

Table S1. 20 μ L reaction system.

Name	Size	Name	Size
5 \times FastPfu Buffer	4 μ L	FastPfu Polymerase	0.4 μ L
2.5 mM dNTPs	2 μ L	BSA	0.2 μ L
Forward Primer(5 μ M)	0.8 μ L	Template DNA	10 ng
Reverse Primer(5 μ M)	0.8 μ L	Replenish dd H ₂ O	20 μ L

Table S2. Attribute table of bacterial community network under Cr stress cultivation mode. The larger the number of edges and nodes, the higher the average degree, the smaller the aggregation coefficient, the smaller the modularity, and the longer the average path length represented, the larger the bacterial network formed, the more complex the interspecific interaction relationship, and the more positive correlation formed on this basis, the more stable the symbiotic network.

Network attribute	Cr stress (sole-cultivated pattern)	Cr stress (two-cultivated pattern)	Cr stress (three-cultivated pattern)
Number of edges	17	36	11
Number of nodes	9	11	11
Average degree	1.93	3.47	1.68
Clustering coefficient	0.57	0.69	0.39
Modularity	0.72	0.86	0.51
Average path length	1.53	3.08	1.36

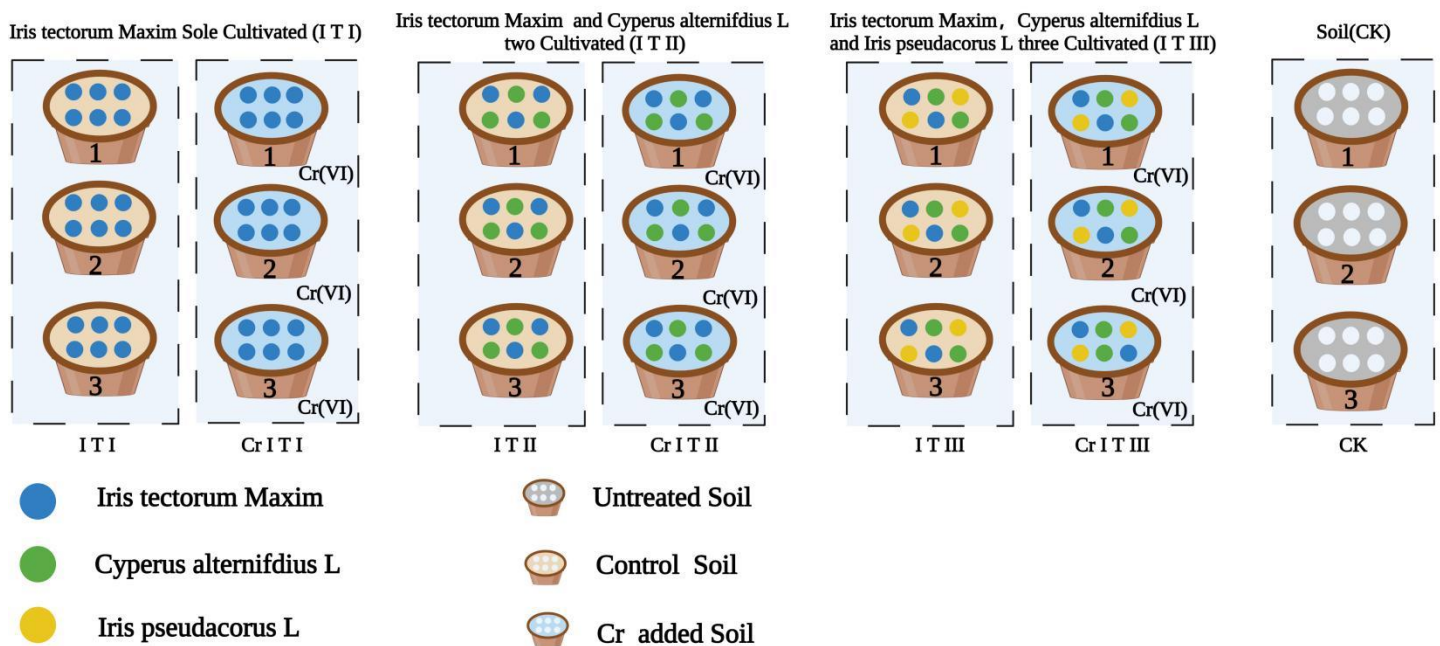


Figure S1. *I. tectorum* pot experiment design. The sole cultivation of *I. tectorum* is ITI group, while of that is CrITI group with adding Cr(VI) 200mg kg⁻¹; The two mixed cultivation of *I. tectorum* and *Cyperus alternifolius* are ITII group, while of those are CrITII group with adding Cr(VI) 200mg kg⁻¹; The three mixed cultivation of *I. tectorum*, *Cyperus alternifolius*, and *Iris pseudacorus* are ITIII group, while of those are CrITIII group with adding Cr(VI) 200mg kg⁻¹; Only the bulk of soil is CK group. There is the above sample group within three repeated samples.

