Cooperation of partially-transformed clones: an invisible force behind the early stages of carcinogenesis

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SUPPLEMENTARY METHODS

S.1. Analytical description of tissue organisation

With the basic assumptions described in **section 3.1** and **Fig. 1**, yhe 1-neighbourhood of an individual cell will contain 6 adjacent cells within the plane and 2 polar cells, one at the top and one at the bottom of the reference cell. The 2-neighbourhood will contain 12 cells within the plane, 6 cells in the above and bottom layers and two polar cells. The 3-neighbourhood will have 18 cells within the plane, 24, 12, 6 and 2 in the other layers. By induction, we infer that the k-neighbourhood of an individual cell in such tessellation is made of ks_0 cells within the plane, the sum of is_0 for each of the above and below layers, with i from 1 to k-1, and the two polar cells:

$$C_k = ks_0 + 2\sum_{i=1}^{k-1} is_0 + 2$$
 Eq. S1.1

To simplify, ks_0 (s_0 here is 6) can be brought within the sum, then allowing to simplify to the correspondent triangular number:

$$C_k = -ks_0 + 2\sum_{i=1}^k is_0 + 2 = k^2s_0 + 2$$
 Eq. S1.2

It should be noted that for intercalated layers, the coordination values can be larger.

Another example, this time including a significant constraint in topology, is represented by the same topology, where only three layers are considered.

$$C_1 = s_0 + 2$$
 Eq. S1.3

$$C_{k>1} = ks_0 + 2(k-1)s_0 = s_0(3k-2)$$
 Eq. S1.4

S.2. Probability of initiation (power function)

Let's assume the probability of tumour initiation is proportional to a concentration gradient, similar to a morphogen, or an oncogenic mitogen/morphogen field decaying as a power function:

$$p_{nk} = \frac{p_{no}}{k^l}$$
 Eq. S.2.1

Where p_{n0} indicate the probability of tumour initiation when cells are attached (the 1-neighbourhood). Therefore, in the case of 3D hexagonal tessellation, we can derive the factor Cp_n :

$$\Omega = \sum_{k=1}^{\infty} \frac{k^2 s_0 + 2}{k^l}$$
 Eq. S.2.2

This sum is carried over an infinite neighbourhood, and the validity of the results will be checked numerically (see **Section 3.2** and **Fig. 2**). First, we can expand p_{tn}:

$$\Omega = s_0 \sum_{k=1}^{\infty} k^{2-l} + 2 \sum_{k=1}^{\infty} k^{-l}$$
 Eq. S.2.3

These series can now be described by Riemann Zeta functions:

$$\Omega = s_0 \zeta(l-2) + 2\zeta(l)$$
 Eq. S.2.4

Let's now consider the thin 3-layer tissue which tessellation was already discussed. In this case, for one cell:

$$\Omega = s_0 + 2 + \sum_{k=2}^{\infty} \frac{s_0(3k-2)}{k^l} = 2 + \sum_{k=1}^{\infty} \frac{s_0(3k-2)}{k^l}$$
 Eq. S.2.5

Following the same process described before, we can obtain:

$$\Omega = 2 - 2s_0 \sum_{k=1}^{\infty} \frac{1}{k^l} + 3s_0 \sum_{k=1}^{\infty} \frac{1}{k^{l-1}}$$
 Eq. S.2.6

And,

$$\Omega = 18\zeta(l-1) - 12\zeta(l) + 2$$
 Eq. S.2.7

This describe the probability of transformation for a cell in the middle layer. We can approximate the result over the tissue equal to this value by N/3 (middle layer) and with half contribution for the top and bottom layer resulting in

$$\Omega = 12\zeta(l-1) - 8\zeta(l) + 4/3$$
 Eq. S.2.8

S.3. Probability of initiation (exponential function)

