

Supplementary 1a. Mathematical modelling for DMH transdermal patches F1–F5 (EC–PVP).

Modelling	Formulae	Parameters	R ² adjusted	AIC	MSC
Zero-Order	F1	k0=6.630	0.1788	84.35	-0.76
	F2	k0=8.939	0.4145	88.09	-0.29
	F3	k0=11.250	-0.5013	100.77	-1.81
	F4	k0=10.536	-1.1067	102.05	-2.67
	F5	k0=10.978	-1.0667	102.88	-2.58
First-Order	F1	k1=0.097	0.4636	79.66	-0.34
	F2	k1=0.159	0.7518	78.65	0.56
	F3	k1=0.328	0.4861	88.98	-0.74
	F4	k1=0.274	-0.0552	94.45	-1.98
	F5	k1=0.324	0.0447	94.39	-1.81
Higuchi	F1	kH=17.861	0.8522	65.48	0.94
	F2	kH=23.891	0.9356	63.81	1.90
	F3	kH=30.901	0.6141	85.83	-0.45
	F4	kH=29.206	0.2845	90.18	-1.59
	F5	kH=30.419	0.3001	90.97	-1.50
Hixson Crowell	F1	kHC=0.029	0.3804	81.25	-0.48
	F2	kHC=0.044	0.6685	81.83	0.27
	F3	kHC=0.083	0.2813	92.67	-1.08
	F4	kHC=0.068	-0.3197	96.91	-2.20
	F5	kHC=0.078	-0.2311	97.18	-2.06
Korsmeyer-P eppas	F1	kKP=25.658 n=0.290	0.9640	50.77	2.28
	F2	kKP=30.913 n=0.352	0.9831	49.92	3.17
	F3	kKP=53.031 n=0.184	0.9907	45.64	3.19
	F4	kKP=57.117 n=0.103	0.9862	47.56	2.28
	F5	kKP=59.077 n=0.107	0.9781	53.72	1.88
Hopfenberg	F1	kHB=0.000 n=1370.731	0.4038	81.66	-0.52
	F2	kHB=0.000 n=2067.878	0.7241	80.65	0.37
	F3	kHB=0.000 n=5320.112	0.4289	90.98	-0.9277
	F4	kHB=0.000	-0.1727	96.45	-2.1636

		n=3632.980			
	F5	kHB=0.000 n=4936.651	-0.0617	96.40	-1.99
Baker-Lonsdale	F1	kBL=0.007	0.8937	61.8571	1.27
	F2	kBL=0.014	0.9694	55.61	2.65
	F3	kBL=0.029	0.8163	77.66	0.28
	F4	kBL=0.025	0.5383	85.36	-1.15
	F5	kBL=0.029	0.5667	85.70	-1.02
Makoid-Banakar	F1	kMB=25.580 n=0.227 k=-0.018	0.9625	51.93	2.17
	F2	kMB=30.950 n=0.321 k=-0.008	0.9816	51.60	3.01
	F3	kMB=53.212 n=0.211 k=0.008	0.9904	46.74	3.09
	F4	kMB=56.042 n=0.019 k=-0.026	0.9953	36.52	3.28
	F5	kMB=58.028 n=0.031 k=-0.024	0.9840	50.93	2.13

R²: Correlation Coefficient; k: Rate Constant; AIC: Akaike Information Criterion; and MSC: Model Selection Criterion. Makoid-Banakar model is the most suitable since R² is the highest and nearest to 1 compared to other models. The Korsmeyer-Peppas release exponent (n) value is <0.5, indicating the Fickian diffusion mechanism for all the formulas.

