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Genetic parameters and selection efficiency using part-records for production traits in strawberries

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Summary. The efficiency of selection for yield and fruit size using parts of the complete-season record was evaluated using data collected for individual strawberry seedlings (*Fragaria* × *annanasa*) in four genetic tests. Part-records were generated for each trait using cumulative weekly sums, and these were compared with complete records to assess the value of extended data collection. In addition, part-records were generated using data from alternate weeks of harvest. Scoring separate sets of seedlings in alternate weeks was assumed to allow a doubling of the unselected population size, halving the selection proportion and increasing selection intensity. Heritabilities estimated for part-records were often larger for mid-season cumulative part-records than for the complete-season records. Seasonal patterns for broad-sense and narrow-sense heritabilities differed, suggesting temporal expression of genes that condition yield and fruit size. Predicted genetic gains were largest using cumulative part-records between 4 and 12 weeks of the 15-week season, depending on trait and breeding objective (breeding value versus clonal value), with 8-9 weeks as a reasonable compromise. Selection using alternate-weeks records was identified as an efficient alternative to selection using total complete-season records. Superiority of the alternate-weeks option depends on the balance between increased selection intensity and decreased individual genetic information, and will differ for specific traits and program designs.

Key words: Indirect selection – Heritability – Genetic correlation – *Fragaria* × *annanasa*

Introduction

Indirect selection, or selection for a secondary trait to obtain a correlated response in a commercially important target trait, has a broad range of applications in plant and animal improvement (Searle 1965). Indirect selection can be an efficient alternative to direct selection for the target trait when: (a) the secondary trait has a superior distribution of genetic and environmental parameters, conferring a greater precision of selection, (b) selection for the secondary trait is more economical, or (c) assessment of the secondary trait can be conducted more quickly, shortening the generation interval (Falconer 1981). Selection based on performance during a portion of the production cycle, defined here as part-record selection, is a version of indirect selection that has been widely studied and applied in animal improvement programs. Theoretical and empirical studies have demonstrated the efficiency of part-record selection for egg production and quality (VanVleck and Doolittle 1964; Lerner and Cruden 1948; Lowe and Garwood 1980; Ayyagari et al. 1980) and for milk yield in dairy cattle (VanVleck and Henderson 1961; Danell 1982). Part-record selection has been less explicitly applied to plant improvement, although mose perennial crops are selected using information from a portion of their commercial production cycle. Determination of an optimal selection age for forest trees, using juvenile-mature correlations, followed procedures analogous to part-record selection in animal programs (Lambeth 1980; Loo et al. 1984).

The most common incentive for part-record selection in both animals and perennial trees has been to shorten the generation interval with minimal reduction of the genetic gain per generation. Alternatively, part-records may provide genetic information that is nearly equal to that obtained from complete records, with a fraction of the data collection effort. A planned decision to collect part-records thus permits redistribution of program effort to tasks that have the highest likelihood of generating selection response. Collection of part-record information may allow an increase in the number of individuals evaluated in each generation when data collection is a program-limiting step. If the number of individuals to be retained after each cycle of selection is predetermined, increasing the initial population size will decrease the selected proportion and increase selection intensity. Part-records may also be advantageous when selected traits are conditioned by genetic and environmental effects that change during the production cycle. Parts of the total record (or functions of these part-records) may provide more precise genetic information than the complete record. Evidence for changes in the relative proportions of genetic and environmental parameters that might affect selection efficiency is available for both plants and animals (Madden et al. 1955; Franklin 1979; Atchley 1984).

In many continuous-cropping plant species (e.g. strawberries and cane-berries), initial selections are made from populations of seedlings evaluated in a single year. Generation intervals are often fixed by flowering cycles or by a need for advanced testing under commercial conditions. Conversely, the large effort required for obtaining individual plant data within a single season is often program-limiting, and planned collection of part-records may be an efficient alternative to collection of records for the complete season. The objective of the study reported below was to investigate the opportunity for improving seedling selection efficiency in a strawberry improvement program by using part-records.

