

Final Report for USFWS MBM Order No. 701812M816

**Investigating the impact of Sampling Effort on
Annual Migratory Bird Subsistence Harvest Survey Estimates**

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SUMMARY

A power analysis was conducted to investigate the impact of two sampling factors, number of villages sampled in an area and percentage of total area households sampled, on the annual harvest of six species of migratory bird, both for bird and egg harvests. The analysis was conducted using historic subsistence harvest survey records from the Yukon-Kuskokwim Delta area and the Bristol Bay area.

An initial analysis of 2001 Bristol Bay area harvest stratified survey data showed that the power analysis could only proceed using (1) a simplified random sampling scheme and (2) combining all observations across years for a village and using nonparametric bootstrap resampling of surveyed households at the village level (see Reynolds 2002a, 2002b). Analyses used all complete household records from simple random sampling the two areas from 1995-2001.

The analysis investigated the impact of the two sampling factors on two characteristics of the resulting sampling distributions for the total annual harvest of a given species and take (bird, eggs): bias and precision. These characteristics were investigated at the region, area, and 'statewide' level.

Overall, the results reveal that the estimation method is generally unbiased and shows little gain in precision, at the area scale, from sampling more than 23 villages in an area at a rate of more than 25% of all area households.

The results and assumptions of the Monte Carlo method are discussed, as are select questions requested by the committee. Sample simulation code and graphical summaries of all region-specific results are included in the appendices.

INTRODUCTION

A power analysis investigates how the bias and precision of a particular statistical estimator, or power of a statistical test, changes as a function of increasing sampling effort or cost. Such analyses allow one to determine any 'thresholds of sampling effort' beyond which the gain in precision or statistical power may not justify the increased sampling effort or cost. Generally, the more complex the sampling design or estimation method then the more complex the power analysis. However, it is exactly these more complex investigations where power analysis becomes most valuable and informative.

A power analysis was conducted using the historic subsistence waterfowl harvest survey data to investigate the impact of two factors,

- (1) the number of villages sampled per area and
- (2) the percentage of households sampled per village,

on two characteristics,

- (i) bias and
- (ii) precision,

of the region, area and state total annual harvests of

- (a) birds and
- (b) eggs

for each of six species of interest: cackling Canada Goose (*Branta canadensis minima*), Emperor Goose (*Chen canagica*), White-Fronted Goose (*Anser albifrons*), Black Scoter (*Melanitta nigra*), Northern Pintail (*Anas acuta*), and Spectacled Eider (*Somateria fischeri*). Two areas were analyzed – the Yukon-Kuskokwim Delta and the Bristol Bay area (Figure 1). Results are given for the areas, each of their component regions, and the sum of the areas (as an approximation of the state total harvest).

As this was the first power analysis conducted on the subsistence waterfowl harvest survey, a significant portion of the effort focused on determining the best approach to pursue (Appendix 1). The general concept of how one conducts a power analysis using historic data is outlined below.

POWER ANALYSIS USING HISTORIC DATA: THE GENERAL CONCEPT

We want to know how the distribution of the total annual harvest estimate is affected by the number of villages sampled in each area and the percentage of area households sampled. For example, what is the gain in precision of the estimate if one samples 12 villages in the area rather than 5, and 30% of the area households rather than 5% (Figure 2)?

In the ideal scenario, we would know the distribution of household total annual harvest for each village in each region of each area, for each species and response (bird or egg):

$$F_{\text{household,annual}}(x \mid \text{village } V \text{ in region } R \text{ of area } A; \text{species } S; \text{response } T).$$

If we knew $F_{\text{household,annual}}$ for each village and species and response, then for each combination of sampling factor levels (J villages sampled, P% of area households sampled), we could simply

Subsistence Migratory Bird Harvest Survey Communities and Regions - Southwest Alaska

