsylvania, Philadelphia, USA; [2]VGX Pharmaceuticals, The Woodlands, Texas, USA; [3]Merck Research Laboratories, Westpoint, PA, USA

Background: We have previously reported dramatic increases in immune responses induced by DNA vaccines delivered by electroporation (EP), resulting in improved control of viral replication following a SIVmac251 challenge. We compared the immunogenicity of DNA+EP to the Ad5 vaccine, the most potent recombinant viral vector for the generation of CTL responses in macaques and humans. Futhermore, we were interested in examining the effect of prime/boost strategies using these two platforms on the magnitude and phenotype of the immune response.

Methods: Three groups of rhesus macaques (n=5) were immunized with consensus SIVmac gag, env, pol constructs with plasmid IL-12 by EP (DNA+EP), Ad5SIVgag, pol, nef (Ad5) or saline alone (Naïve). The DNA+EP group received 4 immunizations and the Ad5 group received 3 immunizations. Five months following the last immunization the DNA+EP group was boosted twice with the Ad5 vaccine and vice versa. Cellular responses were assessed by IFNγ ELISpot, CFSE proliferation, and ICS for polyfunctional populations.

Results: The Ad5 group had an early three-fold enhancement of IFNγ responses compared to the DNA+EP group (1925±610 and 666±297 SFU/106 PBMCs, respectively). Subsequent Ad5 immunizations failed to boost responses while the DNA+EP group reached a robust 9776±1589 SFU/106 PBMCs. Proliferation was five-fold better and the magnitude of the polyfunctional CD8+ T cell response was a log higher in the DNA+EP group compared to the Ad5 group (1.31% and 0.11%, respectively). When boosted with DNA, the Ad5 polyfunctional response increased six-fold (0.67%) and the DNA+EP group had a 7-fold increase (8.28%) following an Ad5 booster immunization.

Conclusion: Following the initial series of immunizations the DNA+EP group surpassed the Ad5 group in terms of magnitude, proliferation, and polyfunctionality. However both groups demonstrated a boost in all responses following crossover immunizations. These results have significant implications for HIV vaccine development and warrant further study.

OA05-03

Efficacy study of a T-cell-based DNA vaccine delivered by intradermal electrotransfer in macaques

N Dereuddre-Bosquet[4], M Baron[4], I Méderlé-Mangeot[4], K Kaldma[1], R Sikut[1], A Männik[1], I Stanescu[2], M Ustav[3], R Le Grand[4], and F Martinon[4]

[1]FIT Biotech, Tartu, Estonia; [2]FIT Biotech Oyj Plc, Tampere, Finland; [3]Institute of Technology, University of Tartu, Tartu, Estonia; [4]CEA / Division of Immuno-Virology, Fontenay aux Roses, France

Background: We recently demonstrated that intradermal (ID) injection with electropororation (EP) of a new HIV DNA vaccine induced strong and persistent specific T-cells in macaques. Here, we used an equivalent vaccine encoding SIVmac251 antigens in order to study its efficacy in SIV mucosal challenge of macaques.

Methods: Eighteen macaques were vaccinated with 1 mg of the auxo-GTU-MultiSIV DNA at week 0, 4 and 12: either by the ID route only (n=6), or by the ID route combined with EP (ID+EP; n=6) or ID+EP with co-injection of a plasmid used as "genetic-adjuvant" (n=6). A control group of unvaccinated animal was included (n=6).

Results: Before challenge, all animals raised SIV-specific T-cells as evidenced by IFN-γ ELISPOT (110±42, 921±310 and 905±252 spots/106 cells in the ID only, ID+EP and ID+EP+genetic-adjuvant groups, respectively). Weak and transient antibody responses were detected. All animals were intrarectally challenged with pathogenic SIVmac251. T-cell responses increased in both ID+EP groups as early as week 1 post-challenge (3,898±395 and 3,031±893 spots, respectively), and up to 12,000 spots by week 2. Macaques immunized ID only raised delayed and lower responses remaining earlier and higher than in controls. At peak of viremia, plasma viral load was significantly reduced (p=0.0104) in the ID+EP group. Interestingly, no reduction of plasma viral load was observed by that time in the genetic-adjuvant group despite high anamnestic responses. Differences in anti-Gag responses may explain this observation. Viremia was not reduced in the ID only group. At set-point, although similar plasma viral load in all groups, reduction of SIV-DNA copies in rectal biopsies was observed in the vaccinated animals.

Conclusion: Electroporation results induced high anamnestic T-cells responses which are better associated with the control of early plasma viremia. Impact of vaccine on disease progression is currently under evaluation.

