Results. Of 70 patients with detectable CMV DNA at randomization (48 LET, 22 PBO), CMV VL was 150 c/mL in 63 patients (range, 150–716). All patients had undetectable CMV VL ≤5 days before randomization. Baseline characteristics were similar to the PEP, except for more patients with myeloablative conditioning (62.9% vs. 48.3%) and longer median days post-HCT to start of study drug (15 days vs. 8 days). Median study drug exposure was 70 days (range, 1–113) in LET group and 14 days (range, 7–99) in PBO group. By HCT Week 14, CS-CMVi occurred in 15 (31.3%) LET-treated patients and 17 (77.3%) PBO patients; CS-CMVi with imputed events were 22 (45.8%) in LET group and 20 (90.9%) in PBO group (difference −44.8%; 95% CI, −64.7% to −24.8%; $P < 0.0001$). Median CMV VL at time of PET was 413 c/mL (range, 150–31,847) and was similar between groups. Eight patients had quantifiable CMV VL (range, 171–1,728 c/mL) 1 week after starting study drug: 6 did not receive PET (5 LET [10.4%], 1 PBO [4.5%]). CMV VL was undetectable subsequently; other 2 withdrew from study. One (2.1%) LET-treated patient developed breakthrough CMV viremia with a *UL56* C325W mutation. HCT Week 48 all-cause mortality was 26.5% in LET and 40.9% in PBO (figure).

Conclusion. LET prevented CS-CMVi compared with PBO among patients with detectable CMV DNA at randomization.

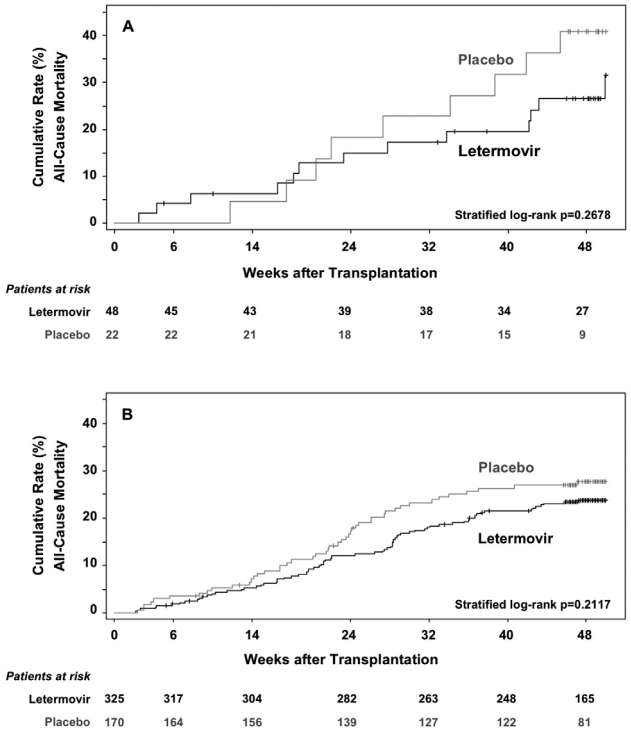

Figure. Time to all-cause mortality in the letermovir HCT phase 3 trial using updated post-study vital status (See Marty FM et al. NEJM 2017;377:2433-44, Supplementary Appendix Section 12 for details). **Panel A**, patients with detectable CMV DNA at randomization (n=70). The event rate for all-cause mortality at HCT Week 24 was 15.0% (95% CI, 4.8%-25.3%) in the letermovir group compared to 18.2% (95% CI, 2.1%-34.3%) in the placebo group (p=0.79); HCT Week 48 rates were 26.5% (95% CI, 13.6%-39.5%) and 40.9% (95% CI, 20.4%-61.5%), respectively. **Panel B**, patients with undetectable CMV DNA at randomization (n=495. primary efficacy population, PEP). The event rate for all-cause mortality at HCT Week 24 was 12.1% (95% CI, 8.6%-15.7%) in the letermovir group compared to 17.2% (95% CI, 11.5%-22.9%) in the placebo group (p=0.04); HCT Week 48 rates were 23.8% (95% CI, 19.1%-28.5%) and 27.6% (95% CI, 20.8%-34.4%), respectively.