Materials and methods

Selection efficiency. The selection efficiency for comparison of part-record and direct selection methods is calculated as the ratio of the gain predicted for the two alternatives (Falconer 1981):

$$E = G_{y/x}/G_y \tag{1}$$

In Eq. (1), G_y is the gain expected in the target trait, y, due to direct selection, and $G_{y/x}$ is the gain expected in trait y by selecting on the secondary trait, x. In this study, direct traits were seasonal totals and secondary traits were the relevant part-records. Efficiencies greater than 1.0 imply superiority of the part-record method. Gains for breeding value from direct mass selection and for mass selection using part-records were predicted as follows (Falconer 1981):

$$G_y = i_y h_y^2 \sigma_y \tag{2}$$

$$G_{y/x} = i_x h_x h_y r_g \sigma_y \tag{3}$$

In Eqs. (2) and (3), i_y and i_x are selection intensities, h_y^2, h_x and h_y are narrow-sense heritabilities (or the square root of narrow-sense heritability), and σ_y is the phenotypic standard deviation, where subscripts y and x denote direct and secondary traits; r_g is the additive genetic correlation between direct and secondary traits. Gains and selection efficiencies were predicted for clonal selection by substituting broad-sense heritabilities (H^2) into Eqs. (2) and (3). Genotypic, or total genetic, correlations (r_{gy}) should be used when predicting gains from clonal selection, but in practice r_g and r_{gy} were nearly identical and only r_g is presented.

Materials and measurements. The materials and measurements used for the present study are a subset of those available from four genetic tests of strawberry seedlings established in September of 1985 and 1986. Results for analyses of genetic and environmental parameters that condition complete-season yield, fruit size and appearance score are given in Shaw et al. (1989), together with detailed descriptions of cultural methods, test locations, experimental design, statistical analyses and the assumptions required for their interpretation. Briefly, data were collected for individual seedlings from 28 and 39 biparental crosses, for the 1985 and 1986 trials, respectively; crosses tested in each year form a partial diallel design with 18 and 15 parents. The parents of all crosses were a random sample of named varieties and advanced selections from the current California breeding population, and quantitative inference relating to selection efficiency must be limited to this reference population. Tests were established for all crosses at two locations in each year. Weekly yields and fruit numbers were recorded for each plant on 15 consecutive weeks, beginning the 2nd week of April and ending in late July of the year follwing planting. These 15 weeks represent the total season's production. Seedlings were distributed between two completely random plots of 6–10 plants per location for the 1985 trials, and the 1986 trials were established using two plots of 6 plants at each location in a randomized complete block design. After losses due to mortality and non-flowering plants, parameters were estimated using records for 610 and 938 seedlings in 1985 and 1986, respectively.

Part-records were generated to test two hypotheses. First, records were generated for each of the 15 weeks of harvest using cumulative weekly yields and fruit sizes (cumulative yield divided by cumulative fruit number). Comparison of gains predicted for selection using cumulative part-records with gains predicted for direct selection provides an assessment of the need for expending program effort on late season harvests. Second, analyses were conducted for part-records generated using cummulative yield and fruit size for alternate weeks (odd and even) of harvest. The rationale here is that evaluation of separate sets of seedlings in alternate weeks permits a doubling of the unselected population size, which will increase selection intensity when the number of individuals retained after each cycle of selection is predetermined. Comparison of gains predicted for selection using alternate-weeks part-records with gain predicted for direct selection tests the relative value of complete genetic and environmental information versus increases selection intensity (see below).