OA05-04

Gp96-Ig-SIV vaccines induce predominant immune responses at mucosal sites

N Strbo[1], M Vaccari[2], S Pahwa[1], MA Kolber[1], E Fisher[1], L Gonzalez[1], BK Felber[2], GN Pavlakis[2], G Franchini[2], and ER Podack[1]

[1]University of Miami Miller School of Medicine, Miami, USA; [2]NCI/NIH, Bethesda, MD, USA

Background: We have developed a vaccine design that utilizes the unique property of the endoplasmic reticulum chaperon, heat shock protein (HSP) gp96, to bind antigenic peptides and deliver them to APCs. Cell-based gp96-Ig vaccines, by prolonged in vivo secretion of gp96-Ig peptide, imitate viral replication and provide immune stimuli comparable to attenuated viruses. In model systems in mice we have shown that gp96-Ig transfected, antigen expressing cells secrete gp96-Ig in vivo and stimulate both systemic and strong mucosal immunity. The aim of our study was to evaluate safety and systemic and mucosal SIV-immunity with secreted gp96-Ig-SIV vaccines in non-human primates.

Methods: Gp96-Ig was generated by replacing the ER retention sequence KDEL with the IgG1-Fc tag. HEK-293 cells were transfected with gp96-Ig and with the cDNAs encoding the SIV antigens gag, pol, env and retanef. Irradiated, transfected 293 cells that secrete 1, 5 or 50 micrograms gp96-Ig-SIV-peptide complexes in 24h, were injected intraperitoneally in Mamu-A*01+ macaques at 0, 4 and 25 weeks.

Results: After the third immunization the SIV-specific CD8 response was boosted to very high levels in the rectum and jejunum (30 - 50% tetramer positive cells in the CD8 gate in LPL and IEL). In vaginal IEL gag-specific CD8 responses reached 4%. Tetramer+ cells expressed appropriate functional (granzymeB) and migration markers (CD103). Control macaques immunized with 293 cells not secreting gp96, showed only background tetramer binding. The mucosal CD8+ and CD4+ T cells from lamina propria and intraepithelial compartment secrete IL-2 or IFN-gamma or both simultaneously in response to peptide stimulation.

Conclusion: We conclude that the cell secreted gp96-Ig-SIV vaccine is safe and can induce strong poly-specific, multifunctional and predominant CD8 responses in mucosal compartments that are thought to be critical for protection from SIV/HIV infection.

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OA05-05

Impact of in vivo CD4 binding during HIV-1 Env trimer immunizations of rhesus macaques

I Douagi[1], MM Forsell[1], C Sundling[1], S O'dell[2], R Seder[2], JR Mascola[2], K Loré[3], RT Wyatt[2], and GB Karlsson Hedestam[1]

[1]Karolinska Institutet, Stockholm, Sweden; [2]Vaccine Research Center, National Institutes of Health, Bethesda, MD, USA; [3]Center for Infectious Medicine, Karolinska Institutet, Stockholm, Sweden

Background: We recently reported that immunization with cleavage-defective soluble HIV-1 envelope glycoproteins (Env) trimers in monkeys, but not in rabbits, results in the elicitation of antibodies directed against the co-receptor binding site of gp120. This finding demonstrates that the high affinity interaction between Env and primate CD4 results in an alteration of Env immunogenicity. To further investigate the impact of Env-CD4 in vivo interactions during vaccination, we immunized rhesus macaques with wild type (wt) and CD4 binding defective Env trimers.

Methods: Groups of five adult rhesus macaques were immunized with wt trimers or CD4 binding defective trimers, with either retained or abrogated capacity to form the co-receptor binding-site. Plasma and PBMCs were collected 2 weeks post-immunization. Frequency of Env-specific B and T cells were assessed by ELISpot analysis and flow cytometry. Serum antibodies were measured by ELISA and neutralization assays. Four weeks following the last immunization, control and vaccinated animals were challenged with SHIVSF162P4.

Results: Antibodies against the co-receptor binding site were elicited in animals immunized with wt trimers, but not in animals immunized with the CD4-binding defective mutants. Elimination of the Env-CD4 in vivo interaction did not affect vaccine-induced Env-specific T cell responses or levels of total elicited binding antibodies. However, differences in the quality of the in vitro neutralizing antibody response were observed between the three groups. A comparable decrease in plasma viral loads compared to unvaccinated controls was also measured following challenge in all three groups.

Conclusion: These results confirm that the wt Env trimers used here interact with host CD4 in vivo affecting the quality of the elicited antibody response. As Env-based vaccines progress from small animals to primates, the effects of high affinity CD4 interaction may need to be considered in regards to immunogen design.