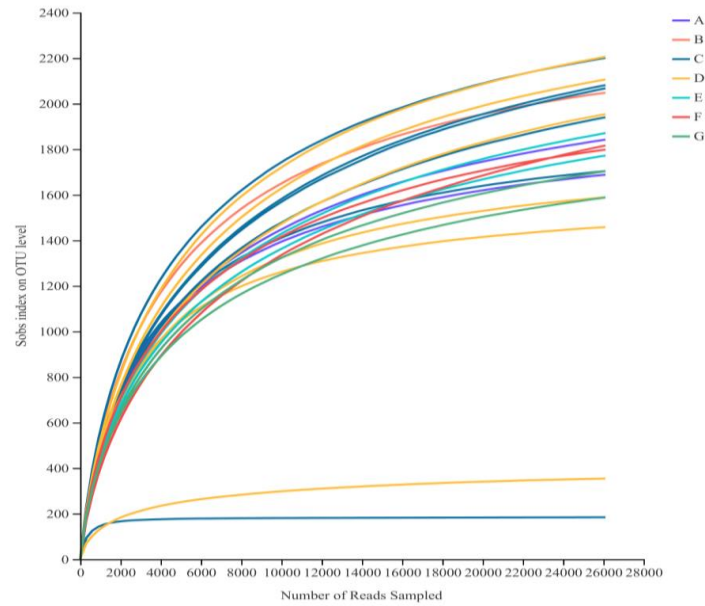


Figure S2. Bacterial community dilution curve of soil sample. The Alpha diversity index was used as the ordinate to draw the curve, and whether the amount of sequencing data was sufficient was judged according to whether the curve was flat. A, C, and E were the control group without Cr in *I. tectorum* single, double, and three plants, respectively. B, D, and F were polluted groups with *I. tectorum* single, double and triple Cr treatments, respectively. G is for unplanted and bulk soil (CK).