Parameter estimates. Parameter estimates for the components of Eqs. (2) and (3) were obtained from the data described above, as follows. Analyses of variance and cross-products were performed for part and complete records using the least-squares procedure DIALL (Shaffer and Usanis 1969). ANOVA and ANCOVA results from supplemental SAS analyses were used to modify DIALL output, to reveal all genetic × location interaction terms (see Shaw et al. 1989, for details), resulting in the form and expected mean squares given in Table 1. Causal components of variance and covariance were estimated from linear functions of these expected mean squares and cross products (Becker 1981). Heritabilities and genetic correlations were estimated as:

$$h^2 = \frac{4(\sigma_{gca}^2)}{2(\sigma_{gca}^2) + \sigma_{sca}^2 + 2(\sigma_{gxl}^2) + \sigma_{sxl}^2 + \sigma_w^2} \tag{4}$$

Table 1. Expected mean squares for the analysis of variance of yield, fruit size and appearance score, with results from the two test locations considered simultaneously

Source	df (1985)	df (1986)	EMS[a]
Location (L)	1	1	$\sigma_w^2 + k_1\,\sigma_{\mathrm{S\times L}}^2 + k_2\,\sigma_{\mathrm{G\times L}}^2 + k_5\,\sigma_{\mathrm{R\,(L)}}^2 + k_6\,\sigma_{\mathrm{L}}^2$
Reps/L	–	2	$\sigma_w^2 + k_5\,\sigma_{\mathrm{R\,(L)}}^2$
GCA (G)	14	14	$\sigma_w^2 + k_1\,\sigma_{\mathrm{S\times L}}^2 + k_2\,\sigma_{\mathrm{G\times L}}^2 + k_3\,\sigma_S^2 + k_4\,\sigma_{\mathrm{G}}^2$
SCA (S)	13	24	$\sigma_w^2 + k_1\,\sigma_{\mathrm{S\times L}}^2 + k_3\,\sigma_{\mathrm{S}}^2$
G × L	12	14	$\sigma_w^2 + k_1\,\sigma_{\mathrm{S\times L}}^2 + k_2\,\sigma_{\mathrm{G\times L}}^2$
S × L	13	24	$\sigma_w^2 + k_1\,\sigma_{\mathrm{S\times L}}^2$
residual	586	858	σ_w^2

[a] σ_{L}^2 – Variance due to locations
$\sigma_{\mathrm{R\,(L)}}^2$ – Variance due to replications in locations
σ_{G}^2 – Variance due to general combining ability (GCA)
σ_{S}^2 – Variance due to specific combining ability (SCA)
$\sigma_{\mathrm{G\times L}}^2$ – Variance due to GCA by location interaction
$\sigma_{\mathrm{S\times L}}^2$ – Variance due to SCA by location interaction
σ_w^2 – Pooled residual variance
k_1–k_6 – are coefficients for model components of variance:

	1985	1986
k_1	11.7	12.0
k_2	42.6	57.2
k_3	23.9	23.4
k_4	90.5	115.4
k_5	–	238.4
k_6	328.0	476.0

$$H^2 = \frac{4(\sigma_{gca}^2 + \sigma_{sca}^2)}{2(\sigma_{gca}^2) + \sigma_{sca}^2 + 2(\sigma_{gxl}^2) + \sigma_{sxl}^2 + \sigma_w^2} \tag{5}$$

$$r_g = \frac{\sigma_{xy\,(gca)}}{[\sigma_{x\,(gca)}^2 * \sigma_{y\,(gca)}^2]^{1/2}}\,. \tag{6}$$

In Eqs. (4) and (5), σ_{gca}^2, σ_{sca}^2, σ_{gxl}^2, σ_{sxl}^2, and σ_w^2 are variances due to general and specific combining ability, interactions of general and specific combining ability with location and an error variance that includes within-family genetic and environmental sources (Hallauer and Miranda 1981). In Eq. (6), $\sigma_{xy\,(gca)}$, $\sigma_{x\,(gca)}^2$, and $\sigma_{y\,(gca)}^2$ are the genetic covariance between traits x and y and their gentic variances based on general combining ability.