OA05-06 LB

First-in-human phase 1 safety and immunogenicity of an Adenovirus Serotype 26 HIV-1 vaccine vector

LR Baden[1], R Dolin[3], KL O'Brien[3], P Abbink[3], A La Porte[3], MS Seaman[3], E Choi[1], R Tucker[1], M Weijtens[2], MG Pau[2], J Goudsmit[2], DH Barouch[3]

[1]Brigham and Women's Hospital, Boston, MA, USA; [2]Crucell, Leiden, Netherlands; [3]Beth Israel Deaconess Medical Center, Boston, USA

Background: Adenovirus serotype 26 (Ad26) is a rare Ad serotype that differs substantially from Ad5 in terms of baseline seroprevalence, receptor usage, tropism, innate immune profile, adaptive immune phenotype, and protective efficacy in the SIV/macaque model. Here we report the initial safety and immunogenicity assessment of a prototype Ad26 vector in humans.

Methods: Ad26 expressing the VRC EnvA test antigen was manufactured by Crucell. 36 Ad26 seronegative, healthy subjects were enrolled in a randomized, double-blinded, placebo-controlled, dose-escalation phase 1 study. Groups of 12 subjects received doses of 10^9, 10^{10}, or 10^{11} vp of the Ad26-EnvA vector (N=10/group) or placebo (N=2/group) at weeks 0, 4, and 24. We performed a pre-specified blinded immunogenicity analysis after the first two immunizations. Validated IFN-gamma ELISPOT assays were performed with positivity criteria of >55 SFC/10^6 PBMC and >4-fold background.

Results: 26/36 subjects were female, and 70/72 vaccinations were administered. Some reactogenicity was observed after the initial immunization in the highest dose group but typically resolved within 24 h. No vaccine-associated AEs or SAEs occurred. In all three dose groups, 2 subjects/group exhibited no detectable vector- or insert-specific immune responses at any timepoint, whereas 10 subjects/group developed positive Ad26 NAb titers, EnvA-specific ELISA titers, and EnvA-specific ELISPOT responses following vaccination. In the 10^9 vp dose group, the median ELISA titer was 1000 (IQR 300-3,000) and the median ELISPOT response was 381 SFC/10^6 PBMC (IQR 125-545) at week 8. In the 10^{11} vp dose group, the median ELISA titer was 5,477 (IQR 3,000-10,000) and the median ELISPOT response was 365 SFC/10^6 PBMC (IQR 85-715) at week 8.

Conclusion: The Ad26 vector is safe and immunogenic in humans at all three doses. Ad26 is therefore a promising new vector for further clinical studies to evaluate novel inserts such as mosaic HIV-1 Gag, Pol, Env antigens.

ORAL ABSTRACT SESSION 06: DYNAMICS OF HIV INFECTION AND THE IMMUNE RESPONSE

OA06-01

Multiplicity of infection by HIV-1 in injection drug users, men who have sex with men and heterosexuals

KJ Bar[1], H Li[1], B Keele[2], T Grayson[1], R Sun[1], A Chamberland[3], C Tremblay[3],JP Routy[3], M Markowitz[4], J Schumacher[1], B Hahn[1], and G Shaw[1]

[1]University of Alabama at Birmingham, USA, Birmingham, Alabama, USA; [2]National Cancer Institute-Frederick, Frederick, Maryland, USA; [3]University of Montreal, Montreal, Canada; [4]Aaron Diamond AIDS Research Center, New York, USA

Background: We have recently shown that transmitted/founder virus(es) can be identified unambiguously using single genome amplification (SGA) (Keele PNAS 2008; Salazar JEM 2009) and that in heterosexual transmissions approximately 80% of patients are infected by a single virus or infected cell (Keele PNAS 2008; Haaland PLoS Pathogens 2009; Abrahams JVirol 2009). Here we explore the characteristics of virus transmission in men who have sex with men (MSM) and injection drug users (IDU).

Methods: Full-length env sequences were derived by SGA from plasma vRNA from 30 acutely infected MSM and 11 IDU from North America. Modes of infection were determined by self-report. Uncloned amplicons were sequenced, aligned, and analyzed by neighbor-joining phylogenies and the Highlighter tool.

Results: Maximum within-patient diversity ranged from 0.08-7.12%. In the MSM group, 19 of 30 (63%) acutely infected subjects had evidence of a single transmitted/founder (t/f) virus and 11 of the 30 had evidence of transmission by a minimum of 2-10 viruses. In the IDU group, 4 of the 11(36%) had evidence of a single t/f virus, while the remaining 7 demonstrated transmission by a minimum of 3-19 variants. In the subjects with multiple transmissions, the median number of t/f variants was 3 for MSM and 5 for IDU. Differences in single versus multiple virus transmissions among HSX, MSM and IDU were statistically significant ($p<0.006$).

Conclusion: The HIV-1 transmission event is different in HSX, MSM and IDU. We see single variant transmission in approximately 80% of HSX, 60% of MSM and 40% of IDU. When multiple transmissions occur, they tend to have a higher number of variants in IDU than in MSM or HSX. These findings indicate that risk of HIV-1 acquisition correlates with numbers of transmitted viruses. This, along with the phenotypic properties of these viruses (especially Env), may be important in vaccine design and assessment.