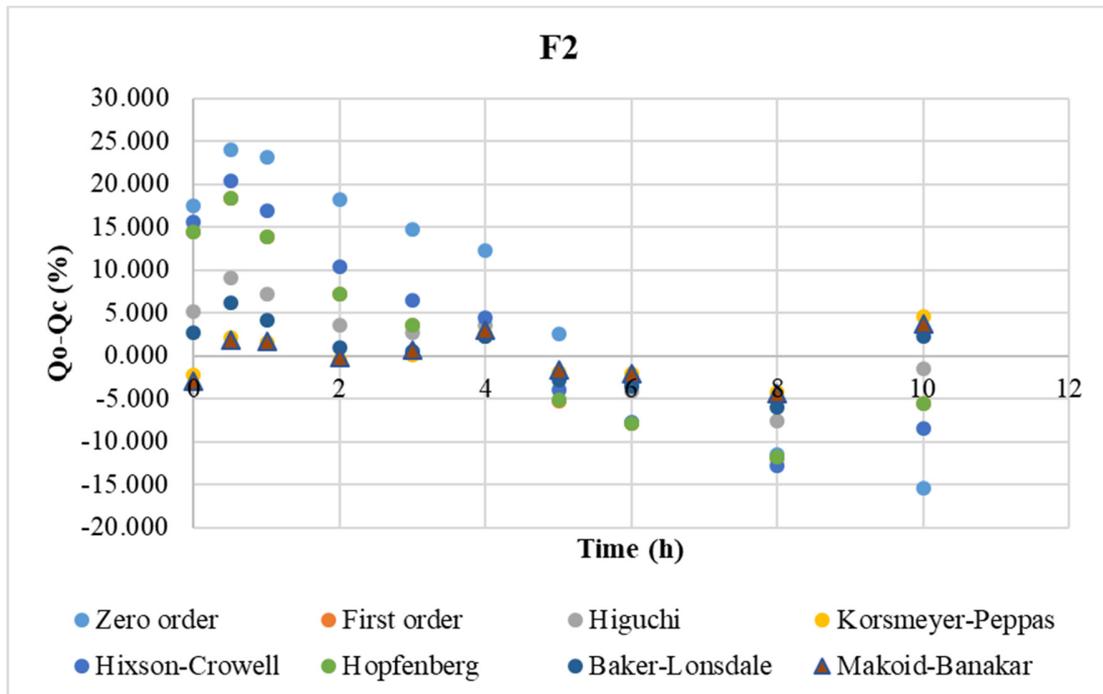
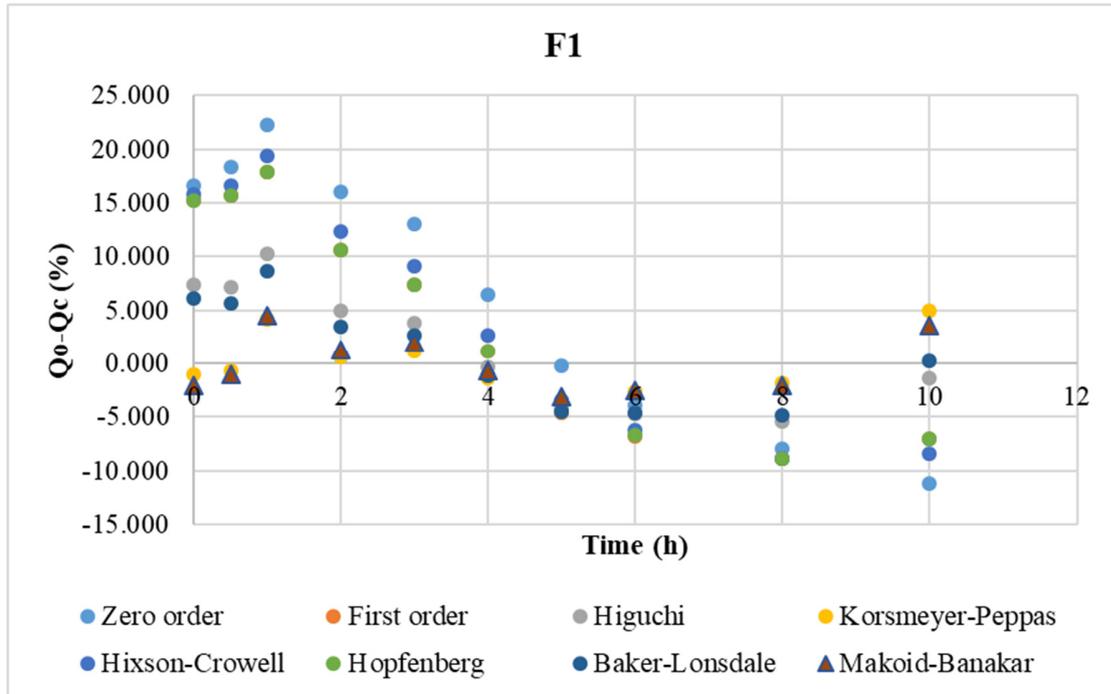
Supplementary 1b. Mathematical modelling For DMH transdermal patches F1–F5 (ES–HPMC).