Selection intensities. Selection intensities are fixed in practice by the initial population size and by the number of plants retained after each cycle of selection (i.e. the selected proportion). Although selection based on cumulative weekly part-records may reduce seasonal data collection effort, weekly data collection is more likely to be program limiting. Initial population sizes, and thus selection intensities, were assumed equal when predicting gains from selection using cumulative part-records and complete-season records. Conversely, planned collection of data in alternate weeks would allow a doubling of the initial population size, if different sets of plants are evaluated in alternate weeks. I assumed that the number of plants retained after selection is not affected by choice of selection method, and that doubling the initial population size will reduce the selection proportion by one-half. An initial selection proportion of 0.05 for direct and cumulative part-record selection, and a reduced selection proportion of 0.025 for alternate-weeks examples were assumed for this study.

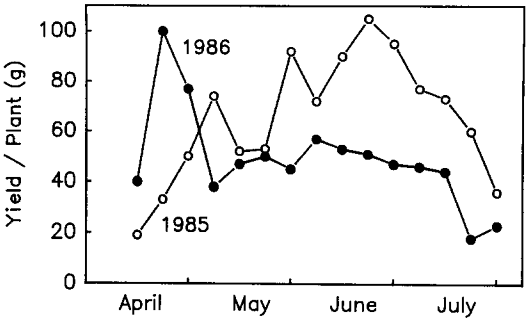

Fig. 1. Distribution of average individual plant yield throughout the production season for genetic tests established in 1985 and 1986

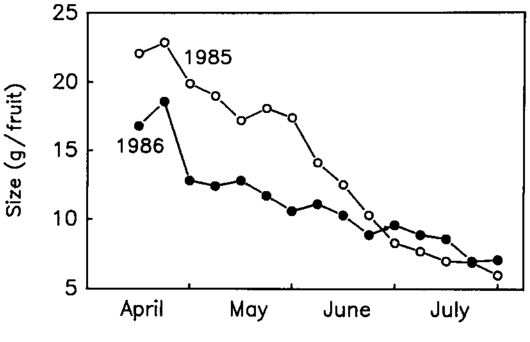

Fig. 2. Distribution of individual plant fruit size throughout the production season for genetic tests established in 1985 and 1986

Results

Seasonal patterns for yield and fruit size differed somewhat between test years (Figs. 1 and 2). Individual plants initiated production between weeks 1 and 10 in the 1985 trial, resulting in a peak for average yield at the 10th week of harvest (4th week of May). Virtually all plants in the 1986 trial had initiated production by the 3rd harvest (4th week of April), and average yield was largest for this harvest. Seasonal patterns for fruit size were similar for both years, but 1985 sizes were larger than those for 1986 through 11 weeks of harvest. Cumulative fruit size was calculated only for plants that had initiated production,

Table 2. Means and standard deviations (SD) for yield (g/plant) and fruit size (g/fruit) based on cumulative weekly assessments, for 15 weeks in two years

Weeks	Yield				Size			
	1985		1986		1985		1986	
	Mean[a]	SD	Mean	SD	Mean	SD	Mean	SD
1	7	23	38	44	22.1	7.8	16.7	10.1
2	52	71	129	104	21.0	8.2	15.8	6.4
3	102	98	212	138	19.5	7.1	14.8	4.8
4	175	129	249	155	18.7	6.9	13.6	4.5
5	222	151	296	174	18.0	6.6	13.5	4.1
6	275	178	345	190	18.0	6.4	13.5	3.9
7	369	230	391	202	17.7	5.2	12.7	3.7
8	440	256	448	218	17.1	4.8	12.4	3.3
9	531	289	501	236	16.2	4.3	12.1	3.1
10	635	322	552	254	14.9	3.9	11.7	2.9
11	700	336	598	271	14.7	3.5	11.4	2.8
12	804	375	644	292	13.8	3.2	11.2	2.6
13	873	404	685	310	13.7	3.0	11.0	2.5
14	929	429	703	319	12.9	2.9	10.8	2.5
15	970	447	724	329	12.5	2.8	10.7	2.4

[a] Means for 1985 and 1986 based on 610 and 938 plants, respectively; standard deviations are included as an indication of the distribution of individual plant values