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1731. Disseminated Metacestode Infection Due to an Unknown *Versteria* Species

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Session: 202. Transplant and Immunocompromised Hosts: Emerging Issues
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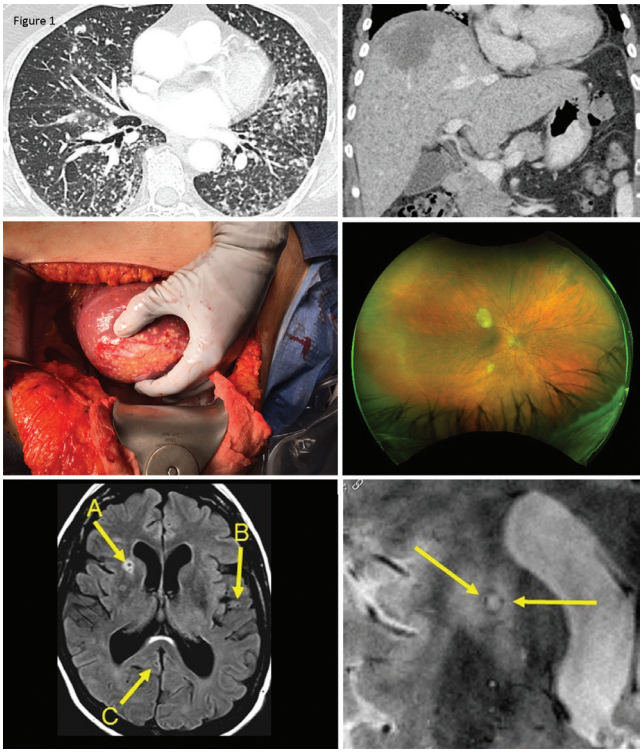
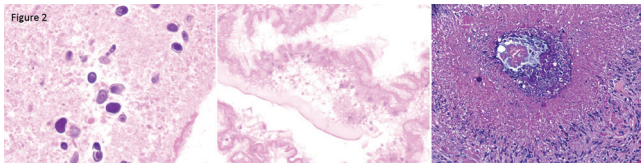
Background. A 68-year-old woman with hypogammaglobulinemia and prior treated lymphoma presented with fever and abdominal pain. Evaluation revealed numerous nodules in the lung, eye, brain, and liver (Figure 1). Initial lung and liver biopsies showed necrotizing granulomas with no organisms and negative serology and cultures. After progression while on broad-spectrum antibiotics for 4 months, an open liver biopsy revealed numerous nodular lesions and a mass made up of multifocal coalescing cystic lesions. The mass consisted of a degenerating 3-layered membrane without scoleces characterized by a wavy protuberant ciliated eosinophilic outer layer, subjacent degenerating cells with pyknotic nuclei, and loose connective tissue suggestive of a bladder wall and calcareous corpuscles in a matrix of granulomatous inflammation with areas of necrosis (Figure 2). This was diagnostic of disseminated metacestodes (larval stage) of a cestode (tapeworm). Treatment with praziquantel and albendazole led to improvement of symptoms and lesions. Disseminated cestode infections other than due to *Echinococcus* species are rare in humans. Sequencing was pursued due to the unusual findings.

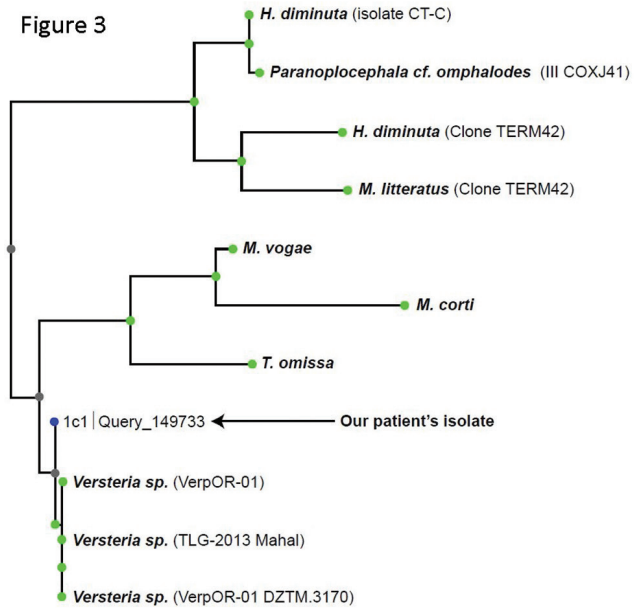
Methods. DNA was extracted from liver tissue followed by targeted amplification of the cestode COX1 gene. PCR products confirmed to be 134 bp, as expected for a cestode COX1 gene, then inserted into a 2.1 Topo vector and cloned. Five separate isolates were sequenced, and 4 were interpretable. The 129-bp consensus sequence is shown in Figure 3. Basic Local Alignment Search Tool (NCBI BLAST) was used to find highly similar sequences.