OA06-02

Monospecific expansion of SIVmac251 during acute infection masks multiple transmitted virus variants revealed during the chronic phase

BK Felber[1], E Kim[2], R Pal[3], RC Desrosiers[4], SM Wolinsky[2], and GN Pavlakis[5]

[1]HRPS, VB, NCI-Frederick, Frederick, MD, USA; [2]Northwestern University, Chicago, IL, USA; [3]Advanced Biosciences Laboratories, Inc., Kensington, MD, USA; [4]New England Primate Research Center, Harvard Medical School, Southborough, MA, USA; [5]HRS, VB, NCI-Frederick, Frederick, MD, USA

Background: Rhesus macaque challenge models to evaluate protection are important in the search for an AIDS vaccine. Many challenge protocols use high dose SIV to ensure infection of all control animals after a single challenge. Many virus variants are predicted to infect the animals under these conditions, which is different than the majority of human infections. It is important to identify both the infecting virus swarm in the stock, and the transmitted and replicating virus, to better evaluate vaccine candidates. It is important to develop macaque models predicting human vaccination outcome.

Methods: We performed single genome amplification (SGA) to identify the full env sequence or a fragment encompassing the highly variable V1/V2 region from naïve SIVmac251-challenged animals using plasma from the acute and chronic phase, as well as from the original SIVmac251 challenge stocks.

Results: The two closely related SIVmac251 stocks sequenced by SGA showed great diversity of env sequences. Most changes were within the V1/V2 region, known to be immunodominant for SIV antibody responses. Despite the stock diversity, only a very narrow selection of similar envs were detected during the acute phase in 7 of 9 animals infected by atraumatic mucosal application. In contrast, multiple diverse env sequences were found in the chronic phase, which can be traced back to the stock.

Conclusion: Multiple species cross the mucosal barrier and infect the host during a high dose mucosal infection. Interestingly, one or very few of these variants propagate early in the acute phase, but other transmitted variants emerge to prominence later. This may be the result of viral fitness, competition, founder effects, or innate mechanisms. These findings also suggest that estimating the number of transmitted virus variants by analysis during the acute phase is inaccurate, and evaluation of both acute and chronic virus is critical to identify the transmitted variants.

OA06-03

Dynamics of CTL epitope escape and reversion in an African subtype C cohort

M Schaefer[1], J Mulenga[2], J Tang[3], P Goepfert[3], P Farmer[1], R Kaslow[3], S Allen[1], and E Hunter[1]

[1]Emory University, Atlanta, GA, USA; [2]Zambia Blood Transfusion Service and ZEHRP, Lusaka, Zambia; [3]University of Alabama-Birmingham, Birmingham, Alabama, USA

Background: HIV immune escape follows a predictable mutational path in response to the HLA alleles carried by an individual. The kinetics of CTL epitope escape and reversion in subtype B HIV-1 infected individuals have recently been reported, however, the inferences drawn from them were limited by the absence of information about the transmitted sequence. To address these issues, we examined Gag, Pol and Nef sequences in both partners of 148 epidemiologically-linked transmission pairs from an African subtype C cohort.

Methods: Cohabiting HIV-1 discordant heterosexual couples from Lusaka, Zambia were followed longitudinally. Despite counseling and condom provision, 7% of uninfected partners became infected each year. At this time and at three-month follow-up intervals, blood and PBMC samples were collected from both the donor (D) and recipient (LR). The gag, pol and nef genes were amplified and sequenced from virus in plasma obtained from both partners. CTL epitopes were identified using previously published HLA-linked polymorphisms.

Results: Analyses of the viruses in the linked transmission pair recipients indicated that a surprising fraction of those transmitted had polymorphisms relevant for the HLA of the LR. Specifically, 29% of LR had viruses with escaped Gag epitopes at the time of seroconversion and these escaped epitopes were present in the D virus at the time of transmission. Thus, we find that Gag escape occurs more slowly than previously reported, with only 5-15% of Gag epitopes exhibiting de novo escape within the first year, and that a majority of HLA-linked polymorphisms at one year were transmitted from the donor.

Conclusion: The study of epidemiologically-linked transmission pairs demonstrates the high rate of transmission of escaped epitopes and that this directly impacts the calculated rates of escape, which could not be accounted for in previous studies. The potential for these non-donor driven mutations to impact viral pathogenesis is under investigation.

OA06-04

The role of early T-cell responses in subjects with acute HIV-1 infection

MK Liu[1], G Ferrari[2], J Salazar[3], B Keele[3], RL Tanner[1], P Hraber[4], E Giorgi[4], VV Ganusov[4], GH Learn[4], MG Salazar[3], SR Moore[1], K Digleria[1], Z Yu[1], T Rostron[1], C DeBoer[5], A Williams[5], C Margaret[5], J Kopycinski[6], SL Campion[1], VE Bourne[1], S Brackenridge[1], B Hahn[3], M Cohen[7], Core B University of North Carolina Duke Research[1], P Borrow[1], K Weinhold[2], A Perelson[4], G Shaw[3], BT Korber[4], N Goonetilleke[1], and AJ McMichael[1]

[1]University of Oxford, Oxford, United Kingdom (Great Britain); [2]Duke University, Durham, North Carolina, USA; [3]University of Alabama, Birmingham, Alabama, USA; [4]Los Alamos National Laboratory, Los Alamos, New Mexico, USA; [5]SCHARP, Seattle, Washington, USA; [6]Imperial College, London, United Kingdom (Great Britain); [7]University of North Carolina, Chapel Hill, North Carolina, USA

Background: Previous studies have shown that T-cells play an important role in the maintenance of virus set-point in early and chronic HIV-1 infection. This study investigates the role of the first T-cell responses in selecting virus escape and controlling the early peak of viremia.

Methods: To identify the single transmitted/founder virus full-length single genome amplification (SGA) virus sequencing was performed when patients were screened before seroconversion during peak viremia. Virus evolution was monitored by further serial SGA sequencing. Ex-vivo IFN-γ enzyme-linked immunospot assays and multi-parameter flow cytometry were used with peptides matching the founder virus sequence to comprehensively map the HIV-1 specific T cell responses in subjects at serial time points over the first 12 months post-screening.

Results: T-cell assays showed that HIV-1 specific T-cell responses selected non-synonymous sequence changes at different rates across the whole of the HIV-1 proteome. The first detectable T-cell responses induced virus escape within 18-34 days of screening. However, these T-cell responses were subsequently lost or diminished after the escape variant became fixed within the virus population. The majority of the later HIV-1 specific T-cell responses induced a slower rate of escape, whilst a minority did not select for escape variants over the study period. Selected sequence changes could also be attributable to reversion, compensatory mutations, other immune responses and linkage to other selected sites. Ongoing studies are exploring the mechanisms behind the few rapid sequence changes found where no T cell response could be identified.

Conclusion: The data shows that the first HIV-1 specific T-cell responses can induce rapid virus escape at times earlier than previously described. Appearing during the decline of viral load from peak viremia these T-cell responses provide some evidence that they contribute to this fall. The role of these first HIV-1 specific T-cell responses will have an impact on vaccine design.

OA06-05

Adaptation of HIV-1 to the human immune system at the population level is driven by protective HLA-B alleles

IM Schellens[1], M Navis[2], HW van Deutekom[3], B Boeser-Nunnink[2], B Berkhout[2], N Kootstra[2], F Miedema[1], C Kesmir[3], H Schuitemaker[2], D van Baarle[1], and JA Borghans[1]

[1]University Medical Center Utrecht, Utrecht, Netherlands; [2]Academic Medical Center, Amsterdam, Netherlands; [3]Utrecht University, Utrecht, Netherlands

Background: HIV undergoes extensive within-host adaptation to HIV-specific Cytotoxic T Lymphocyte (CTL) responses. However, the full extent and importance of CTL escape mutations in driving HIV evolution at the population level remains to be established.

Methods: We included 27 individuals from the Amsterdam Cohort Studies on HIV infection and AIDS with a known seroconversion date in 1985 or 2005/06 (12 and 15 individuals, respectively), of which HIV sequences were derived within a year after seroconversion. CTL epitopes were predicted using a proteasomal cleavage/TAP transport/MHC class I combined predictor. HLA-binding epitopes from the proteins P17, P24, Nef, Protease and RT were predicted for 5 common HLA-A and 3 common HLA-B alleles, as well as for HLA-B27 and HLA-B57, the HLA-B alleles most strongly associated with slow progression to AIDS. To avoid the possibility that observed CTL escape mutations were due to within-host evolution rather than adaptation at the population level, individuals expressing the particular HLA allele under investigation were excluded from the analyses.

Results: HIV strains isolated from recent seroconvertors were found to contain significantly less 9-mers predicted to bind to the 5 HLA-B alleles under investigation compared to historical HIV strains, which was not observed for the 5 HLA-A alleles. Remarkably, the reduction in the number of CTL epitopes during the epidemic was not due to adaptation to the most common HLA-B alleles, but instead to the alleles associated with slow disease progression, HLA-B27 and B57.

Conclusion: These data show that, over the past 20 years, HIV has adapted to the human immune system by decreasing the number of potential CTL epitopes presented via HLA-B, but not HLA-A, alleles, and that such adaptations can become fixed in the population. Adaptation was not related to the population frequency of the HLA alleles, but instead seemed driven by the immune selection pressure of the HLA alleles.