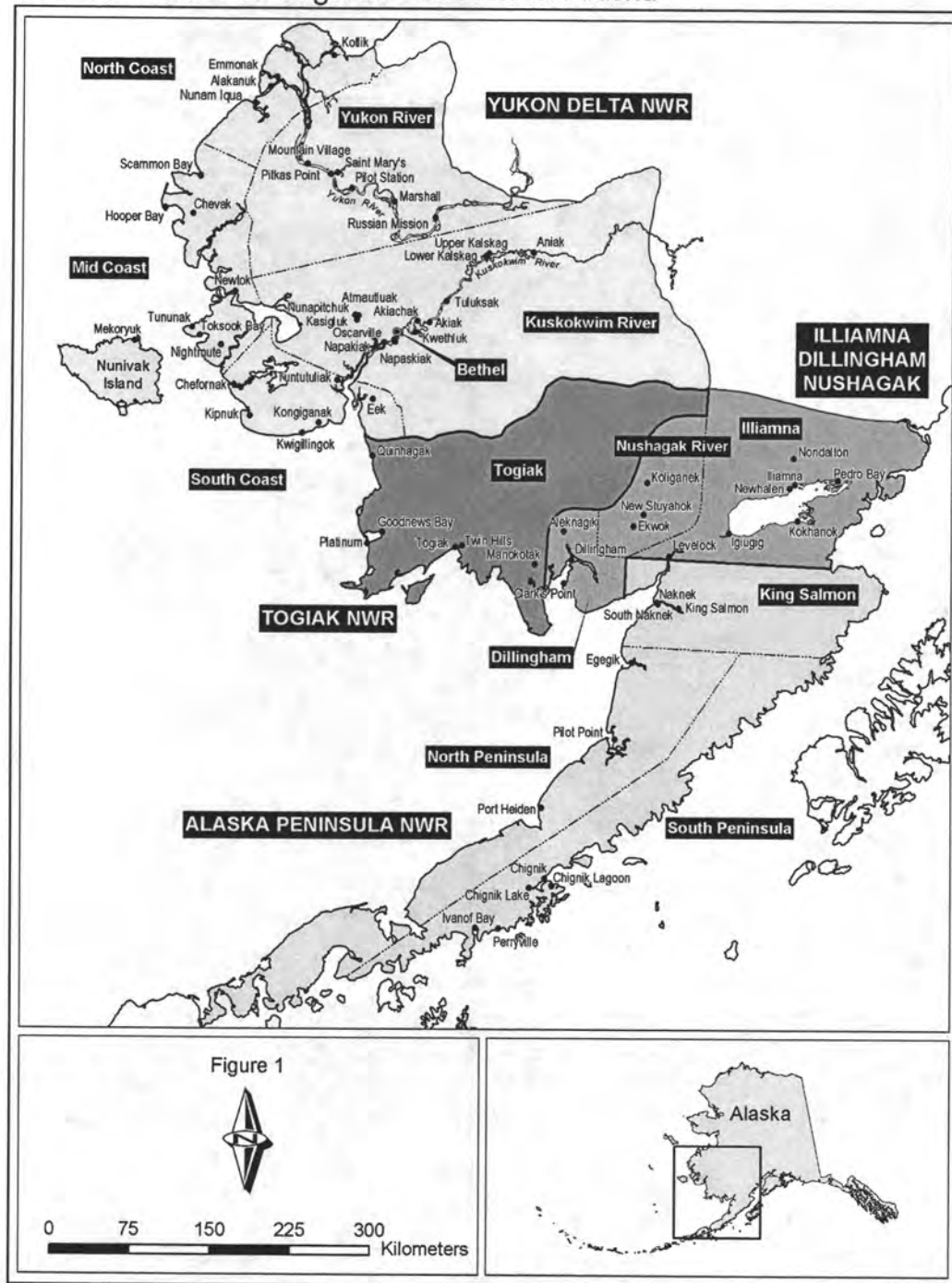


Figure 1. Subsistence Harvest Survey areas and their component regions. The Yukon-Kuskokwim Delta area contains six regions: North Coast, Mid Coast, South Coast, Bethel, Kuskokwim River, and Yukon River. The Bristol Bay area contains seven regions: Togiak, Nushagak, Dillingham, Illiamna, King Salmon, North Peninsula and South Peninsula. Image courtesy of Cynthia Wentworth, USFWS MBM.

- (1) randomly sample $H\%$ households from each of the J chosen villages, where H is calculated from the total number of households in the chosen villages so that $P\%$ of the area households are sampled overall.
- (2) estimate the mean harvest for each sampled village,
- (3) estimate the region mean harvest from the relevant village mean harvest estimates,
- (4) estimate the region total harvest as the product of the region mean harvest and total number of households in the region (based on recent census data),
- (5) sum the region total harvest estimates to get the area estimate,
- (6) sum the area total harvest estimates to get the state total harvest estimate.

Repeating steps (1) – (6) a large number of times (~ 500) for each choice of J and $P\%$ gives an estimate of the sampling distribution of each region total, area total, and state total annual harvest. The characteristics of interest for each sampling distribution, e.g., bias and precision, can then be directly estimated.

This process requires the following information:

- $F_{\text{household,annual}}$, the distribution of total annual household harvests for each village for each species for each response;
- Selecting the type of household sampling to implement (simple random sample (SRS) or stratified random sample);
- Defining the relevant range of J s – the number of villages per area to sample;
- Defining the relevant range of P s – the % of area households to sample;
- The total number of households currently in each village;

Defining the method of estimating the regional mean harvest from the village mean harvest estimates. The analysis used a weighted mean of the village mean estimates, with weighting proportional to the relative number of households in each sampled village.

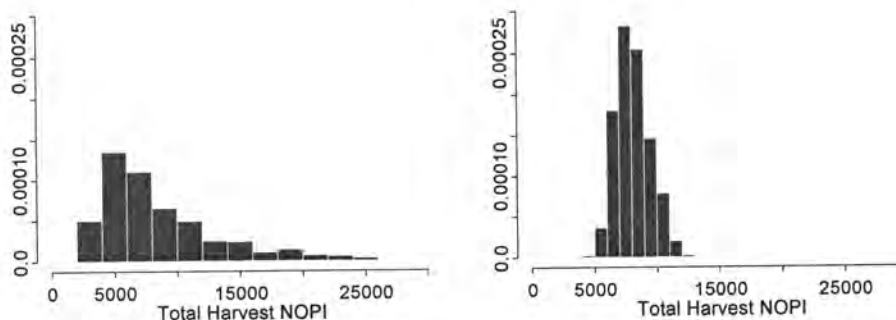


Figure 2. Example sampling distributions of total Northern Pintail (NOPI) harvest estimates from (left) sampling 5 villages in the area and 5% of the area households and (right) sampling 12 villages in the area and 30% of the area households. The increased sampling effort leads to increased precision in the estimate (the right graph shows a narrower distribution). NOTE: the y-axis is scaled so each histogram is a probability distribution with a total area of 1.

The proposal set forth a series of approaches for estimating $F_{\text{household,annual}}$ (Reynolds 2002a). Preliminary investigations revealed that the only currently feasible approach was to estimate $F_{\text{household,annual}}$ using the historic simple random sample survey data. This entailed using simple random sampling in the power analysis (Reynolds 2002b, briefly summarized in Appendix 1). When more years of stratified random sampling survey data are available, the process could be repeated with a stratified sampling scheme, giving more directly transferable results. This point is considered further in the discussion.

MATERIALS

Harvest Data

The analysis used subsistence waterfowl harvest survey data collected from simple random sampling within each village since 1995. The two areas with the largest historic survey databases were analyzed: Yukon-Kuskokwim Delta (YKD) and Bristol Bay (BB) (Figure 1). As some regions were recently sampled using a stratified random sampling design within each village, and villages varied in their past participation in the survey, the temporal coverage of the available data varied across villages (Table 1). The starting time of 1995 was chosen simply for convenience of data access and collation and to minimize the influence of trends affecting year-to-year variation. The analysis utilized per household annual harvest records, created by summing across the relevant seasonal harvest records. Only household records with complete annual surveys were used. That is, only surveys from households that responded every season in a given year were used (YKD -spring, summer, fall harvest surveys; BB – spring, summer, fall, and, for certain regions, winter harvest surveys).