Table 3. Narrow-sense heritability (h^2), broad-sense heritability (H^2) and genetic correlation (r_g) for cumulative weekly yields in two test years

Week	1985			1986		
	h^2	H^2	r_g	h^2	H^2	r_g
1	0.05	0.21	0.25	0.23	0.42	0.72
2	0.21	0.21	0.52	0.36	0.65	0.82
3	0.18	0.18	0.69	0.35	0.64	0.80
4	0.18	0.18	0.75	0.35	0.63	0.81
5	0.23	0.25	0.80	0.33	0.61	0.84
6	0.27	0.27	0.87	0.35	0.58	0.82
7	0.31	0.31	0.94	0.38	0.55	0.87
8	0.39	0.39	0.95	0.31	0.50	0.90
9	0.38	0.38	0.97	0.40	0.48	0.92
10	0.37	0.38	0.98	0.40	0.45	0.94
11	0.34	0.34	0.99	0.38	0.39	0.96
12	0.31	0.31	1.00	0.36	0.36	0.98
13	0.27	0.27	1.00	0.36	0.36	1.00
14	0.24	0.28	1.00	0.36	0.36	1.00
15	0.24	0.23	–	0.35	0.35	–

Table 4. Narrow-sense heritability (h^2), broad-sense heritability (H^2) and genetic correlation (r_g) for fruit size based on cumulative weekly data collected in two test years

Week	1985			1986		
	h^2	H^2	r_g	h^2	H^2	r_g
1	–	–	–	–	–	–
2	0.12	0.39	−0.01	0.09	0.14	0.67
3	0.08	0.39	0.20	0.10	0.19	0.77
4	0.19	0.46	0.78	0.10	0.24	0.85
5	0.16	0.58	0.81	0.10	0.23	0.88
6	0.12	0.65	0.83	0.11	0.24	0.89
7	0.22	0.77	0.85	0.13	0.30	0.89
8	0.23	0.67	0.82	0.14	0.27	0.94
9	0.26	0.43	0.85	0.15	0.24	0.97
10	0.37	0.38	0.87	0.13	0.19	0.99
11	0.34	0.34	0.94	0.13	0.20	1.00
12	0.28	0.34	0.96	0.13	0.20	1.00
13	0.33	0.38	1.00	0.14	0.20	1.00
14	0.34	0.45	1.00	0.13	0.20	1.00
15	0.33	0.46	–	0.12	0.18	–

and was not dependent on time of initiation to the same extent as average weekly yield. Yearly differences in production pattern are reiterated by inspection of cumulative weekly means (Table 2). Plants in the 1986 trials had produced 50% of their seasonal yield after 7 weeks of harvest, whereas plants in 1985 trials had accumulated 50% of their season total after 9 harvests. Cumulative fruit size was larger throughout the 1985 season. Shaw et al. (1989) argued that the between-year differences observed for seasonal yield and fruit size in these trials were due to environment rather than genetic sampling, using data from 5 biparental crosses common to all trials; a similar argument can be made for yearly differences in production pattern.

Maximum estimates of h^2 for yield were obtained after 8 or 9 weeks of harvest in the 1985 ($h^2 = 0.39$) and 1986 ($h^2 = 0.40$) trials, respectively (Table 3). Estimated h^2 for yield decreased after the eighth harvest for the 1985 trial ($h_y^2 = 0.21$), but not for the 1986 trial ($h_y^2 = 0.35$). Late-season yields contributed little to the season total in 1986 and are of little consequence to estimates of genetic parameters. Broad-sense heritabilities (H^2) for yield differed between years both in maximum value ($H_{max}^2 = 0.39$ and 0.65) and in pattern. Importantly, H^2 differed from h^2 for cumulative harvests 1 through 10 in the 1986 trial, but did not differ in 1985. Differential expression of genes between years is common, as evidenced by frequent observations of significant genotype x years interaction variances (Comstock and Moll 1963). Genetic correlations between part- and complete-season yield records increase with the number of harvests in both years, but not linearly. Patterns of heritabilities and genetic correlations for cumulative fruit size were similar for the two years, although parameters differed somewhat in magnitude (Table 4). Differences between H^2 and h^2 for fruit size were present throughout the season and for both years, demonstrating the importance of dominance gene action. Both the pattern and magnitude of genetic correlations between part and seasonal records for fruit size were similar to those for yield (Tables 3 and 4). Differences between H^2 and h^2 changed throughout the harvest

