

Table S1: Effect of different storage durations on reducing sugar

S.no.	Genotypes	Reducing sugar (%)			
		0 DOS (control)	50 DOS	100 DOS	150 DOS
1.	Red Cereole	4.92±0.01 ^P	4.84±0.02 ^{op}	4.56±0.08 ^{mno}	3.98±0.04 ^{jk}
2.	Katarina Red 3	4.71±0.05 ^{nop}	4.63±0.06 ^{mnop}	4.33±0.07 ^{mno}	3.89±0.08 ^{jk}
3.	Katarina Red 7	4.77±0.08 ^{op}	4.67±0.10 ^{mnop}	4.38±0.02 ^{lmn}	3.95±0.06 ^{jk}
4.	Supreme	4.36±0.11 ^{lm}	4.17±0.09 ^{kl}	3.89±0.10 ^{jk}	3.47±0.14 ^{fghi}
5.	Cyrus	4.00±0.05 ^{jk}	3.83±0.05 ^{ijk}	3.50±0.03 ^{fghi}	2.97±0.04 ^{bc}
6.	Lock Roy	3.89±0.18 ^{jk}	3.72±0.14 ^{hij}	3.47±0.19 ^{efgh}	2.96±0.14 ^{bc}
7.	Legend	3.68±0.05 ^{hij}	3.55±0.06 ^{ghi}	3.25±0.02 ^{cdefg}	2.70±0.04 ^{ab}
8.	Wall Brown	4.77±0.05 ^{op}	4.63±0.06 ^{mnop}	4.34±0.06 ^{lm}	3.13±0.45 ^{cde}
9.	Brown Spanish	3.38±0.03 ^{defgh}	3.29±0.03 ^{cdefg}	3.11±0.01 ^{cd}	2.59±0.09 ^a
10.	Local Cultivar	3.52±0.14 ^{fghi}	3.40±0.15 ^{defgh}	3.19±0.10 ^{cdefg}	2.65±0.13 ^{ab}
11.	Nasik Red	3.32±0.09 ^{defg}	3.16±0.05 ^{cdef}	2.97±0.10 ^{bc}	2.56±0.13 ^a
	Range	3.32-4.92	3.16-4.84	2.97-4.56	2.56-3.98

Values are represented as mean ± SE; for each column, different lowercase letters indicate significant differences at p<0.05, as measured by 2-sided Tukey's HSD among genotypes. Values bearing a common superscript (abcd) within the column did not vary significantly.

Table S2: Effect of different storage durations on non-reducing sugar

S.no.	Genotypes	Non-reducing sugar (%)			
		0 DOS (control)	50 DOS	100 DOS	150 DOS
1.	Red Cereole	3.13±0.16 ^{ghijklmn}	3.41±0.14 ^{ghijklmno}	3.87±0.25 ^{lmnopq}	4.92±0.06 ^{tu}
2.	Katarina Red 3	2.65±0.16 ^{cdefghi}	2.86±0.16 ^{defghijk}	3.20±0.10 ^{efghijkl}	4.57±0.12 ^{qrst}
3.	Katarina Red 7	2.82±0.28 ^{defghij}	3.11±0.29 ^{fghijklm}	3.80±0.14 ^{opqrs}	4.83±0.12 ^t
4.	Supreme	3.12±0.20 ^{ghijklm}	3.21±0.15 ^{ijklmno}	3.86±0.23 ^{mnopqr}	4.63±0.03 ^{rst}
5.	Cyrus	2.56±0.39 ^{bcdefgh}	2.86±0.31 ^{defghijk}	3.52±0.25 ^{ijklmno}	4.68±0.13 st
6.	Lock Roy	3.63±0.54 ^{ijklmnop}	3.93±0.50 ^{nopqrs}	4.32±0.56 ^{pqrst}	5.62±0.27 ^u
7.	Legend	2.29±0.14 ^{abcde}	2.64±0.11 ^{cdefghi}	3.66±0.10 ^{klmnop}	4.63±0.10 ^{rst}
8.	Wall Brown	2.54±0.21 ^{bcdefg}	2.86±0.23 ^{defghijk}	3.36±0.30 ^{hijklmno}	4.97±0.63 ^{tu}
9.	Brown Spanish	3.33±0.41 ^{ghijklmno}	3.58±0.36 ^{ijklmnop}	3.97±0.42 ^{mnopqr}	4.98±0.36 ^{tu}
10.	Local Cultivar	1.87±0.19 ^{ab}	2.16±0.21 ^{abcd}	2.66±0.17 ^{cdefghi}	3.61±0.31 ^{ijklmnop}
11.	Nasik Red	1.66±0.15 ^a	1.95±0.10 ^{abc}	2.32±0.13 ^{abcd}	3.37±0.23 ^{ijklmno}
	Range	1.66-3.63	1.95-3.93	2.32-4.32	3.37-5.62

Values are represented as mean ± SE; for each column, different lowercase letters indicate significant differences at p<0.05, as measured by 2-sided Tukey's HSD among genotypes. Values bearing a common superscript (abcd) within the column did not vary significantly.