OA06-06 LB

Evidence of vaccine-induced changes in breakthrough HIV-1 strains from the Step trial

M Rolland[1], S Tovanabutra[3], PB Gilbert[2], E Sanders-Buell[3], L Heath[1], AC deCamp[2], CC Magaret[2], M Bose[3], A Bradfield[3], A O'Sullivan[3], J Crossler[3], W Deng[1], H Zhao[1], K Wong[1], DN Raugi[1], J Hural[2], S Dubey[2], N Frahm[2], NL Michael[3], J Shiver[4], L Corey[2], F Li[2], SG Self[2], J Kim[3], S Buchbinder[5], DR Casimiro[4], MN Robertson[4], MJ McElrath[2], FE McCutchan[3], JI Mullins[1]

[1]University of Washington, Seattle, WA, USA; [2]Vaccine & Infectious Disease Institute, Fred Hutchinson CRC, Seattle, WA, USA; [3]US Military HIV Research Program, Rockville, MD, USA; [4]Merck Research Laboratories, West Point, PA, USA; [5]San Francisco Department of Health, San Francisco, CA, USA

Background: Vaccinations in the Step Study, designed to assess the efficacy of a T cell-based vaccine, were interrupted in 2007 after an interim analysis showed no evidence of efficacy.

Methods: To evaluate the impact of the vaccine on founder/breakthrough viruses, i.e., the viruses obtained from the earliest available specimen around the time of diagnosis, we obtained 0.5-14 HIV-1 whole genome sequences per individual from 40 vaccine and 28 placebo recipients who acquired HIV-1 infection as of December 2007.

Results: To assess whether the vaccine elicited T cells that exerted selective pressure on founder viruses, we identified known and likely class I MHC-restricted CTL epitopes in founder sequences based on each volunteer's HLA type. We calculated protein distances between epitopes in the vaccine and those in the founder sequences. Compared to the vaccine, epitopes from vaccine recipients exhibited more mutations than epitopes from placebo recipients ($p=0.02$). Potential epitopes were then identified across all infected individuals and compared to HXB2. The epitopic distances from the combination of Gag, Pol and Nef sequences (included in vaccine) were significantly higher among vaccine vs. placebo recipients ($p=0.004$). In contrast, there was no distinction between vaccine and placebo if epitopes from Env, Rev, Tat, Vif, Vpr, Vpu (not included in vaccine) were considered together ($p=0.90$). Lastly, ~10 AA signature sites in Gag, Nef, Pol (but none in Env) were found to classify vaccine versus placebo status.

Conclusion: Our data indicate that founder viruses from vaccinees diverged further from the vaccine than viruses from placebo recipients at potentially immune reactive sites. This suggests that the vaccine may have blocked the outgrowth of specific HIV-1 variants that were the most similar to the vaccine sequence and/or elicited immune responses that may have driven specific mutations among vaccinees' viruses post-infection.

ORAL ABSTRACT SESSION 07: T CELL RESPONSES TO VACCINE

OA07-01

HIV-Specific CD8+ T-cells of vaccinees exhibit proliferative and cytotoxic capacities comparable to those of progressors

JE Rood[1], SA Migueles[1], AM Berkley[1], AA Compton[1], RP Joshi[1], A Duerr[2], J McElrath[2], and M Connors[1]

[1]NIH, Bethesda, MD, USA; [2]Vaccine and Infectious Diseases Unit, Fred Hutchinson Cancer Research, Seattle, WA, USA

Background: HIV-specific CD8+ T-cells of long-term nonprogressors (LTNP) exhibit extraordinary per-cell cytotoxic capacity. To adapt cytotoxicity assays for vaccine trials, we compared HIV-specific CD8+ T-cell cytotoxic capacity with proliferation and perforin expression using cells from LTNP, viremic progressors, antiretroviral recipients with <50 HIV RNA copies/ml plasma (Rx<50) and seronegative individuals who had or had not received the Merck Ad5 trivalent vaccine.

Methods: HIV-specific CD8+ T-cell cytotoxic responses to HIV_{SF162}<-infected CD4+ T-cell targets were measured at 1 hour by flow cytometric detection of granzyme (Gr) B delivery to live targets or infected CD4 elimination (ICE). Cytotoxicity, IFN-γ production, perforin expression, and proliferation of HIV-specific CD8+ T-cells were examined following a 6-day stimulation with HIV_{SF162}-infected CD4+ T-cell targets.

