43% mucohaemorrhagic diarrhea. The severity of the diarrhea (Vesikary Scale) was moderate; 54% (n = 73) and 97% of patients were normohydrated; 24% had a household member with diarrhea. Analyzing vaccination history, 74% had received rotavirus vaccine, 89% of them with 2 doses. From 125 samples tested, 29% (n = 36) were NoV positive and, comparing with the negative cases, were younger (19 vs. 22 months; $P < 0.001$) and were associated with higher prevalence of rotavirus vaccination (91% vs. 65%; $P = 0.004$). No statistically difference was found in gender, clinical presentation or severity.

Conclusion. NoV was detected at high frequencies (29%) presenting moderate acute diarrhea, mainly in children that received rotavirus vaccine. Regarding sporadic acute diarrhea cases in children, it is important to consider the role of NoV as a frequent etiological agent. Further surveillance studies at larger populations are needed to elucidate the prevalence, clinical manifestations and risk factors associated with NoV diarrhea in children.

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2508. Absolute Lymphocyte Count and Adenovirus-Specific CD8+ T-cell Immunity as Immunological Predictors of Severe Adenovirus Disease After Kidney Transplantation

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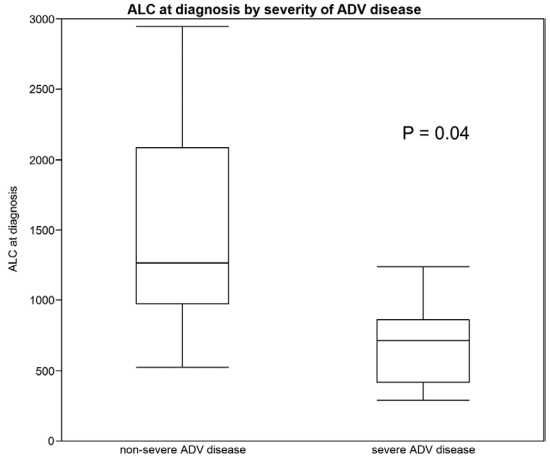
Background. Adenovirus (ADV) infection after kidney transplantation (KT) can range from asymptomatic to severe disease. Cell-mediated immunity plays an important role in preventing disease progression. We aimed to investigate the role of absolute lymphocyte count (ALC) and ADV-specific CD8+ T cell immunity to predict the severity of ADV infection in KT recipients

Methods. We included all adult KT recipients with ADV infection at a single transplant center between January 2015 and March 2018. ADV infection/disease were defined as detectable ADV DNA load in plasma/plus symptoms. We defined severe ADV disease as having plasma ADV DNA load >6.0 log copies/mL and/or disseminated disease (≥2 specific organ symptoms). ADV specific CD8+ T cells were stimulated with whole ADV peptide, stained by intracellular cytokine staining and interrogated by flow cytometry. ALC (all patients) and ADV-specific CD8+ T-cell (7 index cases) were measured at diagnosis. The association of ALC and disease progression were assessed in those with and without severe disease.

Results. ADV infection was diagnosed in 14 KT recipients, 12 (86%) patients were male with a median age of 44 (IQR, 37–58) years. Ten (71%) recipients underwent deceased donor KT and none received anti-thymocyte globulin for induction therapy. ADV infection occurred at median of 14 (IQR, 2–37) months after KT. Eight (57%) recipients were defined as having severe ADV disease including disseminated ADV disease (n = 5). Median peak plasma ADV load was higher in those with severe disease compared with those without severe disease [6.0 (IQR 5.9–6.0) vs. 5.3 (IQR 3.9–5.4) log copies/mL ($P = 0.003$)]. Median ALC and ADV-specific CD8+ T cells at diagnosis were 1,000 (IQR 623–1,350) and 0.003 cells/mm^3, respectively. KT recipients with severe disease had lower median ALC at diagnosis compared with those without severe disease [714 (IQR 419–860) vs. 1,264 (IQR 972–2,086) cells/mm^3; $P = 0.04$) (Figure 1). Those with ALC <1,000 cells/mm^3 at diagnosis had greater risk of severe disease [OR 35 (95% CI, 2.6–1,450); $P = 0.006$].