Table 5. Efficiencies for breeding-value selection (E_{bv}) and clonal selection (E_c), for yield and fruit size based on cumulative weekly data in two years

Weeks	Yield				Size			
	1985		1986		1985		1986	
	E_{bv}	E_c	E_{bv}	E_c	E_{bv}	E_c	E_{bv}	E_c
1	0.12	0.26	0.58	0.79	–	–	–	–
2	0.52	0.54	0.83	1.11	0.10	0.00	0.58	0.59
3	0.59	0.61	0.80	1.08	0.10	0.18	0.70	0.79
4	0.71	0.76	0.81	1.09	0.59	0.78	0.77	0.98
5	0.86	0.83	0.80	1.11	0.56	0.91	0.80	0.99
6	1.00	0.94	0.82	1.06	0.50	0.99	0.85	1.03
7	1.14	1.09	0.91	1.09	0.69	1.10	0.93	1.15
8	1.29	1.24	0.95	1.09	0.68	0.99	0.93	1.15
9	1.33	1.25	0.98	1.08	0.75	0.83	1.08	1.12
10	1.29	1.26	1.00	1.07	0.80	0.83	1.03	1.02
11	1.24	1.20	1.00	1.01	0.83	0.82	1.04	1.05
12	1.14	1.16	1.00	0.98	0.88	1.83	1.04	1.05
13	1.10	1.08	1.03	1.01	0.99	0.90	1.06	1.05
14	1.08	1.10	1.03	1.01	1.02	0.99	1.04	1.05
15	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00

Table 6. Descriptive statistics for yield and fruit size for cumulative alternate weeks data

Weeks	Yield				Size			
	1985		1986		1985		1986	
	Mean[a]	SE	Mean	SE	Mean	SE	Mean	SE
Odd	540	9.7	501	5.9	11.7	0.1	10.5	0.1
Even	624	10.8	534	6.4	12.3	0.1	10.9	0.1

[a] Means for both odd and even weeks treatments are based on 610 and 938 plants for the 1985 and 1986 trials, respectively; standard errors are phenotypic standard deviations divided by the square-root of these sample sizes, and are appropriate for comparison of treatment means

Table 7. Heritabilities and genetic correlations for yield and fruit size based on cumulative data for alternate weeks

	Weeks	1985			1986		
		h^2	H^2	r_g	h^2	H^2	r_g
Yield	Odd	0.19	0.29	0.93	0.28	0.28	1.00
	Even	0.14	0.18	0.95	0.36	0.37	1.00
Size	Odd	0.33	0.33	0.95	0.12	0.18	1.00
	Even	0.33	0.53	0.91	0.07	0.25	1.00

Table 8. Efficiencies for selection for breeding value (E_{bv}) and clonal value (E_c) based on cumulative alternate weeks data[a]

	Weeks	1985		1986	
		E_{bv}	E_c	E_{bv}	E_c
Yield	Odd	1.03	1.18	1.01	1.01
	Even	0.86	0.95	1.15	1.16
	Average	0.94	1.06	1.08	1.09
Size	Odd	1.08	1.08	1.09	1.33
	Even	1.03	1.31	1.09	0.89
	Average	1.06	1.20	1.09	1.11