Census Data

The 2000 census data were used for the number of households currently in each village (Table 1, summarized from Stehn 2002).

Survey Cost Data

Survey cost data was available as a 'per household cost' (provided by Cynthia Wentworth 9 Dec 2002) (Table 1). Household survey cost was defined at the area level for YKD and at the region level for BB.

Software

All simulations, analyses, and figures were generated using the S-Plus 2000 data analysis environment (Insightful, Inc., Seattle, WA.). The simulation code is available from the author upon request (see Appendix 2 for example code).

METHODS

Sampling Simulation

ESTIMATING $F_{\text{HOUSEHOLD,ANNUAL}}$

$F_{\text{household,annual}}$, the distribution of total annual household harvests for each village for each species for each response, was estimated by pooling all complete household survey records for a village from the available simple random sample surveys since 1995 (see Figure 3 for examples). In technical terms, $F_{\text{household,annual}}$ was nonparametrically

Table 1. Per household survey cost and data availability for estimating $F_{\text{household,annual}}$ per village. See text for data sources. For each village in the analysis, every complete household survey from simple random sampling since 1995 was used to estimate $F_{\text{household,annual}}$. Years of coverage denotes first and last year of utilized observations; all intervening years may not be available. Villages in bold had fewer records than their current number of households.

Area	Region	Village	Years of Coverage	Number of Complete Records for Simulations	Current Number of Households	Household Survey cost
YKD	Mid Coast	Bethel	1995-2000	600	1333	\$92.00
		Chefornak	1995-2000	139	64	\$92.00
		Chevak	1995-2000	307	152	
		Hooper Bay	1995-2001	522	210	
		Mekoryuk	1995-2000	136	70	
		Newtok	1995-1999	106	63	
		Nightmute	1996-2000	105	39	
		Scammon Bay	1995-2001	125	89	
		Toksook Bay	1995-2001	168	103	
		Tununak	1997-2001	109	67	
	North Coast	Alakanuk	1995-2001	183	139	\$92.00
		Emmonak	1995-2001	267	168	
		Kotlik	1995-2001	282	110	
		Nunam	1995-2001	148	33	
		Iqua				
		Eek	1995-2000	264	76	\$92.00
	South Coast	Kipnuk	2000	60	133	
		Kongiganak		0	72	
		Kwigillin-gok		0	73	
		Tuntutuliak	1995-2000	257	81	
		Akaichak	1995-1999	253	133	\$92.00
		Akiak		0	65	
		Aniak	1996-2000	215	138	
		Atmaultuak	1997-2000	84	52	
		Lower Kalskag	1995-2000	171	62	
		Upper Kalskag	1996-2000	38	48	
		Kasigluk		0	92	
		Kwethluk	1995-2001	373	128	
	Kuskokwim River					

POWER ANALYSIS FINAL REPORT

<i>Area</i>	<i>Region</i>	<i>Village</i>	<i>Years of Coverage</i>	<i>Number of Complete Records for Simulations</i>	<i>Current Number of Households</i>	<i>Household Survey cost</i>
BB	Lower Yukon River	Napakiak	1995-2000	221	89	\$92.00
		Napaskiak	1998-1999	69	80	
		Nunapit-chuk	1995-2001	195	104	
		Oscarville	1995-2000	53	15	
		Tuluksak	1995-2000	84	83	
		Marshall	1995-2000	150	82	
		Mountain Village	1995-2000	292	155	
		Pilot Station	1997-1999	78	109	
		Pitkas Point	1995-2001	62	26	
		Russian Mission	1995-1999	83	70	
		Saint Marys	1996-2001	188	134	
	South Alaska Peninsula	Chignik City	1996-2001	122	21	\$23.00
		Chignik Lagoon	1996-2001	79	14	
		Chignik Lake	1996-2001	154	35	
		Ivanof Bay	1996-2001	39	9	
		Perryville	1996-2000	128	37	
		Egegik	1996-2001	162	45	
	North Alaska Peninsula	Pilot Point	1996-2001	141	31	\$23.00
		Port Heiden	1996-2000	138	35	
		King Salmon	1995-2000	668	134	
	King Salmon	Naknek	1995-2000	998	202	\$23.00
		South Naknek	1995-2000	212	54	
		Aleknagik	1995-1999	61	55	
	Dillingham					\$140.00

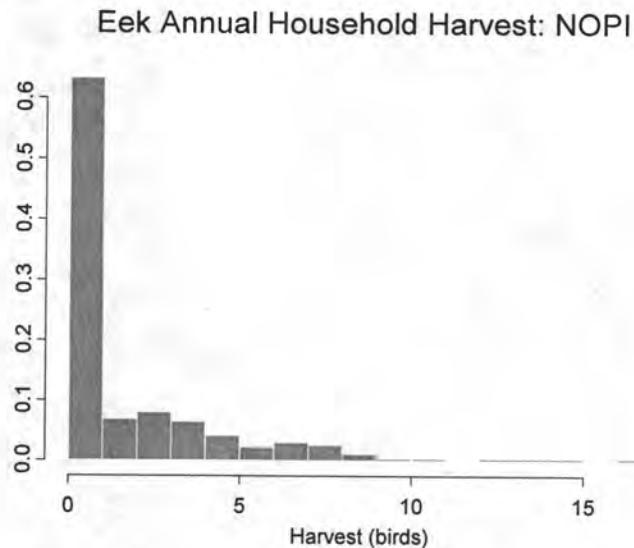
<i>Area</i>	<i>Region</i>	<i>Village</i>	<i>Years of Coverage</i>	<i>Number of Complete Records for Simulations</i>	<i>Current Number of Households</i>	<i>Household Survey cost</i>
		Clarks Point	1995-1999	58	30	
	Nushagak	Dillingham	1995-1999	709	686	
		Ekwok	1995-1999	77	31	\$140.00
		Koliganek	1995-1999	53	42	
		New Stuyahok	1995-1999	114	94	
		Portage Creek		0	7	
	Iliamna	Iguigig	1995-1999	35	10	\$140.00
		Iliamna	1995-1999	80	29	
		Kokhanak	1995-1999	36	36	
		Levelock	1995-1999	47	26	
		Newhalen	1995-1999	48	36	
		Nondalton	1995-1999	85	37	
		Pedro Bay	1995-1999	38	18	
	Togiak	Goodnews Bay	1999-2000	42	56	\$91.00
		Quinhagak	1996-2000	179	113	
		Platinum	1998-2000	52	17	
		Togiak	1995-2001	307	157	
		Twin Hills	2000	14	26	
		Manakotak	1995-2001	187	84	