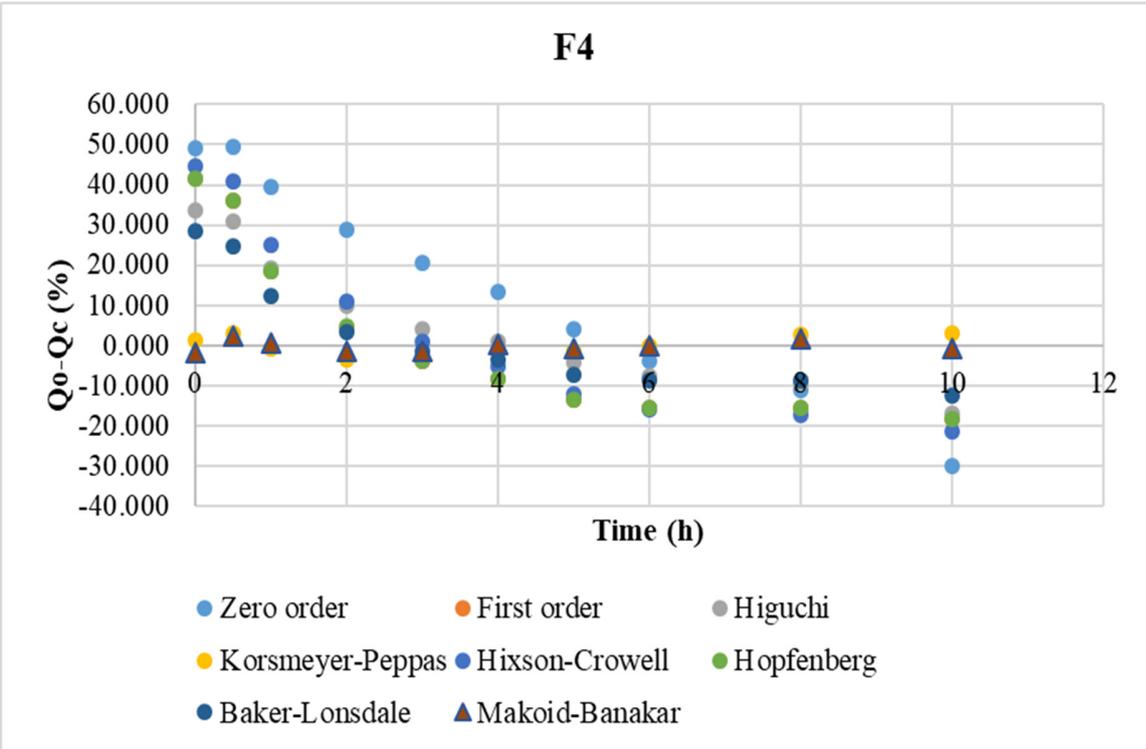
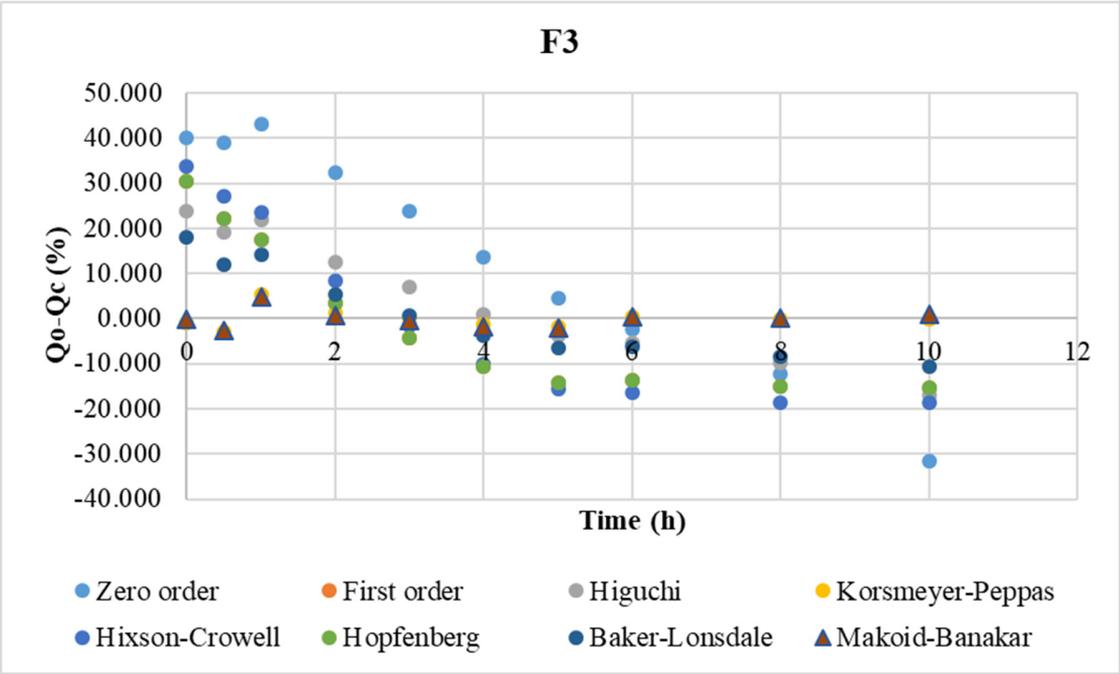
Modelling (ES–HPMC)	Formulae	Parameters	R ² adjusted	AIC	MSC
Zero–Order	F1	k0=9.234	0.1930	82.40	-0.77
	F2	k0=11.573	-0.4798	91.60	-1.78
	F3	k0=12.660	-0.3973	92.88	-1.69
	F4	k0=13.305	-0.3857	93.76	-1.68
	F5	k0=13.926	-0.6508	96.11	-2.02
First–Order	F1	k1=0.175	0.6545	73.92	0.07
	F2	k1=0.366	0.5656	79.34	-0.56
	F3	k1=0.513	0.6586	78.78	-0.28
	F4	k1=0.635	0.7545	76.45	0.04
	F5	k1=1.043	0.8287	73.45	0.24
Higuchi	F1	kH=24.863	0.8828	63.11	1.15
	F2	kH=31.868	0.6467	77.27	-0.35
	F3	kH=34.718	0.6607	78.72	-0.27
	F4	kH=36.493	0.6775	79.18	-0.22
	F5	kH=38.488	0.5667	82.73	-0.68