Results. The sequence matched to *Versteria* sp. (*T. mustelae*) COX1 gene from a mink in Oregon (accession KT223034) with 98% identity.

Conclusion. Metacestodes have the propensity to proliferate and rarely disseminate. There is one reported case of *Versteria* sp. causing a lethal disseminated infection of an orangutan. This is the first report of a *Versteria* sp. disseminated infection in a human and is singular because the patient survived. The patient likely accidentally ingested ova shed from a tapeworm in a mink or similar mammalian host. Histopathologic assessment is crucial in diagnosing cestode infection. COX1 gene sequencing is useful for cestode identification.







Disclosures. **All authors:** No reported disclosures.

1732. Adenovirus Load Dynamics Are Consistently Correlated With Risk of Mortality in Pediatric Allogeneic Hematopoietic Cell Transplant Recipients: Findings From the Landmark AdVance Study

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Session: 202. Transplant and Immunocompromised Hosts: Emerging Issues
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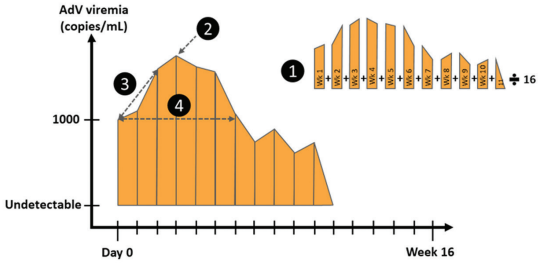
Background. Adenovirus (AdV) infection is an important cause of mortality among allogeneic hematopoietic cell transplant (allo-HCT) recipients. Current European Conference of Infections in Leukemia (ECIL-4) guidelines support weekly AdV screening for those at-risk and pre-emptive antiviral treatment with off-label cidofovir when adenoviremia is detected. However, there is limited understanding of the relative prognostic strength of different dynamic AdV viral load measures. We examined the association between adenovirus viral load dynamics and mortality in pediatric allo-HCT recipients managed under the current standard of care.

Methods. AdVance was a multinational, multicenter study characterizing the current screening and treatment practices for AdV infection in allo-HCT recipients between January 2013 and September 2015. This analysis focused on pediatric (<18 years) patients who experienced AdV viremia ≥1,000 copies/mL within 6 months of HCT. Multivariate Cox Proportional Hazard models, controlling for factors including immune reconstitution, were used to examine the relationship between AdV viral load dynamics (Figure 1) and all-cause mortality in the 6 months after first AdV viremia ≥1,000 copies/mL.

Results. A total of 241 pediatric allo-HCT recipients had AdV viremia ≥1,000 copies/mL in the 6 months following allo-HCT. Among these, 43/241 (18%) died within 6 months of first AdV ≥1,000 copies/mL. AdV viral load dynamics; whether measured by AdV $AAUC_{0-16}$, peak viremia, 2-week change in viremia, or days of viremia >1,000 copies/mL, were consistently correlated with all-cause mortality (Figure 2; hazard ratio [HR] range: 1.3–2.3). Most notably, patients with AdV $AAUC_{0-16}$ in the highest quartile had an HR of 11.6 relative to those in the lowest (confidence interval: 4.7–24.0; Figure 3).

Conclusion. AdV infection is a significant risk for allo-HCT recipients. The AdVance study has identified several dynamic measures of AdV viral load that correlate with the risk of mortality in pediatric allo-HCT recipients. Results show for the first time, that AdV $AAUC_{0-16}$ provides the optimal correlation with mortality in this population and serves as a clinically useful indicator of outcome in patients with AdV infection.