estimated as the empirical distribution function of household harvests - that is, as the relative frequency histogram of the household harvest results for this specific village, species, and response (Lunneborg 2000). The more historic observations available, the more representative the estimate of $F_{\text{household,annual}}$. Villages varied widely in the number of observations available for estimating $F_{\text{household,annual}}$ (Table 1, column 5).

SAMPLING FACTOR RANGES INVESTIGATED

The number of villages sampled per area ranged from a minimum of 1 per region + the area hub to the total number of villages in the area for which data was available, i.e., a complete census at the village level. Specifically, for YKD simulations were conducted with the number of villages sampled per area set as 5 + Bethel (one village per region), 7 + Bethel, 9 + Bethel, ..., 31 + Bethel, or 33 + Bethel (all available villages). For the BB area, simulations were conducted with the number of villages sampled per area set as 7 + Dillingham (one village per region + Dillingham), 9 + Dillingham, 11 + Dillingham, ..., or 29 + Dillingham (all available villages).

Figure 3. Distribution of harvest survey annual values for Eek: Northern Pintail (birds). This is the estimate of $F_{\text{household,annual}}$. The y-axis is relative frequency. Note that one of the 264 observations is a harvest of 16 birds (this bar doesn't appear because it only has a relative frequency of $1/264 < 0.004$).



Simulations were conducted with the percentage of households sampled in each area set as 5%, 10%, 15%, ..., or 75%.

SIMULATION STEPS AND ESTIMATION DETAILS

For each combination of sampling factor settings, 500 sampling events were simulated in each region of each area. Each simulation followed these steps:

1. Set the number of villages to sample in the area, NV .
2. Calculate the number of villages to sample in a specific region R :

$$NV_R = NV \frac{\text{\#of households in Region } R}{\text{\#of households in Area} - \text{\#of households in Hub}}, \text{ with } NV_R \text{ rounded to}$$

the nearest integer and where the area Hub is either Bethel or Dillingham. If $NV_R < 1$, then NV_R is set to 1 so that at least one village is sampled in each region. If $NV_R > \text{the total number of villages available in the region}$, then NV_R is set to the total number of villages available in the region. This last case can only occur when NV is very large and there is great disparity, across the area, in the number of households in each village.

This calculation uses the current number of households in a village and only includes those villages for which historic survey observations were available. The calculation is based on the number of households in a region, not the population size of a region as in Wentworth (1998), as the household is the sampling unit, not the individual.

3. Randomly select NV_R villages from region R for sampling.
4. Set the percentage of households to sample in each area, $P\%$.
5. Calculate the percentage of households to sample in each village, $H\%$, so as to sample $P\%$ of the area households overall:

$H = P \frac{\text{total \# of households in region R}}{\text{total \# of households in villages selected for sampling}}$. If $H\% > 100\%$, then set $H\%$ to 100%.

6. For each selected village V , randomly sample n_v household surveys from the estimate of $F_{\text{household,annual}}$ for that village, where $n_v = H\%$ times the total current # of households in the village (Table 1). Household surveys are sampled with replacement from $F_{\text{household,annual}}$. Note that a sample of household surveys generates a sample for each of the 12 species and response combinations.

7. For each selected village, for each species and response combination, calculate that village's mean household harvest for that species and response:

$$\bar{X}_{\text{Village, Species, Response}} = (1/n_v) \sum_{\text{sampling households}} \text{harvest}_{\text{household } i, \text{ Species, Response}}$$

8. For each region, for each species and response combination, estimate the region's total harvest. First, the region mean household harvest is estimated:

$$\bar{X}_{\text{Region, Species, Response}} = \sum_{\text{sampling villages } V} w_v \bar{X}_{\text{Village } V, \text{ Species, Response}}, \text{ where } w_v = \frac{\text{total households in the sampled villages that occur in village } V}{\sum n_v}$$

This estimator gives more weight to the mean harvest estimates from the larger sampled villages. The region total harvest is then estimated as

$(\text{Total \# of households in the Region}) \bar{X}_{\text{Region, Species, Response}}$. While differing in description, this weighted estimate of total region harvest is identical to that described in Wentworth & Seim (1996) and Wentworth (1998).

9. Sum the total region harvest estimates from each region in the area to estimate the annual area harvest (Wentworth & Seim 1996; Wentworth 1998).

10. Calculate the area survey cost:

$$\text{Survey Cost} = \sum_{\text{Regions } R} \text{Cost}_R (\text{\# of households sampled in Region } R), \text{ where } \text{Cost}_R \text{ is the per household survey cost in region } R \text{ (Table 1).}$$

Villages with no historic observations (0 entry in column 5 of Table 1) were dropped from the simulations. Therefore the total number of households in a region does not include the households in any village whose harvest cannot be simulated. This reduces the total harvest estimates from the following regions: YKD – Kuskokwim River, South Coast; BB – Nushagak.

Five hundred simulations were run for each of 225 sampling scenarios for the YKD area and for each of 180 sampling scenarios for the BB area, for a total of 202500 simulated sampling events.

ANALYSIS DETAILS

In technical terms, the analysis process was a Monte Carlo simulation. The 500 simulations for each combination of sampling factor settings, (denoted as 'sampling scenario'), provided, for that sampling scenario, a Monte Carlo estimate of the sampling distribution of each of the following outcomes of interest: region total annual harvest estimate for each species and response, area total annual harvest estimate for each species and response, and 'statewide' total annual harvest estimate for each species and response.