Hixson Crowell	F1	kHC=0.048	0.5488	76.59	-0.19
	F2	kHC=0.097	0.3983	82.60	-0.88
	F3	kHC=0.127	0.5094	82.41	-0.64
	F4	kHC=0.139	0.6215	80.78	-0.38
	F5	kHC=0.150	0.6059	81.78	-0.59
Korsmeyer–Peppas	F1	kKP=34.720 n=0.302	0.9839	44.08	3.05
	F2	kKP=53.116 n=0.194	0.9977	27.58	4.61
	F3	kKP=57.429 n=0.198	0.9842	48.90	2.70
	F4	kKP=59.989 n=0.202	0.9941	39.93	3.69
	F5	kKP=66.594 n=0.171	0.9979	30.08	4.57
Hopfenberg	F1	kHB=0 n=3545.648	0.6112	75.92	-0.12
	F2	kHB=0 n=3403.549	0.5111	81.34	-0.76
	F3	kHB=0 n=5201.056	0.6159	80.79	-0.48
	F4	kHB=0	0.7238	78.45	-0.15

		n=6167.137			
	F5	kHB=0 n=5645.851	0.8072	75.45	0.04
Baker-Lonsdale	F1	kBL=0.015	0.9395	56.50	1.81
	F2	kBL=0.032	0.8497	68.73	0.49
