

Electronic Supplementary Material

Table S1. Mean (\pm S.E.) number of normal and irregular cells in prophase, metaphase, anaphase, and telophase determined per stand (S) and PEG treatment (T). Different lowercase letters per column indicate statistically significant differences (p -value < 0.05) among S or T based on the Tukey's test.

		Normal dividing cells in the following mitotic phases:			
		Prophase (Mean \pm S.E)	Metaphase (Mean \pm S.E)	Anaphase (Mean \pm S.E)	Telophase (Mean \pm S.E)
Stand (S)	C	154.44 \pm 91.91 a	0.22 \pm 0.22 a	0.00 \pm 0.00 a	2.22 \pm 1.28 a
	A1	455.56 \pm 227.04 a	6.11 \pm 3.20 b	1.89 \pm 1.18 b	7.22 \pm 5.88 a
	B2	254.11 \pm 106.97 a	4.11 \pm 2.18 a,b	0.11 \pm 0.11 a	3.22 \pm 1.31 a
	D3	269.78 \pm 106.39 a	0.67 \pm 0.44 a	0.00 \pm 0.00 a	5.11 \pm 3.00 a
Treatment (T)	0%PEG	435.00 \pm 120.68 a	6.75 \pm 2.74 b	1.25 \pm 0.92 a	7.67 \pm 4.31 a
	10%PEG	305.92 \pm 143.64 a	1.58 \pm 0.45 a	0.25 \pm 0.13 a	5.67 \pm 2.26 a
	20%PEG	109.50 \pm 91.03 a	0.00 \pm 0.00 a	0.00 \pm 0.00 a	0.00 \pm 0.00 a
ANOVA <i>p</i> -value	S	0.4828	0.0282	0.0398	0.6743
	T	0.1686	0.0029	0.1329	0.1279
	S \times T	0.3069	0.0381	0.0613	0.1205
Irregular dividing cells in the following mitotic phases:					
		Prophase (Mean \pm S.E)	Metaphase (Mean \pm S.E)	Anaphase (Mean \pm S.E)	Telophase (Mean \pm S.E)
Stand (S)	C	10.78 \pm 8.57 a	1.37 \pm 0.71 a	0.11 \pm 0.06 a	1.03 \pm 0.54 a
	A1	4.89 \pm 2.18 a	3.59 \pm 1.25 a,b	0.66 \pm 0.17 a	0.33 \pm 0.12 a
	B2	10.74 \pm 5.06 a	5.48 \pm 1.85 b	1.96 \pm 0.51 b	5.64 \pm 1.91 b
	D3	1.37 \pm 0.56 a	4.26 \pm 1.44 a,b	0.33 \pm 0.13 a	0.78 \pm 0.24 a
Treatment (T)	0%PEG	10.36 \pm 6.46 a	5.44 \pm 1.29 b	1.33 \pm 0.39 b	3.77 \pm 1.45 b
	10%PEG	8.83 \pm 3.90 a	5.53 \pm 1.48 b	0.85 \pm 0.18 b	2.06 \pm 0.54 a,b
	20%PEG	1.64 \pm 1.09 a	0.06 \pm 0.06 a	0.03 \pm 0.02 a	0.00 \pm 0.00 a
ANOVA <i>p</i> -value	S	0.4565	0.1566	<0.0001	0.0002
	T	0.3117	0.0007	0.0002	0.0051
	S \times T	0.0718	0.4473	0.0009	0.0051

Table S2. Mean (\pm S.E.) number of irregular dividing cells in different mitotic phases showing various types of anomalies determined per stand (S) and PEG treatment (T). Different lowercase letters per column indicate statistically significant differences ($p\text{-value} < 0.05$) among S or T based on the Tukey's test.