Statewide total annual harvest estimates were approximated as the sum of total annual harvest estimates from the YKD area and the BB area. For each setting of 'number of villages sampled per area' from 8 to 30, and for each setting of 'percentage of total area households sampled', a randomly selected YKD result was added to a randomly selected BB result to obtain an estimate of statewide total annual harvest. Note that the sampling coverage achieved by a given number of villages is not identical across the two areas since they differ slightly in their total number of villages.

There were two characteristics of interest of each of the estimated sampling distributions: the *bias* and the *precision*.

Bias

Bias is the mean total annual harvest estimate minus the true total annual harvest. For these simulations, an area's true total annual harvest for a species and response was calculated as follows. The village mean harvest was calculated from each village's pooled historic harvest survey data. This was the true mean of $F_{\text{household,annual}}$ for the village. The village true total annual harvest was calculated as the village mean harvest times the current number of households in the village. The region true total annual harvest was the sum of the village true total annual harvests; the area true total annual harvest was the sum of the region true total annual harvests. Only villages with historic survey data, i.e., those used in the simulations, were used in this calculation.

Precision — *Sampling : error*

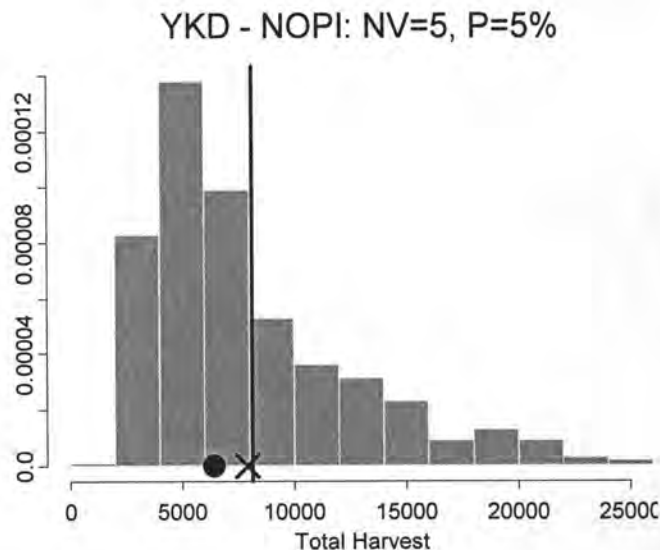
Precision was measured as the length of the central 90% of the Monte Carlo sampling distribution. That is, the 5th and 95th percentiles of the sampling distribution were calculated and the interval between these percentiles, and its total length, used as precision measures (Figure 4). This measure is analogous to the width of the 90% symmetric nonparametric bootstrap confidence interval when estimating (Lunneborg 2000). Taking 500 Monte Carlo simulations guaranteed sufficient accuracy in the resulting bias and precision estimates (Davison & Hinkley 1997). Note that the sampling distributions were not expected to be symmetric, hence the choice of total distance rather than a measure such as radius or standard error whose interpretation entails assumptions of distribution symmetry.

Data Visualization

Data visualization was used to summarize and compare estimated sampling distributions across sampling scenarios. Some graphical summaries display the estimated 5th and 95th percentiles and the estimated mean area total annual harvest, others simply display the

Figure 4. Example sampling distribution estimate from Monte Carlo simulations: YKD area total annual harvest of Northern Pintails (birds), when 5 villages (+ Bethel) are sampled at a rate of 5% of the households in the area. Y-axis is relative frequency.

The vertical line marks the true total annual harvest of Northern Pintails in the YKD area (see text for details), the 'X' marks the mean estimated annual harvest, and the filled circle marks the median annual harvest (50th percentile).



distance between the estimated 5th and 95th percentiles. The first example of each type of display contains a detailed explanation in the legend.

RESULTS

The simulation results for the state and each area were summarized with thirteen graphical displays apiece: one display for each species and response (twelve total) and a summary display of precision results. The simulation results for each region were summarized with similar graphical displays (Appendix 3 contains the YKD results, Appendix 4 the BB results). The area results are given first, followed by the state results.

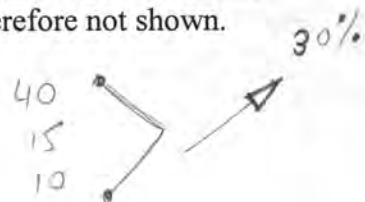
YUKON-KUSKOKWIM DELTA

At the spatial scale of the Yukon-Kuskokwim Delta, the estimator of total annual harvest appeared fairly unbiased for bird take of every species of interest (Figures 5 – 10) as well as for egg take of every species of interest (Figures 11 – 16). Except for those species with the lowest annual harvest rates, Spectacled Eiders (birds and eggs) and Black Scoters (eggs), all responses showed a pattern of 'diminishing returns' with increasing sampling effort (Figures 5 – 16, more clearly displayed in Figure 17). Sampling more than 23 villages in the area + Bethel, or 71% of the villages, at a rate of more than 20-30% of the area households provided only slight improvement in precision (Figure 17).

Region-specific total annual harvest results for the YKD area are in Appendix 3.

Survey cost factors were only available as per household costs. Lacking village-specific or region-specific travel costs, the simulated total survey costs were approximately proportional to the total percentage of area households surveyed, P%. The simulated total survey cost was the same whether 25% of the area households were surveyed across 11 villages or across 23 villages, giving no insight into the true costs associated with increasing precision by sampling more villages. Results are therefore not shown.

BRISTOL BAY AREA



At the spatial scale of the Bristol Bay area, the estimator of total annual harvest gave a nearly unbiased estimate of bird take for every species of interest (Figures 18 – 23). It gave an unbiased estimate of egg take for every species of interest except Northern Pintails, for which is tended to slightly underestimate (Figures 24 – 29). When it occurred, the slight bias was not significant relative to the estimator's imprecision (Figures 18 – 29). Except for those responses with the lowest annual harvest rates, (Spectacled Eider birds and all species' eggs), all responses showed a pattern of 'diminishing returns' with increasing sampling effort (Figures 18 – 29, more clearly displayed in Figure 30). Sampling more than 21 villages in the area + Dillingham, or 73% of the villages, at a rate of more than 25% of the area households provided only slight improvement in precision (Figure 30).

