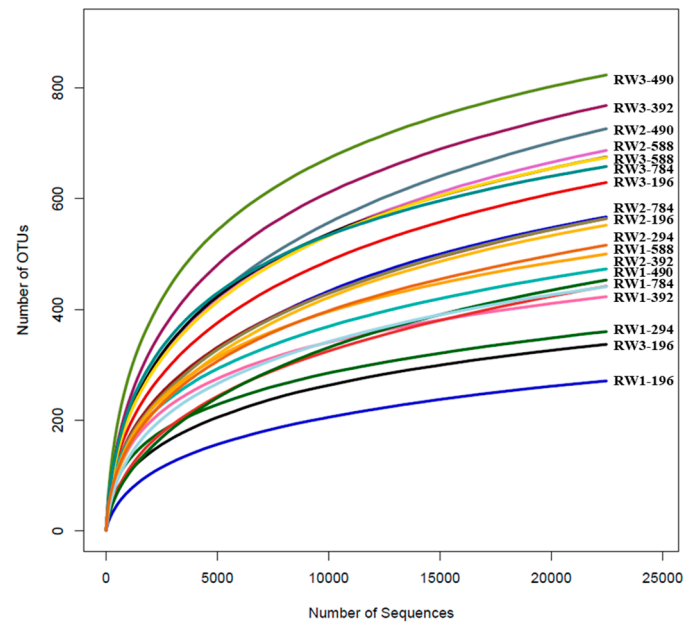
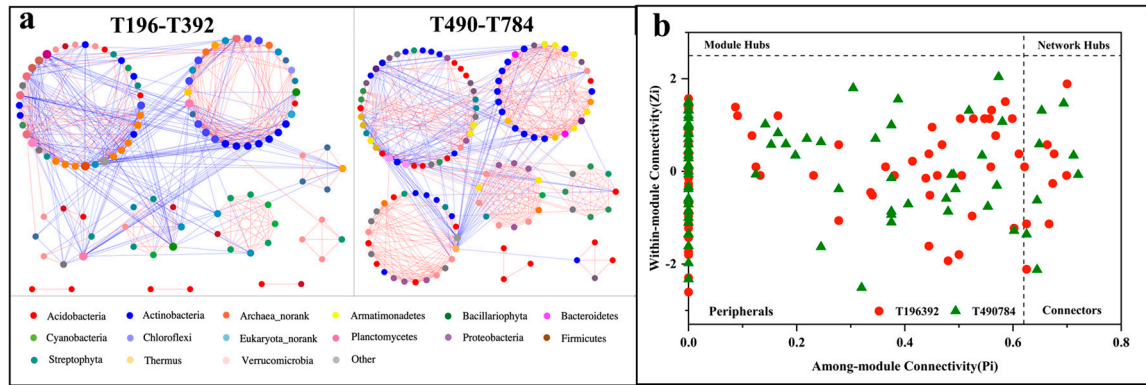


**Figure S1.** Schematic diagram of three sewage treatment processes and reclaimed water agricultural micro-irrigation system.



**Figure S2.** Rarefaction curve



**Figure S3.** Interaction of bacterial networks in biofilms. (a) Visible co-occurrence networks of microorganisms in biofilms formed during T196-T392 and T490-T784, respectively. Red links indicate negative connections and blue links indicate positive connections between the OTUs; (e) Zi-Pi plots based on the topologic roles under different time conditions.