	F3	kBL=0.043	0.8655	69.47	0.64
	F4	kBL=0.050	0.9024	67.23	0.96
	F5	kBL=0.050	0.8460	72.38	0.34
Makoid-Banakar	F1	kMB=34.807 n=0.210 k=-0.024	0.9879	41.89	3.27
	F2	kMB=53.107 n=0.192 k=0.000	0.9974	29.56	4.41
	F3	kMB=56.843 n=0.120 k=-0.023	0.9893	45.67	3.02
	F4	kMB=59.618 n=0.143 k=-0.017	0.9973	32.96	4.39
	F5	kMB=66.407 n=0.151 k=-0.006	0.9981	29.72	4.61

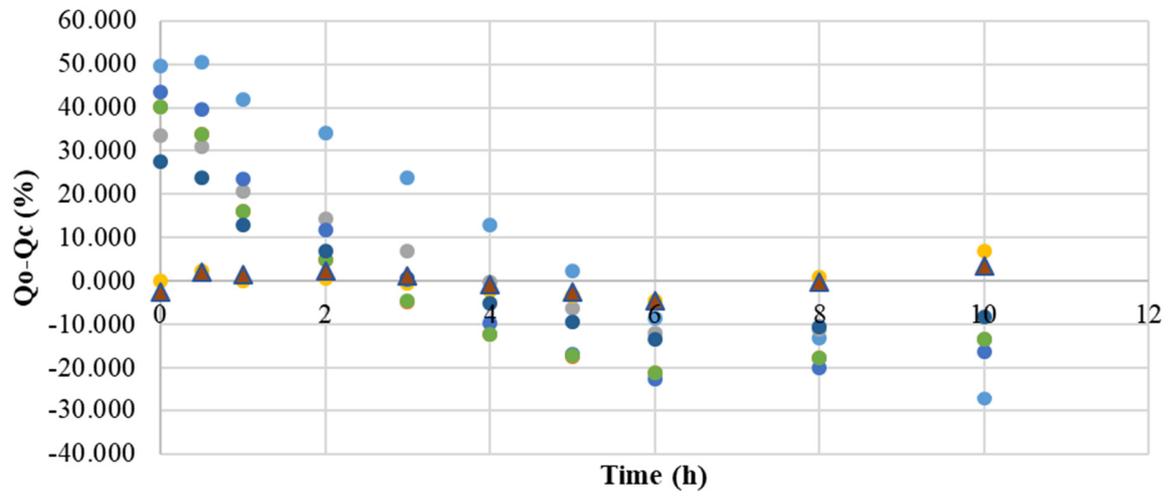
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Supplementary 2a. Goodness of fit (GOF) evaluations based on correlation of residual versus time indicating that the makoid-banakar model is the most suitable model to explain DMH dissolution data from EC-PVP containing patches.