Results: The HIV-specific CD8+ T-cell cytotoxic responses of vaccinees (medians 16.8% GrB activity, 37.2% ICE) were clearly distinguishable from those of seronegative controls (1.7% GrB activity, p<0.001; 0.3% ICE, p<0.001), but were comparable to those of progressors (16.6% GrB activity, p>0.5; 37.4% ICE, p>0.5). Among vaccinees, those with the protective alleles HLA B*27, B*57, or B*58 tended to have higher responses. Vaccinee responses were significantly less than those of LTNP (50.7% GrB activity, p<0.001; 82.5% ICE, p<0.001). GrB activity and ICE were strongly correlated with HIV-specific CD8+ T-cell proliferation (R=0.85, p<0.001 and R=0.87, p<0.001, respectively) and perforin expression (R=0.86, p<0.001 and R=0.9, p<0.001, respectively). When measured on a per-cell basis, cytotoxicity of most vaccinees remained at the level of progressors, even with higher effector:target ratios.

Conclusion: GrB activity and ICE correlate strongly with CD8+ T-cell proliferation and perforin expression in expanded cells suggesting these parameters are reasonable surrogate measurements of CD8+ T-cell-mediated killing requiring fewer cells. GrB activity and ICE of vaccinees were similar to those of progressors, suggesting these low responses might contribute to suboptimal control in cases of HIV infection following vaccination.

OA07-02

Adenovirus vectors induce expansion of memory CD4 T cells with a mucosal homing phenotype that are readily susceptible to HIV-1 infection

A Benlahrech[1], J Harris[2], A Meiser[1], T Papagatsias[1], J Hornig[1], P Hayes[1], A Lieber[3], T Athanasopoulos[2], V Bachy[4], R Daniels[5], K Fisher[6], F Gotch[1], L Klavinskis[4], L Seymour[6], K Logan[1], R Barbagallo[1], G Dickson[2], and S Patterson[1]

[1]Imperial College, London, United Kingdom (Great Britain); [2]Royal Holloway University of London, Surrey, United Kingdom (Great Britain); [3]University of Washington, Seattle, USA; [4]King's College London, London, United Kingdom (Great Britain); [5]National Institute for Medical Research, London, United Kingdom (Great Britain); [6]Hybrid Systems Ltd., Oxford, United Kingdom (Great Britain)

Background: In the recently halted human immunodeficiency virus type 1 (HIV-1) vaccine STEP trial individuals that were seropositive for adenovirus serotype 5 (Ad5) showed increased rates of HIV-1 infection on vaccination with an Ad5 vaccine. We undertook a series of ex vivo strategies to address the hypothesis that immunisation of Ad5 seropositive individuals with adenoviral vectors may result in activation, expansion, and trafficking of Ad5-specific memory CD4 T cells to mucosal tissues thereby increasing the number of HIV-1 susceptible targets at the initial sites of infection.

Methods: Ad5 and Ad11 antibody titers were measured in 20 healthy volunteers. Dendritic cells (DC) were generated from these individuals, pulsed with replication defective Ad5 or Ad11 and co-cultured with autologous lymphocytes. Cytokine profiles, proliferative capacity and the migration potential of the adenovirus-stimulated memory T cells were measured. The susceptibility of re-stimulated memory Ad-specific T cells to infection with a CCR5-utilising HIV-1 was also assessed by multi-colour flow cytometric analysis and p24 ELISA assays.

Results: Stimulation of T cells from Ad5 seropositive but Ad11 seronegative individuals with Ad5, or serologically distinct Ad11 vectors induced expansion of adenovirus memory CD4 T cells expressing alpha 4 beta 7 and CCR9, indicating a mucosal-homing phenotype. CD4 T cell proliferation and IFN-gamma production in response to Ad stimulation correlated with Ad5 antibody titers. In contrast, Ad5 serostatus did not correlate with total cytokine production upon re-challenge with Ad5 or Ad11. Expanded Ad5 and Ad11 memory CD4 T cells showed an increase in CCR5 expression and higher susceptibility to infection by R5 tropic HIV-1.

Conclusion: Adenoviral-based vaccination against HIV-1 in individuals with pre-existing immunity against Ad5 may result in preferential expansion of HIV-susceptible activated CD4 T cells that home to mucosal tissues, increase the number of virus targets and lead to a higher susceptibility to HIV infection.

OA07-03

Influence of preexisting vaccinia immunity on a DNA/MVA SIV vaccine, decreased cellular immunity but enhanced control of a pathogenic SIV challenge

S Kannanganat[4], P Nigam[4], V Velu[4], P Earl[1], L Lai[4], B Lawson[4], L Chennareddi[4], R Wilson[2], P Kozlowski[2], B Moss[1], H Robinson[3], and R. Amara[4]

[1]Laboratory of Viral Diseases, NIH, Bethesda, USA; [2]Louisiana State University Health Sciences Center, New Orleans, USA; [3]Geovax Inc., Atlanta, USA; [4]Yerkes National Primate Center of Emory University, Atlanta, USA

Background: The influence of preexisting immunity to viral vectors is a major issue for the development of viral vectored vaccines. Here we report that for a DNA/MVA vaccine, preexisting immunity to vaccinia virus (Dryvax) decreases cellular immune responses but enhances control of an intrarectal SIV challenge.