Region-specific total annual harvest results for the BB area are in Appendix 4.

Survey cost factors were only available as per household costs. Lacking village-specific or region-specific travel costs, the simulated total survey costs were approximately proportional to the total percentage of area households surveyed, P%. The simulated total survey cost was the same whether 25% of the area households were surveyed across 11 villages or across 23 villages, giving no insight into the true costs associated with increasing precision by sampling more villages. Results are therefore not shown.

STATEWIDE APPROXIMATION

At the spatial scale of the state, or at least those portions covered by the YKD and BB areas, the estimator of total annual harvest gave a nearly unbiased estimate of bird take for every species of interest (Figures 31 – 42). All responses showed a pattern of 'diminishing returns' with increasing sampling effort (Figures 31 – 42, more clearly displayed in Figure 43). Sampling more than 23 villages in the area + the hub, i.e., about 70% of the villages + the hub, at a rate of more than 25% of the area households, provided only slight improvement in precision (Figure 43).

DISCUSSION

Sampling Effort Summary

All results show a point of diminishing returns beyond which the added sampling effort brings little reduction in estimate imprecision. In general, this is approximately the same across areas and responses (species, harvest types), for those species and takes whose harvest is of sufficient frequency to demonstrate ANY improvement in precision with increased sampling effort: sampling 23 villages in the area (+ the Hub) at a rate of 25% of the area households.

While this result propagates up from the area to the state level, so far as data is available, specific regions may show lower levels are sufficient for specific species and takes. Note that the YKD and BB areas may not accurately represent the true pattern in other areas of the state.

Relation to Stratified Random Sampling

The simulation results assume simple random sampling of households within villages. In general, stratified random sampling provides an estimator whose variance is no worse than simple random sampling. Therefore these results provide an *upper bound* on the uncertainty expected under stratified random sampling. I.e., sampling effort required to reach comparable precision using stratified random sampling should be less, and at worse nor more, than that shown here with simple random sampling. The committee should consider repeating this analysis when sufficient stratified random sampling data becomes available.

Sampling Cost Estimates

The available survey cost information was insufficient to provide insight into the relationship between survey cost, sampling design, and estimate precision. The simulated cost results increased approximately in direct proportion to the percentage of area households sampled, regardless of the number of villages sampled. While it will not be simple to calculate, the committee should consider estimating the fixed sampling costs associated with each specific village, such as travel to and from the village. They would then be in a position to rerun the analysis and obtain relevant insight into the tradeoffs among cost, design, and precision.

Methodological Issues

Bias

The BB area results show some slight bias, differing across species and takes. Ignoring errant bias due to too little sampling (number of villages sampled < 15), there is a tendency to overestimate Northern Pintail bird takes and Emperor Goose bird takes, and a tendency to underestimate Spectacled Eider bird takes, Black Scoter bird takes, and Northern Pintail egg takes (Figures 18, 21, 19, 20 and 24, respectively). All the biases have their source in specific regions, generally arising due to inadequate sampling effort to fully capture the highly skewed harvest distributions of the region's villages.

The bias in Northern Pintail bird takes is due to biased estimation in the Dillingham and Nushagak regions (Appendix 4), all of which declines as sampling effort increases. This is likely due to the necessity of fairly intensive sampling to account for the extremely skewed harvest distributions of each of the regions' villages (Figure 45).

The bias in Emperor Goose bird takes is due to biased estimation in the South Peninsula region (Appendix 4), arising from the very low number of harvests and hence highly skewed harvest distributions. Note that the South Peninsula contains only ~11% of the BB area households (excluding Dillingham), hence the number of villages sampled under any of the scenarios is 0.11 times NV, rounded to the nearest whole number (refer to the simulation steps detailed above). This is only 1, 2, or, for the highest settings of NV, 3 villages from the region's total of 5. This low to moderate sampling effort fails to adequately capture the region's skewed harvest distributions and hence true harvest.

The bias in Spectacled Eider bird takes is due to biased estimation in the South Peninsula region, and to a slight extent the Togiak region (Appendix 4). Again, there are very few harvests of Spectacled Eiders, the vast majority of harvest survey results being 0: Chignik

City – 100% 0, Chignik Lagoon – 100% 0, Chignik Lake – 94% 0, Ivanof Bay – 97% 0, Perryville – 96% 0. The low to moderate sampling effort applied to this region fails to adequately capture the region's very rare nonzero harvests, producing underestimates of the true harvest.

The bias in Black Scoter bird takes is due to biased estimation in the Nushagak region (Appendix 4), again arising from the very few nonzero takes and the low to moderate sampling effort this region received.

The bias in Northern Pintail egg takes is due to biased estimation in the Dillingham region (Appendix 4), again arising from the very skewed harvest distributions in this region, with their few nonzero takes.

Sufficiency of the historic survey observations for estimating $F_{\text{household,annual}}$

The vast majority of villages had more historic observations available for estimating $F_{\text{household,annual}}$ than the number of samples that would be drawn from this distribution (i.e., at most, the current number of households) (Table 1). There was moderate variation among villages as to the relative number of historic observations available for estimating $F_{\text{household,annual}}$ relative to the current number of households in the village. However, this relative variation among villages was approximately equal across areas (BB has somewhat higher ratios of number of observations to number of households), suggesting that the area results are comparably influenced by variation in data richness.

Simulation cap on number of households sampled in a village

As stated in the simulation steps detailed above, there was a maximum to the number of simulated households samples drawn from each chosen village: 100% of the current number of households in that village (see step 5). If there was a large disparity across villages in a region in the total number of households in each village, then this maximum could be attained. Note that area hubs were excluded from this calculation. This may be the source of some of the bias seen in the Dillingham region results at settings with low numbers of villages and moderately high percentage of area households sampled.

