**Michael's late 2014 simplified model \*\* that provides recursion relation equations that generalise across individual gametes.**

Alleles: Assumptions of phenotype:

H-locus = {H, h} H 🡪 dominant Heg homing, dominant telomere shortening

T-locus = {T0, T1, T2, T3} T0 🡪 dominant lethality

* Gamete frequency at stage *N*:

*p*0 = HT0 *q*0 = hT0  
*p*­1 = HT1 *q*1 = hT1

*p*2 = HT2 *q*2 = hT2

*p*3 = HT3 *q*3 = hT3

* Allow for random mating
  + **CASE 1:** hT*i* meets HT*j* || *qi pj*
  + Allow for recombination  
    ( hT*i* ) & (HT*j* ) || *qi pj* (1-r)  
    ( hT*j* ) & (HT*i* ) || *qi pj* r
  + Allow for homing  
    ( hT*i* ) & (HT*j* ) || *qi pj* (1-r) (1-e)  
    ( HT*i* ) & (HT*j* ) || *qi pj* (1-r) e  
    ( hT*j* ) & (HT*i* ) || *qi pj* r (1-e)  
    ( HT*j* ) & (HT*i* ) || *qi pj* r e
  + Allow for telomere shortening (dominant)  
    ( hT*i*-1) & (HT*j*-1 ) || *qi pj* (1-r) (1-e)  
    ( HT*i*-1) & (HT*j*-1 ) || *qi pj* (1-r) e  
    ( hT*j*-1) & (HT*i*-1 ) || *qi pj* r (1-e)  
    ( HT*j*-1) & (HT*i*-1 ) || *qi pj* r e
  + Final gamete frequency  
    hT*i*-1 || *qi pj* ½ (1-r) (1-e)  
    hT*j*-1 || *qi pj* ½ r (1-e)  
    HT*i*-1 || *qi pj* ½ ( e - er + r )  
    HT*j*-1 || *qi pj* ½ ( 1 - r + er )
  + **CASE 2:** HT*i* meets HT*j* || *pi pj*
  + No role for recombination  
    ( HT*i* ) & (HT*j* ) || *pi pj*
  + No role for homing  
    ( HT*i* ) & (HT*j* ) || *pi pj*
  + Allow for telomere shortening (dominant)  
    **( HT*i* ) & (HT*j* )** || *pi pj*
  + Final gamete frequency  
    **HT*i*** || *pi pj* ½   
    **HT*j*** || *pi pj* ½
  + **CASE 3:** hT*i* meets hT*j* || *qi qj*
  + No role for recombination  
    ( hT*i* ) & (hT*j* ) || *qi qj*
  + No role for homing  
    ( hT*i* ) & (hT*j* ) || *qi qj*
  + No telomere shortening   
    ( hT*i* ) & (hT*j* ) || *qi qj*
  + Final gamete frequency  
    hT*i* || *qi qj* ½   
    hT*j* || *qi qj* ½

Summing over everything in the punnet square gives:

