SEL DIGEST

Abundance cannot represent antibiotic resistance risk

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Fig. 1 Quantification of ARGs risk in soil-plant system.

Antibiotic resistance is increasing in the soil environments (Chen et al., 2019a; Zhu et al., 2019) and transferring into human body via plant microbiome, which can be exacerbated by the food chain, direct contact pathway, and globalization process (Chen et al., 2019b). However, antibiotic resistance is not the newborn from anthropogenic activities, as it has been detected in the permafrost (D’Costa et al., 2011) and human

paleofeces (Wibowo et al., 2021). More interestingly, some of the ancient antibiotic resistance genes did not exhibit the resistance to antibiotics (Martínez et al., 2015), but showed a range of environmental functions, such as liberating phosphorus from phosphate (McRose and Newman, 2021), or encoding efflux pumps (Piddock, 2006). All these evidences indicated that we cannot just assess the health risk of soil

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antibiotic resistome based on their abundance. In *Nature Communications*, Zhang et al. (2021) developed a metagenome-based framework to comprehensively assess the health risk of 2579 antibiotic resistance genes (ARGs) into four ranks by considering the human-associated-enrichment, gene mobility, and host pathogenicity. Only 3% of total assessed ARGs were considered as the top risky ones, which were enriched in the human-associated ecosystems, carried by mobile genetic elements and hosted by pathogens. This framework provided a viable approach to evaluate the health risks of current and future ARGs and made a step forward in comprehensive investigation of antibiotic resistome profile in diverse ecosystems. Based on this framework, future study in soil can focus on how to quantify the health risk, rather than ranking into several groups of each ARGs, and more importantly, trying to replace the abundance with “risk index” to evaluate the health risk of global soil antibiotic resistome as well as their interaction with plant microbiome and human body.

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