**Table S1** Water quality indexes (mg/L)

Water quality index	RW1	RW2	RW3
Total number of bacteria (cells×ml <sup>-1</sup> )	(8.2~9.5) ×10 <sup>4</sup>	(1.4~3.8) ×10 <sup>4</sup>	(9.3~15.8) ×10 <sup>4</sup>
COD <sub>Cr</sub>	54.5~60.8	36.9~45.2	51.2~59.6
BOD <sub>5</sub>	10.9~16.3	5.8~8.7	12.8~20.9
Total Nitrogen (TN)	22.8~28.5	20.7~24.7	24.9~32.1
Total Phosphorus (TP)	2.62~4.02	0.28~2.57	3.77~4.15
Suspended Substance (SS)	21.2~26.9	13.4~15.7	19.2~23.5
Total Hardness (TH)	280.3~320.9	153.5~195.8	73.1~92.4
pH	7.8~8.3	7.3~8.6	7.4~8.8
CO <sub>3</sub> <sup>2-</sup> +HCO <sub>3</sub> <sup>-</sup> (TC)	166~260	190~274	287~387
Cl <sup>-</sup>	106~125	100~115	50.3~66
SO <sub>4</sub> <sup>2-</sup>	91.1~109.5	85~98	101~119
NO <sub>3</sub> <sup>-</sup>	1.61~3.25	0.27~2.45	3.25~3.64
Ca <sup>2+</sup>	45.8~67.5	37.6~50.6	12.1~18.3
Mg <sup>+</sup>	15.9~26.0	13.4~20.5	8.87~15.2
Fe <sup>3+</sup>	0.02~0.98	0.07~0.25	0.02~0.28
Mn <sup>2+</sup>	0.028~0.019	<0.001	<0.001

**Table S2.** The relative abundances and standard errors of bacteria in phylum, class, order, family and genus (%) (490h).

Phylum		Chroococcaceae	
Acidobacteria	1.28±0.35	Comamonadaceae	2.62±0.89
Actinobacteria	11.48±1.33	Erythrobacteraceae	1.72±0.20
Bacteroidetes	1.32±0.20	Flavobacteriaceae	0.60±0.14
Chloroflexi	2.08±0.73	Leptolyngbyaceae	0.67±0.35
Cyanobacteria	4.67±1.98	Methylophilaceae	0.58±0.22
Firmicutes	0.83±0.19	Microbacteriaceae	9.10±1.22
Proteobacteria	13.93±1.42	Moraxellaceae	0.46±0.24
Class		Nocardiaceae	
Actinobacteria	11.36±1.34	Planococcaceae	0.55±0.18
Alphaproteobacteria	8.18±0.76	Pseudanabaenaceae	1.33±0.77
Betaproteobacteria	3.69±0.93	Sphingomonadaceae	2.87±0.37
Acidobacteriia	0.31±0.09	Genus	
Flavobacteriia	0.63±0.13	Acinetobacter	0.46±0.24
Gammaproteobacteria	1.72±0.20	Altererythrobacter	1.72±0.20
Bacilli	0.79±0.19	Rhodococcus	1.22±0.37
Cytophagia	0.21±0.09	Chroococcus	0.44±0.34
Order		Flavobacterium	0.43±0.11
Burkholderiales	3.03±0.90	Hydrogenophaga	1.94±0.85
Flavobacteriales	0.60±0.14	Leptolyngbya	0.60±0.31
Micrococcales	9.20±1.23	Leucobacter	0.68±0.13
Pseudomonadales	0.79±0.24	Methylophilus	0.58±0.22
Rhizobiales	0.99±0.17	Microbacterium	6.42±0.95
Sphingomonadales	4.59±0.46	Phreatobacter	0.41±0.08
Synechococcales	2.09±1.01	Pseudomonas	0.33±0.08
Corynebacteriales	1.63±0.42	Sphingomonas	2.09±0.30
Oscillatoriales	1.66±0.81	Sphingopyxis	0.58±0.20
Family		Yonghaparkia	1.19±0.37
Bradyrhizobiaceae	0.43±0.13		

**Table S3.** Microbial community molecular ecological network topology parameters.

Treatment	Similarity threshold (St)	Network size (n)	R <sup>2</sup> of power law	Average connectivity (avgK)	Average clustering coefficient (avgCC)	Average path distance (GD)	Modularity	Module No.
T196-T392	0.830	108	0.325	12.241	0.395	2.675	0.388	10
T490-T784	0.830	123	0.294	10.862	0.472	2.900	0.525	7