Supplementary Materials for Modeling the competing effects of the immune system and EMT on epithelial cancers

Daniel R. Bergman[1], Matthew Karikomi [1], Qing Nie [1,2,*] and Adam L. MacLean [3,*]

[1]Department of Mathematics, University of California, Irvine, Irvine, CA 92697, USA
[2]Department of Cell and Developmental Biology, University of California, Irvine, Irvine, CA 92697, USA
[3]Department of Biological Sciences, University of Southern California, Los Angeles, CA 90089, USA
*Correspondence: qnie@uci.edu (Q.N.); macleana@usc.edu (A.L.M.)

Contents

1 Definition of parameters specifying the model **2**

2 Parameter values used for simulation **3**

1 Definition of parameters specifying the model

Name	Description
p	proliferation rate of tissue cells
d_C	death rate of tissue cells
Δ_{MIE}	mesenchymal immune evasion
Δ_{MGA}	mesenchymal growth arrest
Δ_A	mutant cells decreased apoptosis
Δ_{IE}	mutant cells increased immune evasion
Δ_P	mutant cells increased proliferation
K_0	EC50 term for negative feedback of tissue cells on own proliferation
K_1	EC50 term for probability of NK cell finding mutant cell
K_2	EC50 term for Treg inhibition of cytotoxic functions
K_3	EC50 term for how much TGF-β each cell has
K_4	EC50 term for TGF-β activation of Tregs
E_{NK}	rate of NKs clearing mutants
E_{CTL}	rate of CTLs clearing mutants
σ_{NK}	NK source rate
σ_{CTL}	CTL source rate per cleared mutant cell
σ_{Treg}	Treg source rate per cleared mutant cell
d_{NK}	NK death rate
d_{CTL}	CTL death rate
d_{Treg}	Treg death rate
k_{EMT}	EMT/MET rate
σ	standard deviation of noise in TGF-β each cell receives
τ_{max}	max amount of TGF-β any cell can receive
τ_{MUT}	rate of TGF-β production by mutant cells
τ_{Treg}	rate of TGF-β production by Treg

Table S1: The model parameter names and descriptions. Note that many of these values are affected by the inflammation state of the system.

2 Parameter values used for simulation

Name	Description	INFL Low Value
p	weight of proliferation for tissue cells	0.28
d_C	weight of apoptosis for tissue cells	0.14
Δ_{MIE}	MIE	0.6
Δ_{MGA}	MGA	0.2
Δ_A	proportional decrease to weight of apoptosis for cells with mutated apoptosis pathway	0.3
Δ_{IE}	proportional increase to weight of immune evasion for cells with mutated immune evasion pathway	0.48
Δ_P	proportional increase to weight of proliferation for cells with mutated proliferation pathway	0.36
K_0	EC50 term for negative feedback of tissue cells on own proliferation	80 cells
K_1	EC50 term for probability of NK cell finding mutant cell	8 cells
K_2	EC50 term for Treg inhibition of cytotoxic functions	5 cells / volume
K_3	EC50 term for cumulative absorption of TGF-β	200 amount / volume
K_4	EC50 term for TGF-β activation of Tregs	50 amount / volume
E_{NK}	weight of NKs clearing mutants	10
E_{CTL}	weight of CTLs clearing mutants	200
σ_{NK}	NK source rate	1.3 cells / cycle
σ_{CTL}	CTL source rate per cleared mutant cell	100 cells / (cleared mutants × c
σ_{Treg}	Treg source rate per cleared mutant cell	200 cells / (cleared mutants × concentration
d_{NK}	NK death rate	0.13 / cycle
d_{CTL}	CTL death rate	0.0260 / cycle
d_{Treg}	Treg death rate	0.0260 / cycle
k_{EMT}	EMT/MET rate	0.01 / concentration of TGF
σ	standard deviation of noise in TGF-β each cell receives	6 concentration of TGF-β
τ_{max}	max amount of TGF-β any cell can receive	500 concentration of TGF-β
τ_{MUT}	rate of TGF-β production by mutant cells	0.05 concentration of TGF-β / cel
τ_{Treg}	rate of TGF-β production by Treg	0.5 concentration of TGF-β / cell
	RP Cancer Line	0.5
	INFL High Duration	30 cycles
	INFL Low Duration	30 cycles
	Mes Threshold	0.7
	maximum initial mutation damage after warmup	0.01
	increase in probability to mutate for non-mutating proliferating cells	0.0001

Table S2: The model parameter names, descriptions, and values during both low and high inflammation. Parameters with only one value do not change with the inflammatory state.