Conclusion. Lack of ALC and ADV-specific CD8+ T cell immunity (limited data) at diagnosis could potentially be immunological predictors of severe ADV infection in KT recipients.



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2509. High-Risk Human Papillomavirus Infection and the Risk of Cardiovascular Disease: A Cohort Study

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Background. A study using National Health and Nutrition Examination Survey (NHANES) 2003 to 2006 demonstrated the association between high-risk (oncogenic) human papillomavirus (HPV) and an increased prevalence of the self-reported cardiovascular diseases (CVD). However, this study was limited by temporal ambiguity between HPV and CVD, because of its cross-sectional design. We investigated the longitudinal effect of HPV infection on the development of CVD events in a cohort study of Korean women free of CVD at baseline.

Methods. We conducted a cohort study of 63,411 women aged 30 or older without CVD at baseline who underwent a high-risk HPV test and were followed annually or biennially from 2011 to 2016 for new-onset CVD. CVD was ascertained through the linkage to the Health Insurance and Review Agency database. A Cox-proportional hazards regression model was used to estimate adjusted hazard ratios (HRs) with 95% confidence intervals (CIs) of incident CVD.

Results. The prevalence of high-risk HPV infection was 7.6%. During 261,598.9 person-years of follow-up, 1,122 cases of new-onset CVD were identified (incidence rate of 4.3 per 10^3 person-years). The age-adjusted HR (95% CI) comparing high-risk HPV-positive- to high-risk HPV-negative participants was 1.26 (1.03–1.53). After further adjustment for possible confounders, a significant association between high-risk HPV infection and incident CVD was still observed, with a corresponding HR (95% CI) of 1.25 (1.03–1.53). This association was stronger in obese (BMI ≥25 kg/m^2) compared with non-obese individuals (BMI <25 kg/m^2). Otherwise, the associations between high-risk HPV infection and incident CVD did not differ by various clinically relevant subgroups.

Conclusion. In this large cohort of apparently healthy young and middle-aged women, high-risk HPV infection was significantly associated with an increased risk of developing CVD, indicating a possible role for high-risk HPV in the pathogenesis of CVD.

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2510. Epidemiological Change of Cytomegalovirus Diseases in the Developed Country With High Cytomegalovirus–Seropositive Rate: Nationwide, Whole Population-Based Study

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Background. The cytomegalovirus (CMV) can cause tissue-invasive diseases in various organs through primary infection or reactivation of latent status over a lifetime. Even though individuals with risk of CMV diseases such as elderly or immunocompromised patients are constantly increasing, the recent epidemiologic change of it is not fully evaluated, especially on a grand scale.

Methods. We used the Korean Health Insurance Review and Assessment Service (HIRA) claim nationwide database of about 50 million individuals, nearly entire population, between 2010 and 2015. The South Korean National Health Insurance Service operates the "Relieved Co-payment Policy" program as out-of-pocket relief in patients with rare intractable diseases including CMV. The unique code of CMV end-organ diseases in the program is completely matched with ICD-10 B25 except congenital CMV infection and mononucleosis. By this process, the cohort of CMV diseases was established from the HIRA data warehouse. The 628 case (with CMV) and 3,140 control (without CMV disease) group matched with age and sex were selected in same dataset to evaluate the effect of CMV diseases on all-cause death.

Results. The standardized prevalence rates of CMV diseases adjusted with age and sex have continuously increased from 0.55/100,000 in 2010 to 1.41/100,000 individuals in 2015. The crude prevalence was the highest in youngest group of less than 9-year-old every year for 6 years (4.34/100,000 in 2015) and second highest in individuals with 60–69-year-old (2.28/100,000 in 2015). Male population had the higher crude and standardized prevalence than female in all age groups every year. The individuals in lowest income status had the highest standardized prevalence (7.1/100,000 in 2015). In model adjusted by age, sex, low income, diabetes, hypertension and dyslipidemia, case group had 4.8 of hazard ratio (95% CI, 3.3–7.0) to all-cause of death compared with control group. The Kaplan–Meier survival curve revealed the significantly higher rate of all-cause mortality in case group ($P < 0.001$).

Conclusion. The occurrence of CMV disease is steadily on rise during the past 6 years in nationwide data, especially in male infant and childhood as well as elderly individuals, with association of high mortality.

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