Supplementary methods

Bacterial and viral DNA extraction, sequencing, and analysis

Bacterial DNA extraction, metagenomic sequencing, and analysis were performed according to Zheng et al. (1). Briefly, bacterial DNA was extracted using the FastDNA Spin kit for soil (MP Bio, Solon, OH, USA) following the manufacturer's instructions. The viral DNA extraction methods are as follows (2, 3): to separate viral DNA from bacterial DNA, suspending soil samples in potassium citrate buffer (1.92 $g \cdot L^{-1}$ $Na_2HPO_4 \cdot 12H_2O$, 10 $g \cdot L^{-1}$ $C_6H_5K_3O_7$ and 0.24 $g \cdot L^{-1}$ KH_2PO_4; pH = 7) at 4°C for 15 min. The mixture was sonicated (100W, 47kHz, 3min) on ice, and then was centrifuged (7000 rpm, 10 min) to obtain a supernatant containing commixtures and virus particles. The supernatant was centrifuged again (7000 rpm, 15 min) and filtered to remove commixtures larger than 0.22 μm. The virus particles were enriched by using tangential flow filtration technology (TFF, Sartorius Vivaflow50 30,000 MWCO PES, USA). The obtained viral particles were treated with a DNase I:RNase A (37°C; 30 min) mixture in 2:1 to remove free DNA and RNA fragments. Viral DNA was extracted using Takara MiniBEST Viral RNA/DNA Extraction Kit 5.0, and the viral DNA was performed to whole genome amplification (KAPA HiFi HotStart ReadyMix).

The amplification viral DNA and bacterial DNA were subjected to metagenomic sequencing, and each library of 400 bp insert-size fragments was used to generate 150 bp paired-end reads using the HiSeq 4000 platform (Illumina, San Diego, CA, USA). The quality control of raw reads of bacteria and viruses ware performed using Cutadapt 1.2.1, followed by *de novo* assembly using Megahit 1.2.6 (k-mer~ parameter settings)

(4, 5). Open reading frames (ORFs) were predicted using MetaGeneAnnotator (6), and then non-redundant sequences were constructed using CD-HIT (90% sequencing similarity and 90 % coverage) (7). Bacterial taxonomy at species levels were annotated using the lowest common ancestor (LCA) algorithm in MEGAN 5 through the NCBI-NT reference database (8). Viral contigs were identified using VirSorter 1.0.5, and viral sequences >5 kb were further filtered using the vhmm pipeline (9). KEGG (kobas3.0.3) and CAZyme (cazydb.07312018.fa) databases were used to annotate non-redundant proteins of bacterial and viral genomes (10, 11). The possible AMGs in viral gene sequences were identified by DRAM-V with default parameters as previously described (1).

Reference:

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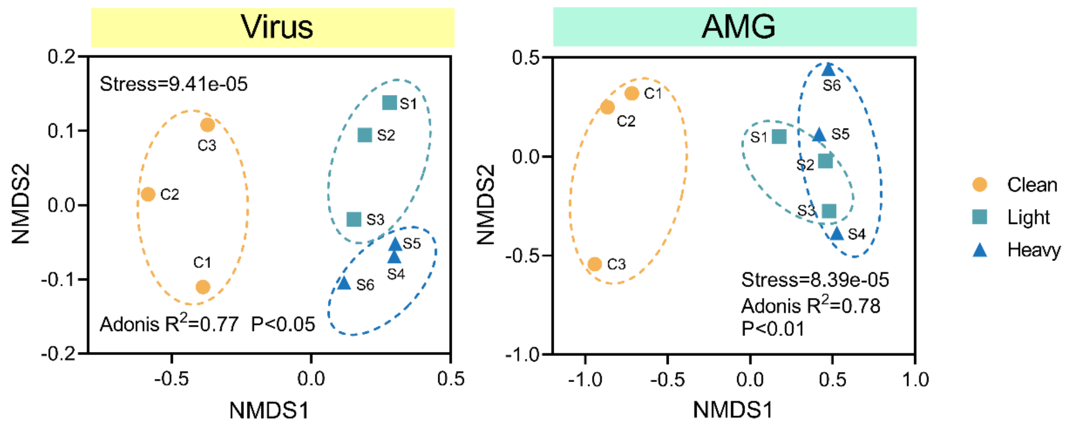
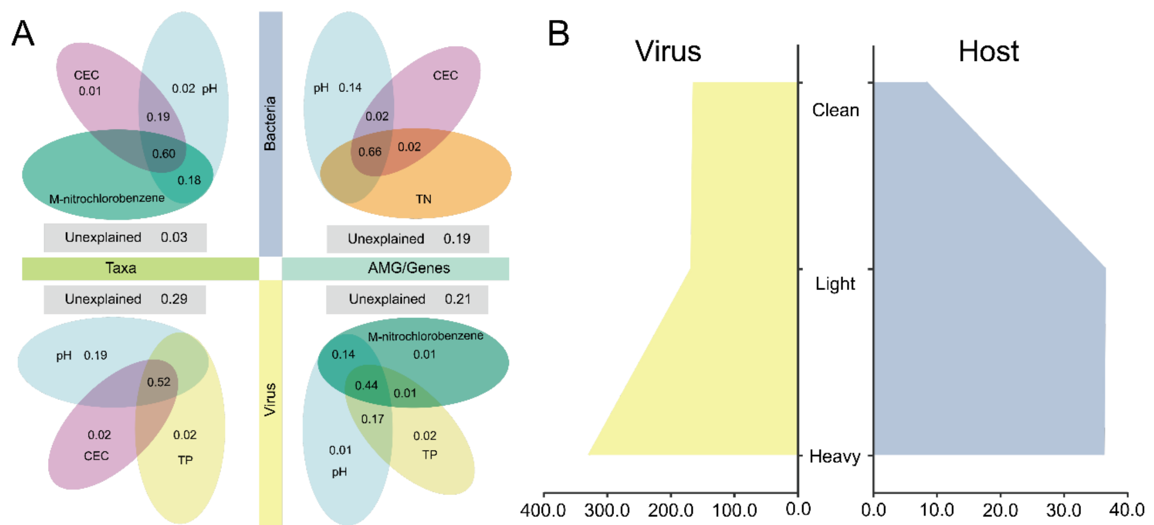
Supplementary figures



Supplementary Fig. S1. NMDS analysis of virus taxa and AMGs.



Supplementary Fig. S2. (A) Variation partitioning analysis (VPA) to indicate the impact of environmental factors on bacterial and viral taxa and functional genes. Venn diagram show the degree of separate and joint explanation of variation in bacterial and viral taxa and functional gene composition by environmental factors. Values < 0 are not shown. TP: total phosphorus; TN: total nitrogen; CEC: cation exchange capacity; m-nitrochlorobenzene; pH. **(B)** Differences in niche breadth of virus and host in clean and OCP-contaminated soil.