		Prophase anomalies:		
		Stickiness of chromatin	Presence of micronuclei	Binucleate cell
Stand (S)	C	32.33 \pm 25.08 a	0.00 \pm 0.00 a	0.00 \pm 0.00 a
	A1	12.89 \pm 5.73 a	1.67 \pm 1.18 a	0.11 \pm 0.11 a
	B2	29.67 \pm 13.44 a	0.67 \pm 0.47 a	1.89 \pm 1.09 b
	D3	4.00 \pm 1.33 a	0.11 \pm 0.11 a	0.00 \pm 0.00 a
Treatment (T)	0%PEG	30.75 \pm 18.48 a	0.33 \pm 0.14 a	0.00 \pm 0.00 a
	10%PEG	24.58 \pm 10.49 a	1.00 \pm 0.91 a	0.92 \pm 0.83 a
	20%PEG	3.83 \pm 3.24 a	0.50 \pm 0.36 a	0.58 \pm 0.31 a
ANOVA <i>p</i> -value	S	0.3293	0.2358	0.0660
	T	0.1976	0.6622	0.4153
	S \times T	0.0332	0.2154	0.6214
Metaphase anomalies:				
		Stickiness of chromatin	C-mitosis	Disturbed chromosomal orientation
Stand (S)	C	0.78 \pm 0.47 a	3.33 \pm 1.99 a	0.00 \pm 0.00 a
	A1	1.33 \pm 0.75 a	8.67 \pm 3.08 a	0.78 \pm 0.66 a
	B2	6.44 \pm 2.31 b	8.78 \pm 4.83 a	1.22 \pm 0.98 a
	D3	3.11 \pm 1.66 a,b	9.33 \pm 3.46 a	0.33 \pm 0.23 a
Treatment (T)	0%PEG	5.33 \pm 2.03 b	10.17 \pm 2.68 b	0.83 \pm 0.75 a
	10%PEG	3.42 \pm 0.85 b	12.25 \pm 3.66 b	0.92 \pm 0.50 a
	20%PEG	0.00 \pm 0.00 a	0.17 \pm 0.17 a	0.00 \pm 0.00 a
ANOVA <i>p</i> -value	S	0.0126	0.3730	0.5323
	T	0.0050	0.0027	0.4160
	S \times T	0.1283	0.0589	0.5336

Table S2. (continued)

		Anaphase anomalies:				
		Stickiness of chromatin	Laggard chromosomes	Chromatin bridges	Polarity disturbances	Disturbed chromosomal orientation
Stand (S)	C	0.11 ± 0.11 a	0.00 ± 0.00 a	0.22 ± 0.15 a	0.22 ± 0.22 a	0.00 ± 0.00 a
	A1	0.33 ± 0.24 a	1.33 ± 0.65 b	0.33 ± 0.23 a	0.00 ± 0.00 a	0.78 ± 0.36 b
	B2	4.11 ± 1.98 b	1.56 ± 0.63 b	3.11 ± 1.22 b	0.33 ± 0.23 a	0.67 ± 0.33 a,b
	D3	0.44 ± 0.24 a	0.44 ± 0.44 a,b	0.22 ± 0.15 a	0.33 ± 0.33 a	0.22 ± 0.22 a,b
Treatment (T)	0%PEG	2.75 ± 1.53 b	1.50 ± 0.54 b	2.00 ± 0.97 b	0.17 ± 0.17 a	0.25 ± 0.18 a
	10%PEG	1.00 ± 0.51 a,b	1.00 ± 0.51 a,b	0.83 ± 0.41 b	0.50 ± 0.29 a	0.92 ± 0.34 b
	20%PEG	0.00 ± 0.00 a	0.00 ± 0.00 a	0.08 ± 0.08 a	0.00 ± 0.00 a	0.08 ± 0.08 a
ANOVA <i>p</i> -value	S	0.0037	0.0499	0.0003	0.6858	0.1031
	T	0.0285	0.0245	0.0107	0.1952	0.0232
	S × T	0.0180	0.0984	0.0120	0.3168	0.3435
Telophase anomalies:						
		Stickiness of chromatin	Chromatin bridges	Laggard chromosome	Disturbed chromosomal orientation	
Stand (S)	C	3.11 ± 2.02 a	0.22 ± 0.22 a	0.78 ± 0.47 a	0.00 ± 0.00 a	
	A1	0.67 ± 0.37 a	0.11 ± 0.11 a	0.00 ± 0.00 a	0.56 ± 0.24 a,b	
	B2	18.00 ± 6.00 b	0.44 ± 0.24 a	2.78 ± 1.19 b	1.33 ± 0.80 b	
	D3	0.89 ± 0.46 a	0.67 ± 0.55 a	0.89 ± 0.56 a	0.67 ± 0.37 a,b	
Treatment (T)	0%PEG	12.42 ± 5.06 c	0.50 ± 0.23 a	2.08 ± 0.95 b	0.08 ± 0.08 a	
	10%PEG	4.58 ± 1.86 b	0.58 ± 0.42 a	1.25 ± 0.49 a,b	1.83 ± 0.56 b	
	20%PEG	0.00 ± 0.00 a	0.00 ± 0.00 a	0.00 ± 0.00 a	0.00 ± 0.00 a	
ANOVA <i>p</i> -value	S	< 0.0001	0.5873	0.0078	0.0248	
	T	< 0.0001	0.2582	0.0126	< 0.0001	
	S × T	< 0.0001	0.1754	0.0113	0.0068	