Let's now assume the oncogenic field decays as an exponential function:

$$p_{nk} = p_{n0}e^{-(k-1)k_c^{-1}}$$
 Eq. S.3.1

Where k_c is a decay constant expressed in terms of k-neighbourhood for simplicity. If two cells are in contact, the probability of initiation will be p_{n0} as per definition of p_{n0} . When cells are at a k_c+1 distance, this probability is 1/e lower, *i.e.* ~30% lower. In the case of 3D hexagonal tessellation, the factor Cp_n can be now expressed as:

$$\Omega = \sum_{k=1}^{\infty} (k^2 s_0 + 2) e^{-(k-1)k_c^{-1}}$$
 Eq. S.3.2

Or the sum of the series:

$$\Omega = 2\sum_{k=1}^{\infty} e^{-(k-1)k_c^{-1}} + s_0 \sum_{k=1}^{\infty} k^2 e^{-(k-1)k_c^{-1}}$$
 Eq. S.3.3

The first series converges to:

$$\sum_{k=1}^{\infty} e^{-(k-1)k_c^{-1}} = \frac{e^{k_c^{-1}}}{e^{k_c^{-1}} - 1}$$
 Eq. S.3.4

The second series can be represented as:

$$\sum_{k=1}^{\infty} k^2 e^{-(k-1)k_c^{-1}} = e^{k_c^{-1}} \sum_{k=1}^{\infty} k^2 e^{-k/k_c} = \frac{e^{2k_c^{-1}} \left(e^{k_c^{-1}} + 1 \right)}{\left[e^{k_c^{-1}} - 1 \right]^3}$$
 Eq. S.3.5

Therefore,

$$\Omega = e^{k_c^{-1}} \frac{(2+s_0)e^{2k_c^{-1}} + (4+s_0)e^{k_c^{-1}} + 2}{\left[e^{k_c^{-1}} - 1\right]^3}$$
 Eq. S.3.6

With $s_0 = 6$, once again to confirm mathematical consistency, $\lim_{k_c \to 0} \Omega = 8$, as in the case where only adjacent cells are important. Shallower decays will again increase this value (see **Fig. 2**).

S.4 Probability of initiation (generalisation)

We have characterised the oncogenic field in relation to typical descriptions of morphogenic gradients [22]. While relevant for specific cases, steady-state concentration gradients of shared resources in space, generated by passive diffusion and linear or non-linear degradation, can adopt different shapes. One useful analytical description is represented by concentrations that decay as the product of exponential and power-law functions, for instance as:

$$p_{nk} = \frac{p_{n0}}{k^l} e^{-(k-1)k_c^{-1}}$$
 Eq. S.4.1

With the same formalism and strategies described in **Sections S.2** and **S.3** we can show that, for a three-dimensional tissue:

$$\Omega = \sum_{k=1}^{\infty} (k^2 s_0 + 2) k^{-l} e^{-(k-1)k_c^{-1}}$$
 Eq. S.4.2

This analytical representation of Ω can be expressed as sums of polylogarithm functions:

$$\Omega = e^{k_c^{-1}} \left[2Li_l(e^{-k_c^{-1}}) + s_0 Li_{l-2}(e^{-k_c^{-1}}) \right]$$
 Eq. S.4.3

This representation converges to those shown in **Sections S.2** and **S.3** in the cases where k_c is very large or where l is very small, respectively, i.e. when the power-law or the exponential decay components are negligible. The case l=1 represents an oncogenic field induced by continuous point-sources in an unconstrained three-dimensional space in the presence of linear degradation. In this geometry:

$$\Omega = e^{k_c^{-1}} \left[-2\log(1 - e^{-k_c^{-1}}) + s_0 \frac{e^{-k_c^{-1}}}{\left(1 - e^{-k_c^{-1}}\right)^2} \right]$$
 Eq. S.4.4

S.5. Cell-autonomous time-horizon (discrete-time Markov chain)

The mutational process illustrated in this work can be modelled as a discrete-time Markov process (see also **Sup. File 'firstpassageproblem_v2.nb'** or '**firstpassageproblem_v2.pdf'** in the GitHub repository *alesposito/CloE-PE* [50] for the Mathematica Notebook used in this work and the **peer-review open documentation** for related discussion). Each cell is described by four states: wild-type (W), mutant X, mutant Y, and double-mutant (XY). At any given time, the transition matrix between these states is:

$$T = \begin{pmatrix} 1 - (x+y)\rho_0 - xy\rho_0^2 & x\rho_0 & y\rho_0 & xy\rho_0^2 \\ 0 & 1 - y\rho_0 & 0 & y\rho_0 \\ 0 & 0 & 1 - x\rho_0 & x\rho_0 \\ 0 & 0 & 0 & 1 \end{pmatrix}$$
 Eq. S.5.1

where the probability of acquiring the mutation X or Y are independent and directly proportional to the mutational rate ρ_0 with proportionality constants x and y, respectively. Initially, the system is described by the state vector $S_0 = \begin{pmatrix} 1 & 0 & 0 \end{pmatrix}$, *i.e.* all cells are wild-type. The probability of observing a double-mutant XY at day t (with $t \in \mathbb{N}$) is:

$$p_{XY}(t) = 1 - \frac{(1 - x\rho_0)^t}{1 + x\rho_0} - \frac{(1 - y\rho_0)^t}{1 + y\rho_0} + \frac{(1 - xy\rho_0^2)(1 - x\rho_0 - y\rho_0 - xy\rho_0^2)^t}{(1 + x\rho_0)(1 + y\rho_0)}$$
 Eq. S.5.2

As $\rho_0 \ll 1$, $p_{XY}(t)$ can be well-approximated with a second-order (or the order matching the number of mutations for **Eq. S.5.9**) element of a Taylor series:

$$p_{XY}(t) \approx t^2 x y \rho_0^2$$
 Eq. S.5.3

The probability of not observing any XY mutant in a population of N cells will be therefore $(1 - t^2 x y \rho_0^2)^N$, and the probability of observing a double-mutant after t days will be thus:

$$P_{XY}(t) \approx 1 - (1 - t^2 x y \rho_0^2)^N \approx 1 - e^{-t^2 N x y \rho_0^2}$$
 Eq. S.5.4

The probability $d_{XY}(t)$ to observe a first XY mutant can be then evaluated by differentiating **Eq. S.5.4**.

$$d_{XY}(t) = \frac{\partial P_{XY}}{\partial t} = 2tNxy\rho_0^2 e^{-t^2Nxy\rho_0^2}$$
 Eq. S.5.5

The expectation for the average latency of the first double-mutant XY can be then evaluated as:

$$\langle t_{XY} \rangle = \int_0^\infty t d_{XY}(t) dt = \frac{1}{2\rho_0} \sqrt{\frac{\pi}{xyN}}$$
 Eq. S.5.6

For a two-hits model, the cell-autonomous time-horizon (t_a) and the time at which the first CD clone might appear can be then described by **Eq. S.5.6** with x=1, and y=1 or y= Ω , respectively.

$$t_a = \langle t_{AB} \rangle = \frac{1}{2\rho_0} \sqrt{\frac{\pi}{N}}$$
 Eq. S.5.7

$$\langle t_{CD} \rangle = \frac{1}{2\rho_0} \sqrt{\frac{\pi}{\Omega N}} = t_\alpha \Omega^{-0.5}$$
 Eq. S.5.8

We note that the scaling factor $\Omega^{-0.5}$ in **Eq. S.5.8** is the factor (xy)^{-1/2} in **Eq. S.5.6** with x=1 and y= Ω . In the Mathematica notebook we also show that for three mutations (X, Y, Z) the scaling factors is (xyz)^{-1/3}. We infer that if we define an average or apparent oncogenic field effect Ω , the scaling factor between the first passage time of a clones cooperating by paracrine effects and clone accruing a similar number of mutations within a single cell would be of the form:

$$\Omega^{-d/m}$$
 Eq. S.5.9

in which m is the number of mutations required for transformation and d is the number of mutations which effect is mediated through, for example, diffusible molecules.