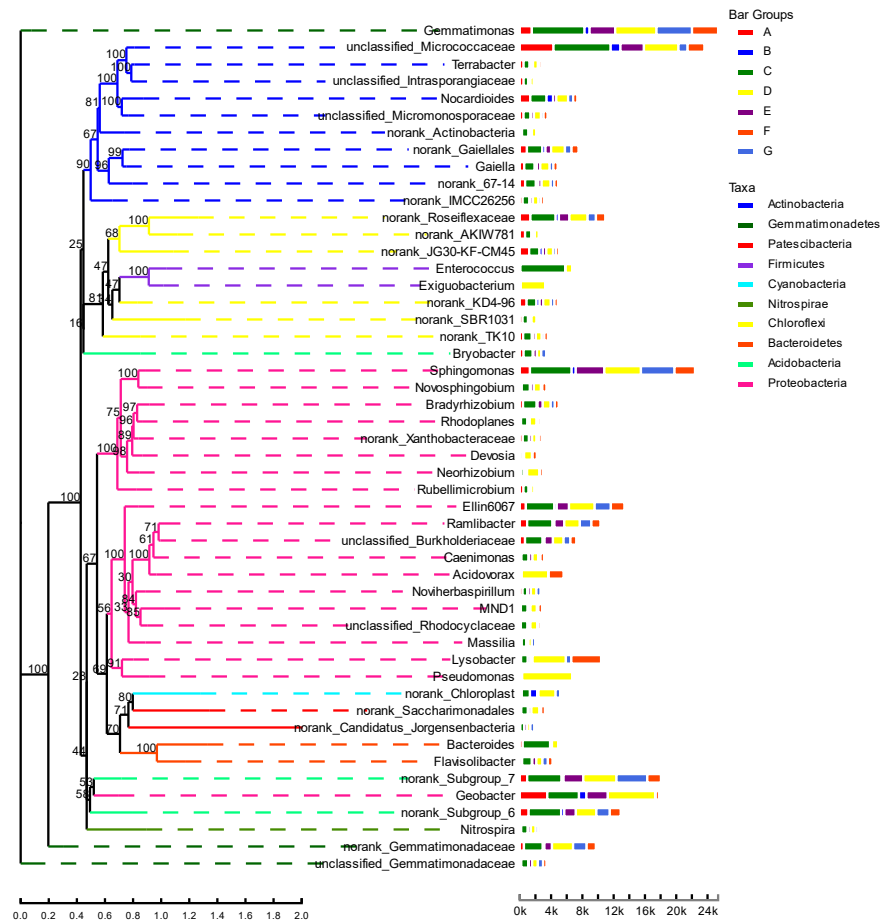


Figure S3. Evolution tree of rhizosphere microbial community of *I. tectorum*. On the left is the phylogenetic evolutionary tree. Each branch represents a species, and the branches are colored according to the higher taxonomic level to which the species belongs. The length of the branches is the

evolutionary distance between the two species, that is, the degree of species difference. The bar chart on the right shows the proportion of Reads in different groups.

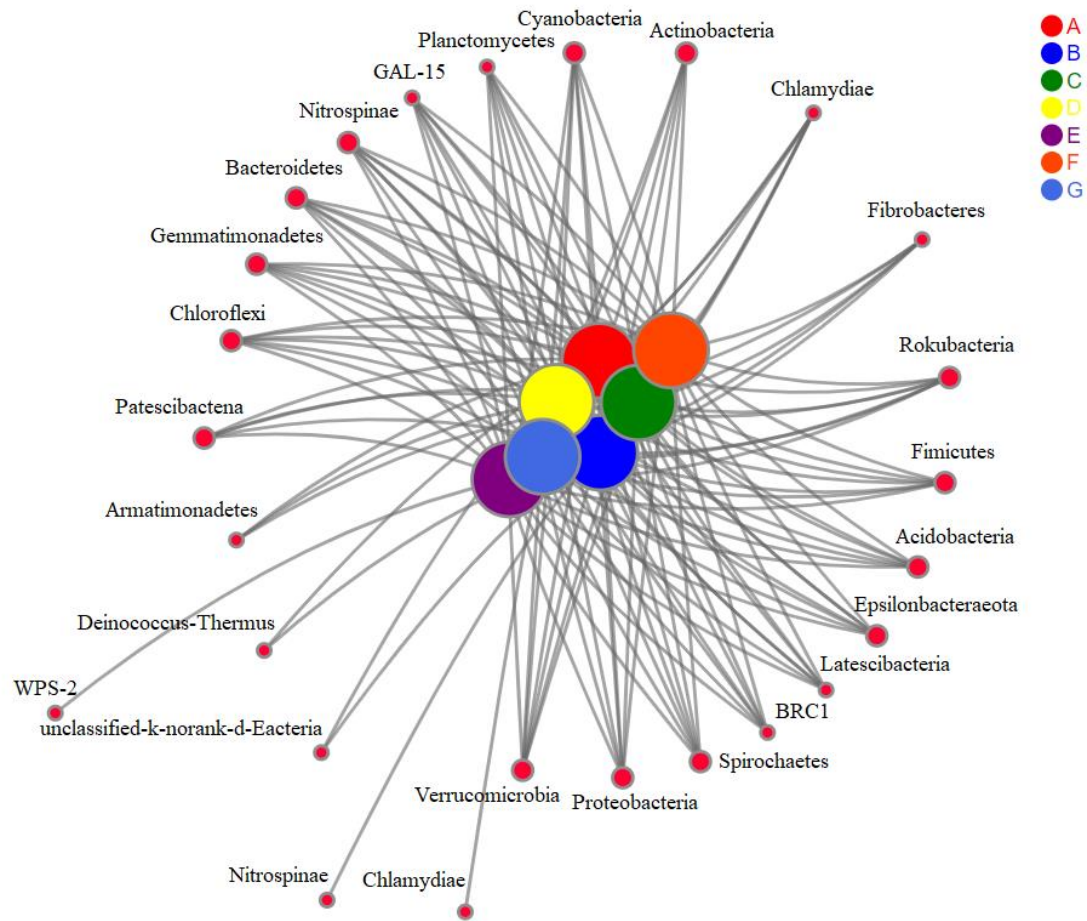


Figure S4. Collinear network graph. It mainly reflects the co-existence of species in environmental samples. A, C, and E were the control group without Cr in *I. tectorum* single, double, and three plants, respectively. B, D, and F were polluted groups with *I. tectorum* single, double and triple Cr treatments, respectively. G is for unplanted and bulk soil (CK).