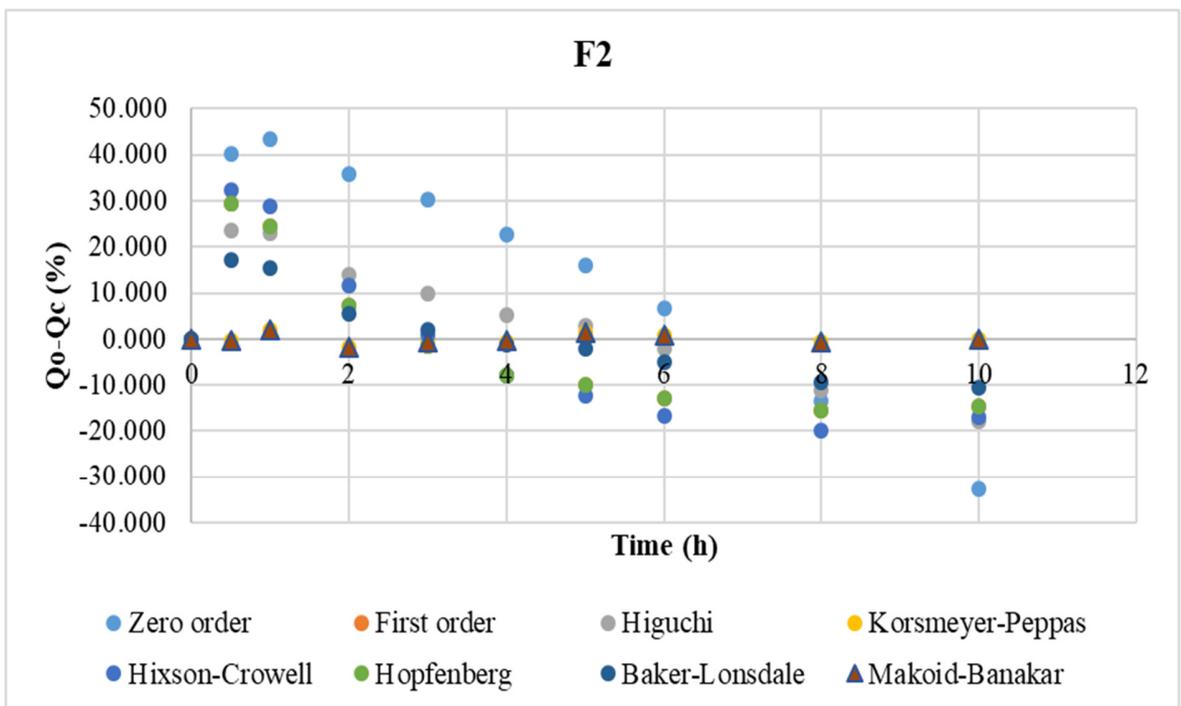
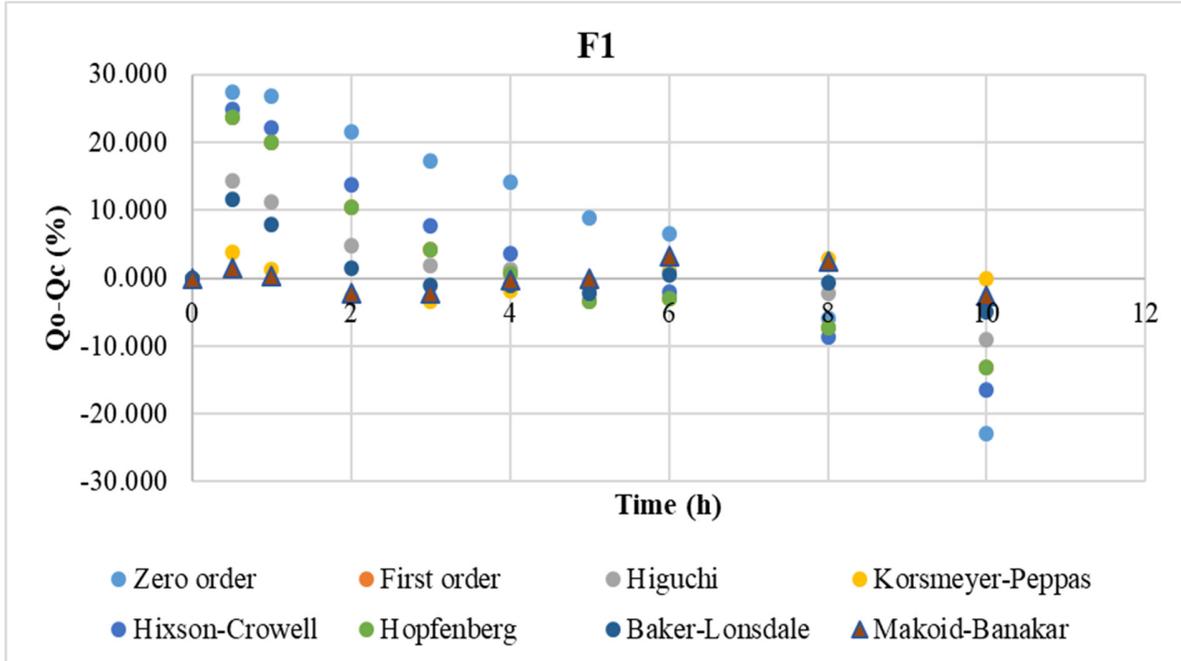


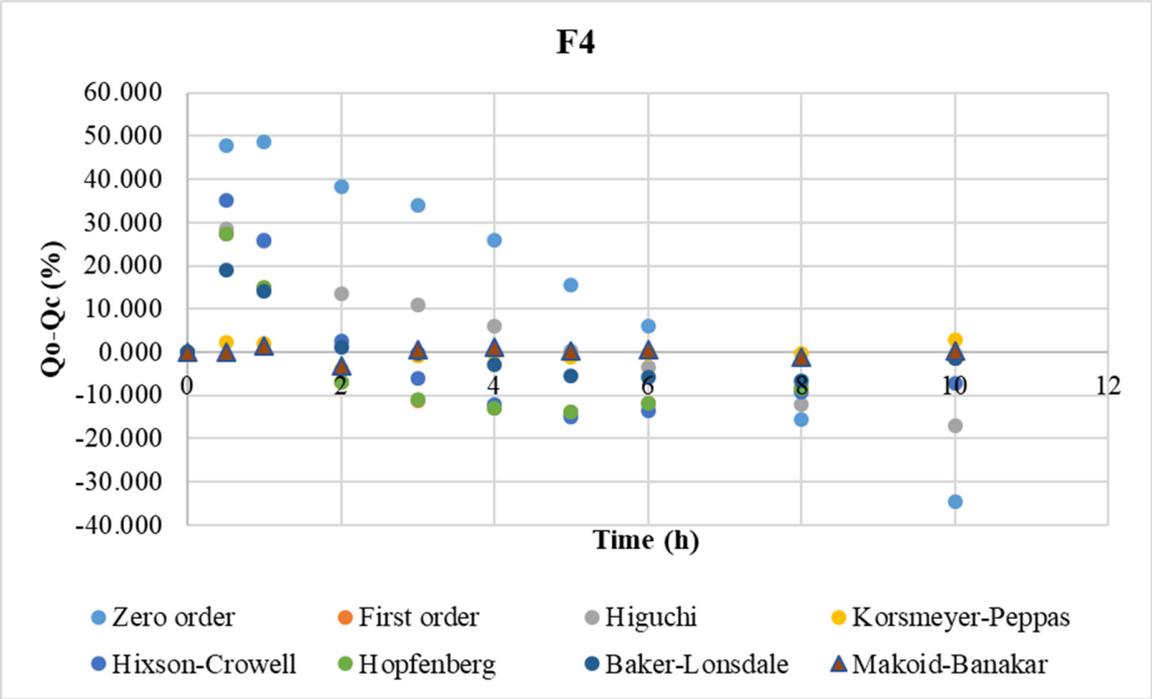
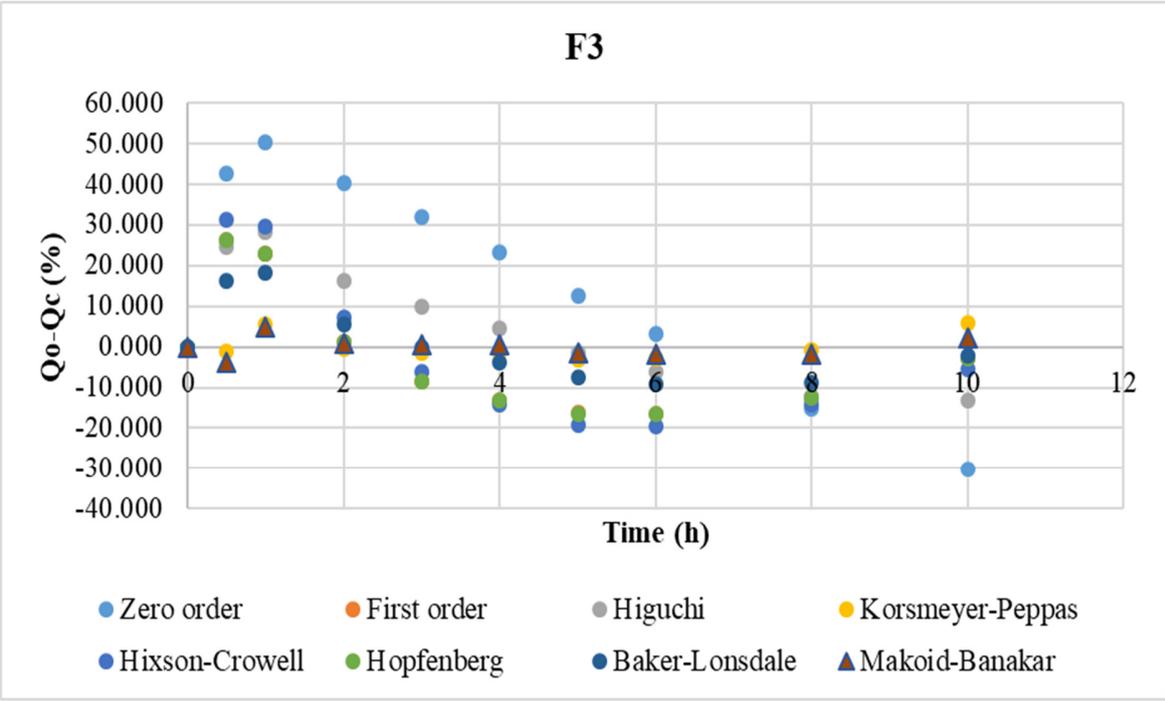
F5



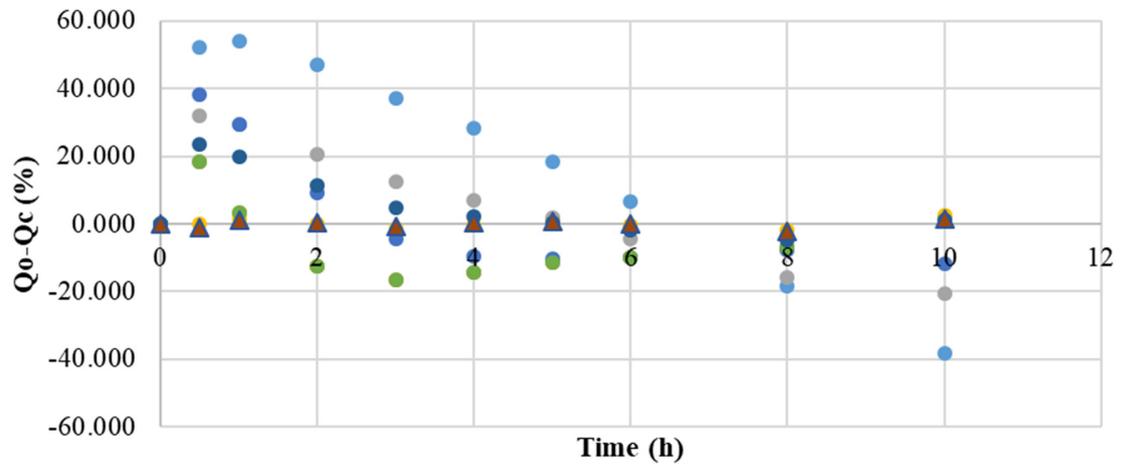
- Zero order
- First order
- Higuchi
- Korsmeyer-Peppas
- Hixson-Crowell
- Hopfenberg
- Baker-Lonsdale
- ▲ Makoid-Banakar

Supplementary 2b. Goodness of fit (GOF) evaluations based on correlation of residual versus time indicating that the makoid-banakar model is the most suitable model to explain DMH dissolution data from ES-HPMC containing patches.





F5



- Zero order
- First order
- Higuchi
- Korsmeyer-Peppas
- Hixson-Crowell
- Hopfenberg
- Baker-Lonsdale
- ▲ Makoid-Banakar