[a] This treatment assumes retention proportion of 0.05 for the base population ($i = 2.06$) vs. 0.025 for a doubled population ($i = 2.34$)

season, for both yield and fruit size. This difference was largest for size after 7 weeks of harvest in both years, and after 3 weeks of harvest for yield in the 1986 trial. These observations suggest that genes conditioning genetic variation for these traits were expressed temporally. Selection efficiencies differed somewhat between traits, years and selection objectives (Table 5). However, part-record selection efficiency for yield was larger than direct selection efficiency for all cases by the 10th week of harvest (E_{bv} and $E_c > 1.0$), and was larger in 3 of 4 cases after the 7th harvest. Efficiencies for clonal selection of fruit size were maximum in both years for 7 weeks of harvest, whereas selection efficiency for breeding value was greater than 1.0 after 14 and 9 weeks of harvest for the 1985 and 1986 trials, respectively.

Means for alternate-weeks part-records differed by between 4% and 15% and these differences were significant for traits in both years (Table 6). Heritabilities estimated for alternate-weeks part-records differed in magnitude, but complementary estimates were within one standard error (Table 7), with the exception of H^2 for fruit size in 1985 ($H^2_{\mathrm{odd}} = 0.33$, $H^2_{\mathrm{even}} = 0.53$). Also, heritabilities for alternate-weeks part-records were uniformly smaller than the maximum heritability for cumulative part-records, and were usually smaller than heritabilities estimated for seasonal totals. For example, h^2 maximum was 0.40 at weeks 9–10, h^2_y was 0.35 and the average h^2 for odd and even weeks was 0.33 for yield in 1986 (Tables 3 and 7). Genetic correlations between alternate-weeks part-records and season totals ranged between 0.91 and 1.00 which, together with observations on means and heritabilities, suggests that each assessment captured a similar fraction of the production season. Efficiencies for selection using alternate-weeks information ranged from 0.86 to 1.33, and were larger than 1.00 for 13 of the 16 cases presented in Table 8.

Discussion

Selection using cumulative or alternate-weeks part-records can be efficient alternatives to direct selection for improvement of yield and fruit size in strawberries. The relative contribution of genetic and environmental effects to the phenotypic variance of individual traits differed between production seasons and changed throughout each production season as well. Because the parents and environments tested were sampled from a single reference population, the differences observed between trials established in consecutive years reflects genetic, climatic and statistical sources of variation. Limitations to inference should recognize that genetic variances and correlations typically have large associated standard errors. Further refinement of the operational recommendations derived from this study should proceed by continued sampling and estimation of these parameters. Frequent monitoring is needed because genetic variances and correlations are expected to change as the result of successful selection. Regardless of such limitations, several observations were consistent for trials evaluated in both years. Heritabilities for season totals were lower than those for early-season part-records, suggesting that environmental effects were relatively more important to late-season production. Changes in the relative values of narrow-sense and broad-sense heritabilities were observed for both yield and fruit size throughout the production season and suggest temporal expression of genes that condition these traits.

Because selection efficiency depends on the distribution of genetic and environmental parameters, and because these parameters vary within and between seasons, choice of a single selection option necessarily requires a compromise. Conservatively, scoring for cumulative yield could be terminated by week 10, and perhaps much earlier. Clonal selection efficiency for cumulative fruit size was largest using part-records for 7 weeks of harvest for both years; early part-record selection for breeding value would be an efficient option only for the 1986 trials. For cumulative part-records, selection using 8 or 9 weeks harvest information represents a reasonable compromise: selection efficiencies for the examples presented were near maximum for all traits, selection objectives and years, and data collection effort would be reduced by 6–7 harvests. Selection using part-records generated by sampling in alternate weeks was also identified as an efficient compromise. Data collection in alternate weeks samples the entire production cycle, and may be advantageous when genetic variation is temporally expressed or when production patterns differ among years. Sampling the entire cycle may be especially important when genetic effects are temporally variable, and when selections for varietal potential (clonal value) and parental potential (breeding value) must be made from the same genetic test.