Name	Description	INFL Low Value	INFL High Value
p	proliferation rate of tissue cells	0.28	
d_C	death rate of tissue cells	0.14	
Δ_{MIE}	MIE	0.6	
Δ_{MGA}	MGA	0.2	
Δ_A	mutant cells decreased apoptosis	0.3	
Δ_{IE}	mutant cells increased immune evasion	0.48	
Δ_P	mutant cells increased proliferation	0.36	
K_0	EC50 term for negative feedback of tissue cells on own proliferation	80	
K_1	EC50 term for probability of NK cell finding mutant cell	8	
K_2	EC50 term for Treg inhibition of cytotoxic functions	5	0.025
K_3	EC50 term for how much TGF-β each cell has	200	
K_4	EC50 term for TGF-β activation of Tregs	50	
E_{NK}	rate of NKs clearing mutants	10	30
E_{CTL}	rate of CTLs clearing mutants	200	600
σ_{NK}	NK source rate	1.3	
σ_{CTL}	CTL source rate per cleared mutant cell	100	
σ_{Treg}	Treg source rate per cleared mutant cell	200	
d_{NK}	NK death rate	0.13	
d_{CTL}	CTL death rate	0.0260	
d_{Treg}	Treg death rate	0.0260	
k_{EMT}	EMT/MET rate	0.01	
σ	standard deviation of noise in TGF-β each cell receives	6	
τ_{max}	max amount of TGF-β any cell can receive	500	
τ_{MUT}	rate of TGF-β production by mutant cells	0.05	
τ_{Treg}	rate of TGF-β production by Treg	0.5	
	RP Cancer Line	0.5	
	INFL High Duration	30	
	INFL Low Duration	30	
	Mes Threshold	0.7	
	maximum initial mutation damage after warmup	0.01	
	increase in probability to mutate for non-mutating proliferating cells	0.0001	

Table S3: The model parameter names, descriptions, and values during both low and high inflammation. Parameters with only one value do not change with the inflammatory state.

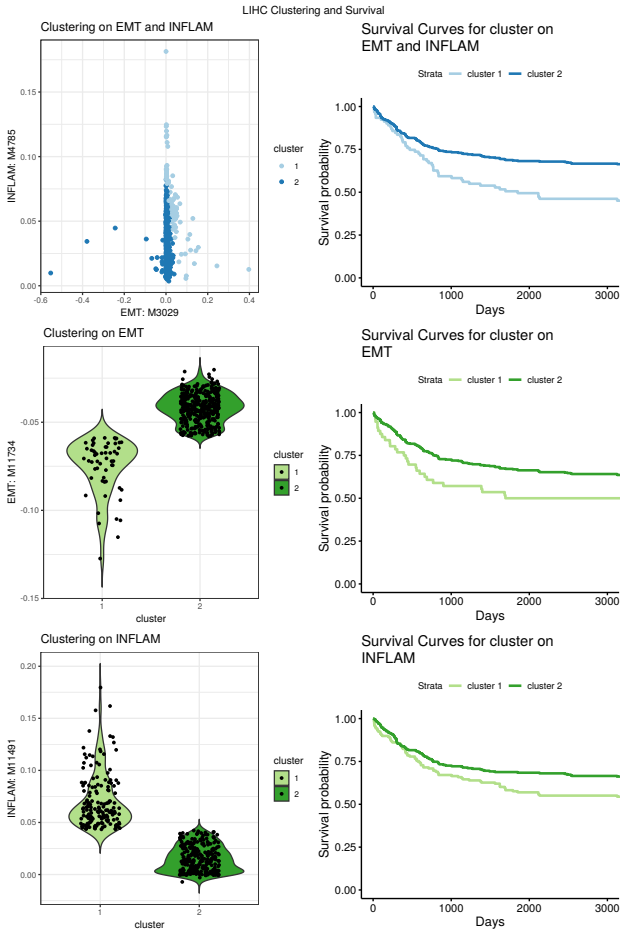

Figure S1: A. K-means clustering of LIHC using gene ontology terms indicative of EMT and inflammation signatures ($k = 2$). B. Survival plots corresponding to the clustering on EMT and inflammation. C. K-means clustering of LIHC using gene ontology terms indicative of an EMT signature ($k = 2$). D. Survival plots corresponding to the clustering on EMT. E. K-means clustering of LIHC using gene ontology terms indicative of inflammation ($k = 2$). F. Survival plots corresponding to the clustering on inflammation.