Figure 1: Adenovirus viral load dynamics



1 $AAUC_{0-16}$:
Log_{10} of the time-averaged area under the AdV viremia curve over the 16 weeks following first AdV viremia ≥1000 copies/mL

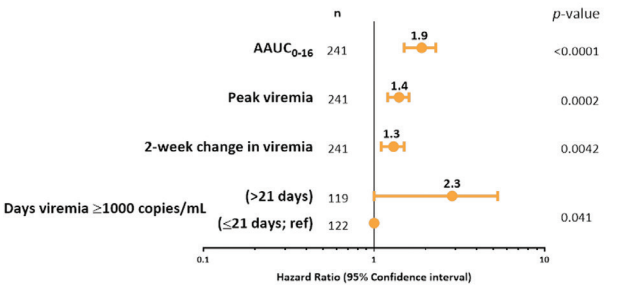
2 Peak viremia:
Peak Log_{10} AdV viremia over the 16 weeks following first AdV viremia ≥1000 copies/mL

3 2-week change in viremia:
Change in Log_{10} AdV viremia in the first 2 weeks from first AdV viremia ≥1000 copies/mL

4 Days viremia ≥1000 copies/mL:
Number of days where AdV viremia was ≥1000 copies/mL over the 16 weeks following first AdV viremia ≥1000 copies/mL

AdV, adenovirus

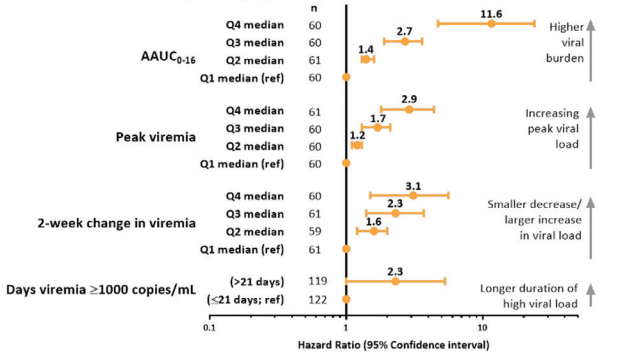
Figure 2: All adenovirus viral load dynamics were associated with a significantly higher risk of all-cause mortality in the 6 months following first adenovirus viremia ≥1000 copies/mL



$AAUC_{0-16}$, Log_{10} of the time-averaged area under the AdV viremia curve over the 16 weeks following first AdV viremia ≥1000 copies/mL; Days viremia ≥1000 copies/mL, number of days where AdV viremia was ≥1000 copies/mL over the 16 weeks following first AdV viremia ≥1000 copies/mL; Peak viremia, peak Log_{10} AdV viremia over the 16 weeks following first AdV viremia ≥1000 copies/mL; ref, reference group; 2-week change in viremia, change in Log_{10} AdV viremia in the first 2 weeks from first AdV viremia ≥1000 copies/mL (see figure 1)

Note: Other factors with $p<0.10$ in the $AAUC_{0-16}$ multivariate analysis were retained in the final multivariate models for other measures. Lymphocyte count, sex, and renal replacement therapy were significant ($p<0.05$) prognostic factors in each of the final models.

Figure 3: Pediatric allogeneic hematopoietic cell transplant recipeints with longer or more intense adenovirus infection had a significantly higher risk of all-cause mortality



$AAUC_{0-16}$, Log_{10} of the time-averaged area under the AdV viremia curve over the 16 weeks following first AdV viremia ≥1000 copies/mL; Days viremia ≥1000 copies/mL, number of days where AdV viremia was ≥1000 copies/mL over the 16 weeks following first AdV viremia ≥1000 copies/mL; Q, quartile; Peak viremia, peak Log_{10} AdV viremia over the 16 weeks following first AdV viremia ≥1000 copies/mL; ref, reference group; 2-week change in viremia, change in Log_{10} AdV viremia in the first 2 weeks from first AdV viremia ≥1000 copies/mL (see figure 1)

Note: Other factors with $p<0.10$ in the $AAUC_{0-16}$ multivariate analysis were retained in the final multivariate models for other measures. Lymphocyte count, sex, and renal replacement therapy were significant ($p<0.05$) prognostic factors in each of the final models.

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