Methods: Three groups of rhesus macaques, eight per group, were studied. The Dryvax-naive and Dryvax-immune groups received the DNA/MVA SIV vaccine (DNA at weeks 0 and 8, and rMVA at weeks 16 and 24). In addition, the Dryvax-immune group received the Dryvax vaccine 1.5 years prior to the DNA prime. The control group did not receive any vaccine. All macaques were challenged intrarectally with SIV251 at 9 months after the final MVA.

Results: Following vaccination, the frequency of SIV Gag-specific CD4 and CD8 T cells were 5-10 fold lower in the Dryvax-immune group than the Dryvax-naive group. Despite their low SIV-specific T cell responses, the Dryvax-immune macaques exhibited the best control of SIV challenge with viremia 480-fold lower at peak and 40-fold lower at set point than in the unvaccinated control animals (p=0.01). The enhanced control in the Dryvax-immune animals was not restricted to Mamu A*01+ animals and was strongly associated with reduced colorectal virus at 2 weeks post challenge. Factors that correlated with early colorectal viral control included the magnitude of vaccine-elicited CD4 T cells displaying the CCR5 viral co-receptor, which was dampened in the Dryvax-immune animals; the presence of anti-viral mucosal IgA, which was more frequent in the Dryvax-immune animals, and the avidity of the anti-Env Ab response. The frequency of anti-viral CD8 T cells did not correlate with early colorectal viral control.

Conclusion: These results highlight important roles for vaccine-elicited CCR5+ CD4 T cells in augmenting, and mucosal IgA and high avidity anti-Env IgG in restricting the early replication of a colorectal immunodeficiency virus challenge.

OA07-04 LB

Immunogenicity of ALVAC-HIV® (vCP1521) and AIDSVAX® B/E prime boost vaccination in RV144, the Thai phase III HIV vaccine trial

MS de Souza[1], R Trichavaroj[1], A Schuetz[1], W Chuenarom[1], Y Phuang-ngern[1], S Jongrakthaitae[1], S Ratto-Kim[2], S Nitayaphan[1], L Dally[3], S Rerks-Ngarm[4], J Tartaglia[5], D Francis[6], NL Michael[2], RM Paris[1], JH Kim[2]

[1] U.S. Military HIV Research Program/AFRIMS, Bangkok, Thailand; [2]U. S. Military HIV Research Program, Rockville, Maryland, USA; [3]EMMES Corporation, Rockville, Maryland, USA; [4]Ministry of Public Health, Nonthaburi, Thailand; [5]Sanofi Pasteur, Toronto, Canada; [6]Global Solutions for Infectious Diseases, San Francisco, California, USA

Background: The Phase III trial of ALVAC-HIV®and AIDSVAX®B/E in Thailand began in October 2003 and concluded in June 2009. Both vaccine candidates express HIV-1 circulating recombinant form (CRF) 01_AE and subtype B antigens. This study assessed whether the Phase III vaccine lots show immunogenicity comparable to the previous Phase I/II study of the identical immunization regimen.

Methods: A list of blinded samples from persons completing all 4 injections with either placebo or vaccine and remained HIV negative at the end of the trial was provided. Peripheral blood mononuclear cells (PBMC) or plasma were tested to CRF 01_AE and subtype B vaccine antigens in the following validated assays: (1) Interferon-gamma (IFN-γ) ELISpot; (2) IFN-γ/interleukin-2 intracellular cytokine staining (ICS); (3) Binding antibody (BAb). ELISpot and ICS assays measured responses to Env (92TH023) and Gag (LAI) peptide pools prior to and 6 months following the completion of immunization. BAb was measured using reciprocal dilution EIA to A244 and MN gp120 and BH10 p24 prior to and at 2 weeks following the completion of immunization.

Results: Data will be un-blinded to treatment assignment by October 2009. Analyses of post-injection responses to Env and Gag by ELISpot revealed an overall frequency of 14%, with Env responses (11%) predominating over Gag (5%). The overall frequency of ICS responses to HIV peptides in samples studied to date was 35% and was greater for CD4 (26%) than CD8 (9%) T cells, with responses to Env again predominating: 26% versus 1% Gag for CD4 and 6% Env versus 2% Gag for CD8 T cells. The frequency of BAb responses to p24 was 37% and was identical for CRF01_AE and MN gp120 (70%).

Conclusion: Cellular and humoral immune responses to the ALVAC-HIV® + AIDSVAX® B/E regimen were predominantly to HIV Env and appear similar to those seen in the earlier Phase I/II study.