**Table S1 Reaction system conditions for genomic DNA removal.**

| Reagent | Amount |
|---|---|
| 5 ×*g* DNA Eraser buffer | 2.0 μl |
| gDNA Eraser | 1.0 μl |
| Total RNA | 800 ng |
| RNase-free $dH_2O$ | up to 10 μl |

**Table S2 Reverse transcription reaction system.**

| Reagent | Amount |
|---|---|
| Reaction mixture | 10.0 μl |
| PrimeScriptRT enzyme Mix I | 1.0 μl |
| RT primer Mix | 1.0 μl |
| 5× PrimeScriptBuffer 2 (for real time) | 4.0 μl |
| Rnase-free $dH_2O$ | 4.0 μl |
| Total concentration | 20 μl |

**Table S3** Reverse transcription PCR program.

| Temperature (°C) | Time |
|---|---|
| 37 | 15 min |
| 85 | 5 s |
| Save at 4 ° C | |

**Table S4** Summary of the sequencing data of *H. erectus*.

| Group | Control group | HM-group t | MP-group |
|---|---|---|---|
| Number of original sequences (n) | 49 556 386 | 49 404 042 | 48 043 100 |
| Number of sequences after filtering (n) | 47 880 348 | 47 987 534 | 46 520 778 |
| Number of bases after filtration (bp) | 7 182 052 200 | 7 198 130 100 | 6 978 116 700 |
| Q30 (%) | 94.03 | 94.08 | 94.32 |

**Table S5** Assembly results.

| Length range (bp) | Trinity | Unigene |
|---|---|---|
| 200–600 | 33 659 | 22 513 |
| 600–1 000 | 11 264 | 5 247 |
| 1 000–2 000 | 19 264 | 6 887 |
| > 2 000 | 22 525 | 7 617 |
| Count | 86 712 | 42 264 |
| Minimum length | 201 | 201 |
| Maximum length | 18 307 | 18 307 |
| Mean length | 1 443.25 | 1 122.71 |
| N50 | 2 485 | 2 223 |
| N90 | 646 | 406 |

**Table S6 Summary of comments in each database.**

| Database | Number of single gene clusters | Percentage (%) |
|---|---|---|
| Non-redundant protein database (Nr) | 22 671 | 53.6 |
| Nucleic acid sequence database (Nt) | 18 801 | 44.5 |
| Tokyo Encyclopedia of Genes and Genomes (KO) | 12 046 | 28.5 |
| Protein sequence database (Swiss-Prot) | 18 276 | 43.2 |
| Protein family domain database (Pfam) | 14 248 | 33.7 |
| Gene Ontology Data (GO) | 19 506 | 46.2 |
| Gene evolutionary lineage: unsupervised orthologous group (eggNOG) | 17 228 | 40.8 |
| Clustering of Eukaryotic Protein Adjacent Classes (KOG) | 15 454 | 36.6 |
| Total single gene cluster (Total unigenes) | 42 264 | 100 |

**Appendix S1. Preparation of MP bait**

**Attachment of MPs to mysid**

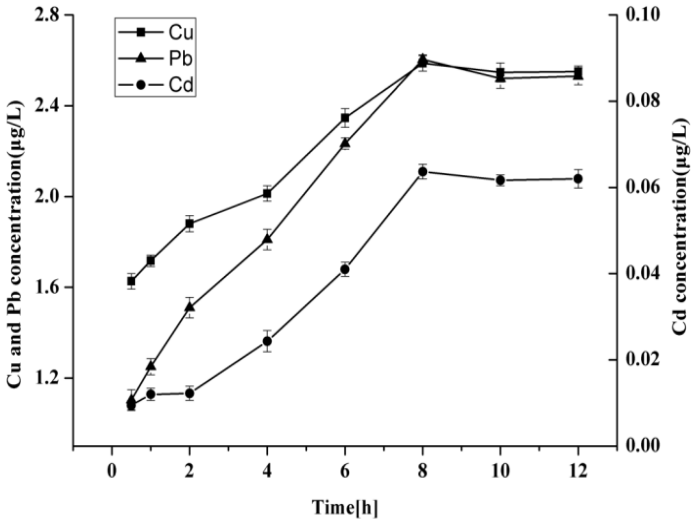
After thawing the frozen mysid shrimp and washing the intact individuals, 10 g of mysid was weighed, and 20 mg of MPs was added and thoroughly mixed. Thereafter, the mixture was poured into a glass jar containing 60 L of seawater, and 1 g of mysid sample was collected at 0, 0.5, 1, 1.5, and 2 h at 25–26 °C. The attachment of MPs to mysid was determined via musing ultrasonic cleaning to elute the MPs particles attached to the mysid individuals, and the MPs were counted under the microscope to determine the number of MPs particles attached to a unit mysid.