Simulation cap on number of villages sampled in a region

As stated in the simulation steps detailed above, there was a maximum to the number of villages sampled from each region – it could not exceed the total number of villages in the region! If there was a large disparity across regions in their number of households, excluding the area hub, then the requested number of villages to sample could exceed the available number of villages (see step 2). In these rare cases, then the results from the sampling all villages in the region (the previous setting of 'number of villages to sample') were simply copied over in the simulation results. This is the source of the parallel line structure at the very high NV values of, say, Spectacled Eider egg takes or Cackling Canada Goose egg takes in Figure 30. This structure arose because all villages in Togiak, the main harvest region for these takes, were being sampled by the 'sample 25 villages in the area' setting was reached.

Relation of Monte Carlo precision estimates to sample-based variance estimates (Finite Population Correction issue)

The main characteristic of interest in the simulation results is the precision of the total annual harvest estimate; this an alternative measure of the variance of the sample statistic of interest (total annual harvest). It was chosen instead of the variance as it is more directly comprehended by lay audiences and does not require assumptions of distribution symmetry to interpret. Note that all the simulation data is available should the committee decide to calculate variances.

It is well known that when (i) the sample statistic of interest is the mean, (ii) you are sampling a finite population, and (iii) you are calculating a *sample-based estimate of the variance of the sample mean*, then you should use a finite population correction factor (Cochran 1977, pg 24). The sample statistic of interest in this case, the total annual harvest, is a function of the sample mean household harvest rate for each village. However, note the results of interest are not sample-based estimates of the variance. We are not estimating the unknown sampling variance of the annual harvest from each sample. Rather we are using Monte Carlo simulations to directly estimate the whole sampling distribution of the annual harvest. One can then directly calculate any characteristic of interest from this distribution. We chose the central 90% of the distribution.

Extending the Simulation Analysis: Missing Data

The analysis could be repeated with a missing data process overlain at the household level. Doing so requires specifying how the estimation process will handle the missing data: ignore, impute values from sample observations, impute values from historic observations, or some other approach.

Extending the Simulation Analysis: Trend Assessment

Trend assessment is of ultimate interest, but it was not attempted as part of the current project because: (i) insufficient time and project funds, (ii) insufficient data. Trend assessment is heavily influenced by the trends in sampling precision across time under different population growth scenarios. The analysis of the simple random sample observations gives an upper bound on the imprecision expected under stratified random sampling. However, the *trends* in imprecision from simple random sampling is likely to not provide very accurate information on the *trends* in imprecision from stratified random sampling. Without a clear relationship between the two, it seems misdirected to undertake such an extensive, and expensive, project whose results will not be clearly related to the true objective of interest (trends under stratified random sampling).

When more extensive data is available from stratified random sampling, the committee may want to undertake such a project. They may want to consider trend assessment methods that entail less restrictive models than simple linear relationships with time, such as methods from industrial quality control literature and the time series literature.

Figure 5. Simulated sampling distribution of Yukon-Kuskokwim Delta area total annual harvest estimates for Northern Pintails. Starting at the lower left panel: the bottom rectangular box covers the central 90% of the distribution of simulated total annual area harvest estimates of Northern Pintails when only 5 villages (+ Bethel) are sampled (y-axis label "Nv5" = Number of villages sampled is 5) – one per region of the Yukon-Kuskokwim area. That is, the left edge of the box marks the 5th percentile estimate (3025 birds, on the x-axis) and the right edge marks the 95th percentile estimate (18289 birds). The 'X' marks the mean estimated total annual area harvest; the filled circle denotes the median (50th percentile) estimated total annual area harvest; the solid vertical line denotes the true area total annual harvest, calculated as described in the text. Each row (box) in a panel displays the results for sampling a different number of villages in the area, with the number of villages sampled increasing as one moves upwards in each panel. Each panel displays the results for sampling a different portion of the total area household: 5% (lower left panel), 10% (panel to the immediate right of it), 15%, and so on, denoted P5, P10, P15...in the panel headers. There is little if any bias once 9 or more villages (+ Bethel) are sampled (Nv9 row and above in any panel).