The principle advantage of the alternate-weeks option was assumed to be a doubling of the evaluation potential, which halves the proportion selected and increases indirect selection intensity ($i_{y/x}$) relative to that for direct selection (i_y). Selection intensity does not change linearly with the proportion selected (Falconer 1981), and direct comparisons are best made between specific alternatives. For the cases presented, reducing the proportion selected from 0.05 to 0.025 increased selection intensity from 2.06 to 2.34, a change that was usually enough to confer an advantage for the alternate-weeks option. The relative advantage of the alternate-weeks option would be greater when the initial selected proportion is large, because halving the selected proportion has a larger effect on selection intensity. For example, reducing an initial selected proportion from 0.2 to 0.1 changes selection intensity from 1.40 to 1.76, a 26% change, compared to a 14% increase for the example above.

One potential disadvantage of the alternate-weeks method is that sets of seedlings sample different portions of the production season, and individuals in different sets may not be directly comparable when making individual plant selections. One solution to this problem is to distribute selection intensity evenly among sets. Another is to use sets as units of blocking, correcting individual values for estimated block effects prior to selection. The most serious confounding will result from genes that condition the initiation and pattern of production, a problem that might be partially corrected using estimated family × set interaction effects, again prior to selection. Comparing the performance of individuals with different production patterns is a general problem for selection of continuous-cropping species, and programs will benefit from knowledge about the inheritance of such traits.

References

Atchley WR (1984) Ontogeny, timing of development, and genetic variance-covariance structure. Am Nat 123: 519–540

Ayyagari V, Mohapatra SC, Venkatramaiah A, Thiagasundaram T, Choudhuri D, Johri DC, Renganathan P (1980) Selection for egg production on Part records: 1. Evaluation of short term selection response. Theor Appl Genet 57: 277–283

Becker WA (1984) Manual of quantitative genetics. Academic Enterprises, Pullman

Comstock RE, Moll R (1963) Genotype-environment interactions. In: Hanson WD, Robinson HF (eds) Statistical genetics and plant breeding. Natl Acad Sci Nat Res Council Pub no. 982, pp. 164–194

Danell B (1982) Studies on lactation yield and indifidual test day yields of Swedish dairy cows: II. Estimates of genetic and phenotypic parameters. Acta Agrie Scand 32: 83–92

Falconer DS (1981) Introduction to quantitative genetics. Longman, New York

Franklin EC (1979) Model relating levels of genetic variance to stand development of four North American conifers. Silvae Genet 28: 207–212

Hallauer AR, Miranda JB (1981) Quantitative genetics and maize breeding. Iowa State University Press, Ames

Lambeth CC (1980) Juvenile-mature correlations in Pinaceae and implications for early selection. For Sci 26: 571–580

Lerner IM, Cruden DM (1948) The heritability of accumulative monthly and annual egg production. Poultry Sci 27:67–78

Loo JA, Tauer CG, Van Buijtenen JP (1984) Juvenile-mature relationships and heritability estimates of several traits in Loblolly pine (*Pinus taeda*). Can J For Res 14:822–825

Lowe PC, Garwood VA (1980) Efficiency of selection based on segments of the early record for improving annual lay rate. Poultry Sci 59:677–680

Madden DE, Lush JL, McGilliard LD (1955) Relations between parts of lactations and producing ability of Holstein cows. J Dairy Sci 38:1264–1271

Searle SR (1965) The value of indirect selection: I. mass selection. Biometrics 21:682–707

Shaffer HE, Usanis RA (1969) General least-squares analysis of diallel experiments. A computer program – DIALL. Genetics Dept Res Rep No. 1, North Carolina State University, Raleigh

Shaw DV, Bringhurst RS, Voth V (1989) Genetic parameters estimated for an advanced-cycle strawberry breeding population at two test locations. J Am Soc Hortic Sci (in press)

VanVleck LD, Henderson CR (1961) Estimates of genetic parameters for some functions of part lactation milk records. J Dairy Sci 44:1073–1084

VanVleck LD, Doolittle DP (1964) Genetic parameters of monthly egg production in the Cornell controls. Poultry Sci 43:560–567