**Heavy metal MPs preparation**

MPs (0.10 g) were washed sequentially with 2% HNO3 and ultrapure water, and placed in a 4 L glass jar containing 3 L of filtered seawater, which was covered with aluminum foil. After 36 h aeration at 25–26 °C when all MPs had been fully infiltrated and even distributed in the seawater, a mixture of 0.05 mg/L Cu, 0.01 mg/L Cd and 0.05 mg/L Pb was added, followed by aeration to facilitate the attachment of the heavy metal ions to MPs. At the same time 50–200 MPs were samples at 0.5, 1, 2, 4, 6, 8, and 10 h, and the MPs within the water samples were collected through a 1-μm nitrocellulose filter membrane (Shanghai Xinya Purification Material Factory, China). The concentrations of Cu, Cd, and Pb ions on the surface of MPs on the filter membranes was determined using a PE NexION 300X inductively coupled plasma emission mass spectrometer (ICP-MS). The saturated time and concentration of each heavy metal by microplastic attached were measured.

**Results**

This result indicated that the attachment of heavy metals to the surface of the MPs saturated after 8 h at 25–26 °C. Based on the pre-laboratory basis it is known that there was a gradual increase in the concentrations of heavy metals attached to the surface of MPs with increasing aeration time, peaking 8 h, and plateauing afterwards. The adsorption of centrally located shrimp by MPs leveled off after 1.5 h, when the number of MPs on the bait was 1600/g.



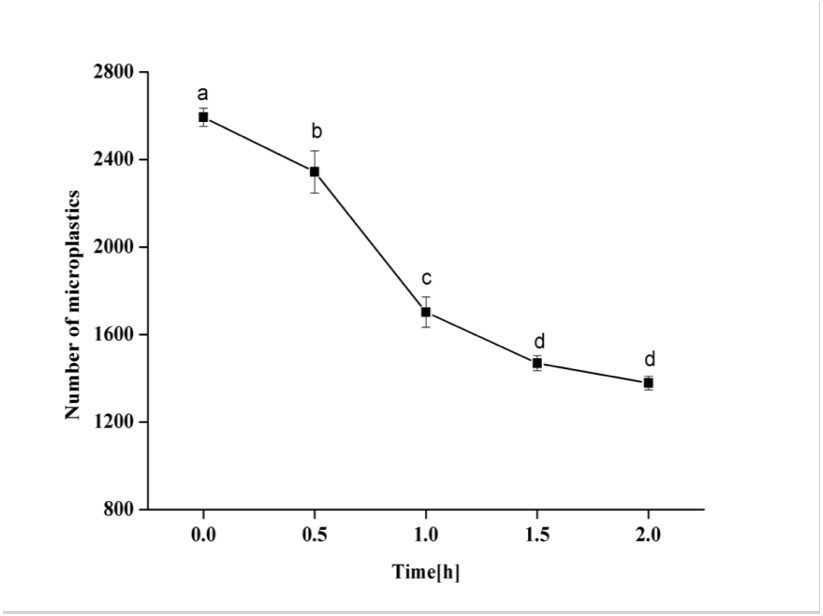



Figure. The attachment dynamics of heavy metal(a) and mysid to PE microplastics(b)
Different letters indicate significant differences at $p < 0.05$.