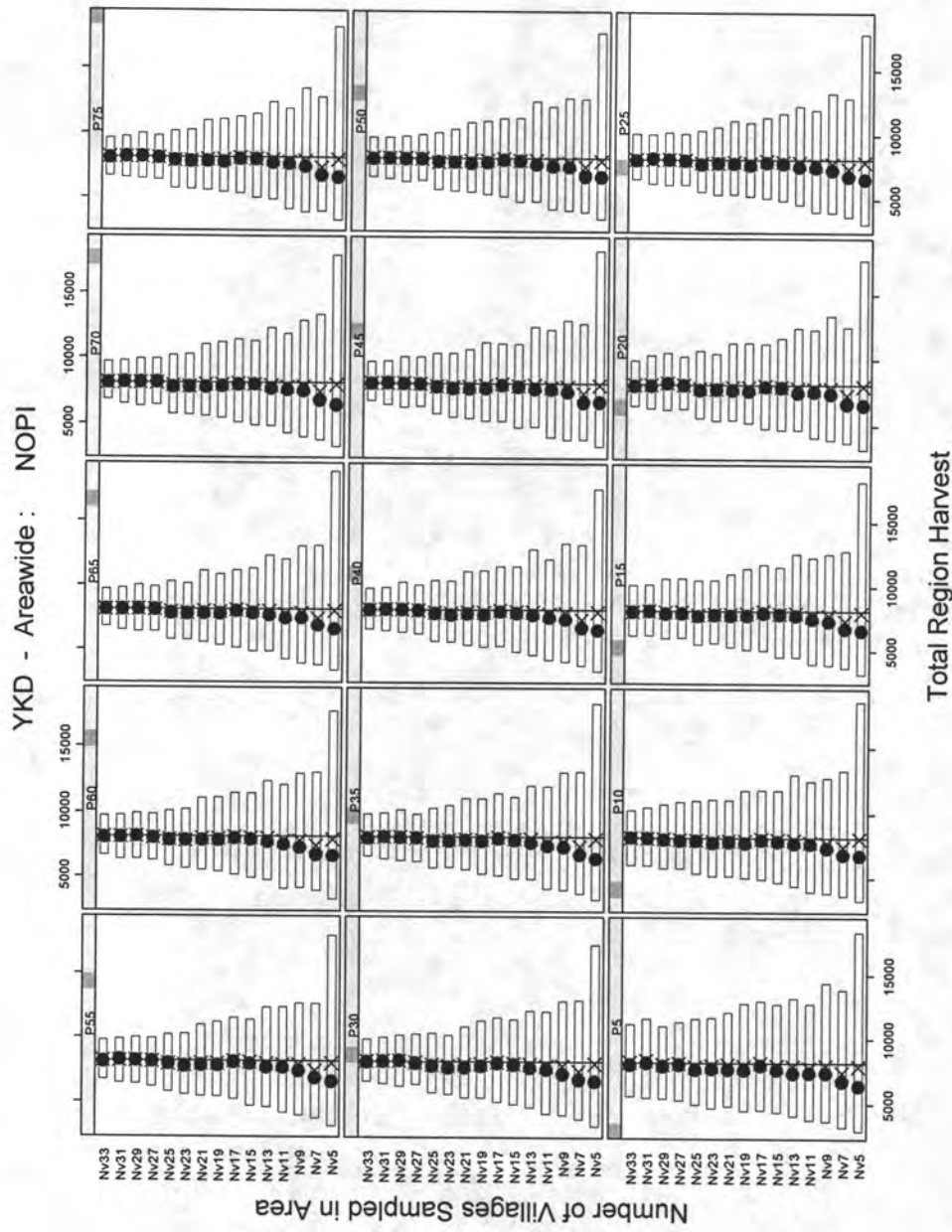


Figure 6. Simulated sampling distribution of Yukon-Kuskokwim Delta area total annual harvest estimates for Spectacled Eiders. There are too few non-zero harvests to produce a gain in precision by sampling more villages. Little precision is gained from sampling more than 25-30% of the area households.

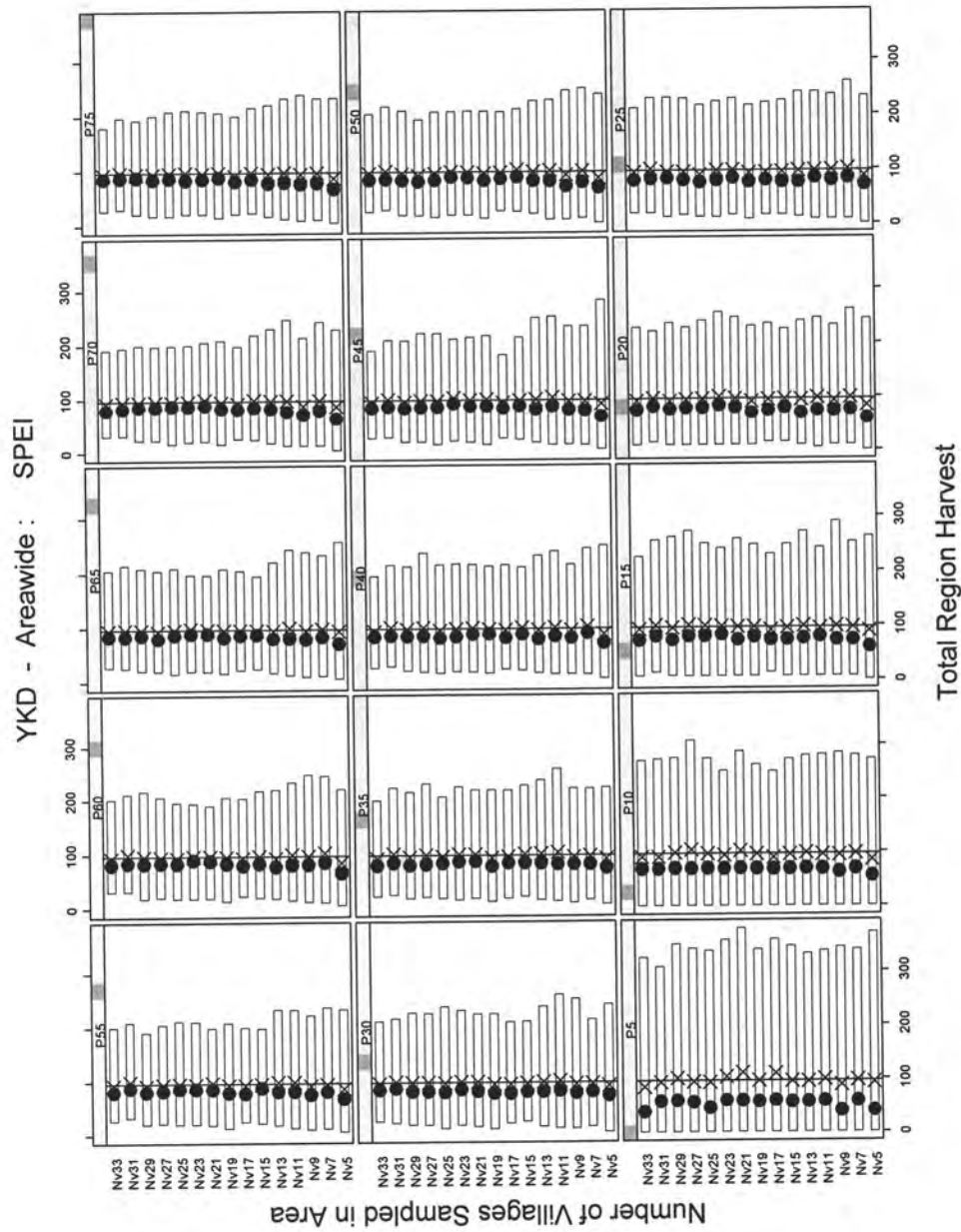


Figure 7. Simulated sampling distribution of Yukon-Kuskokwim Delta area total annual harvest estimates for Black Scoters. There is little gain in precision from sampling more than either 17 or 23 villages in the area (+ Bethel), at a rate of more than 15-25% of the area households.

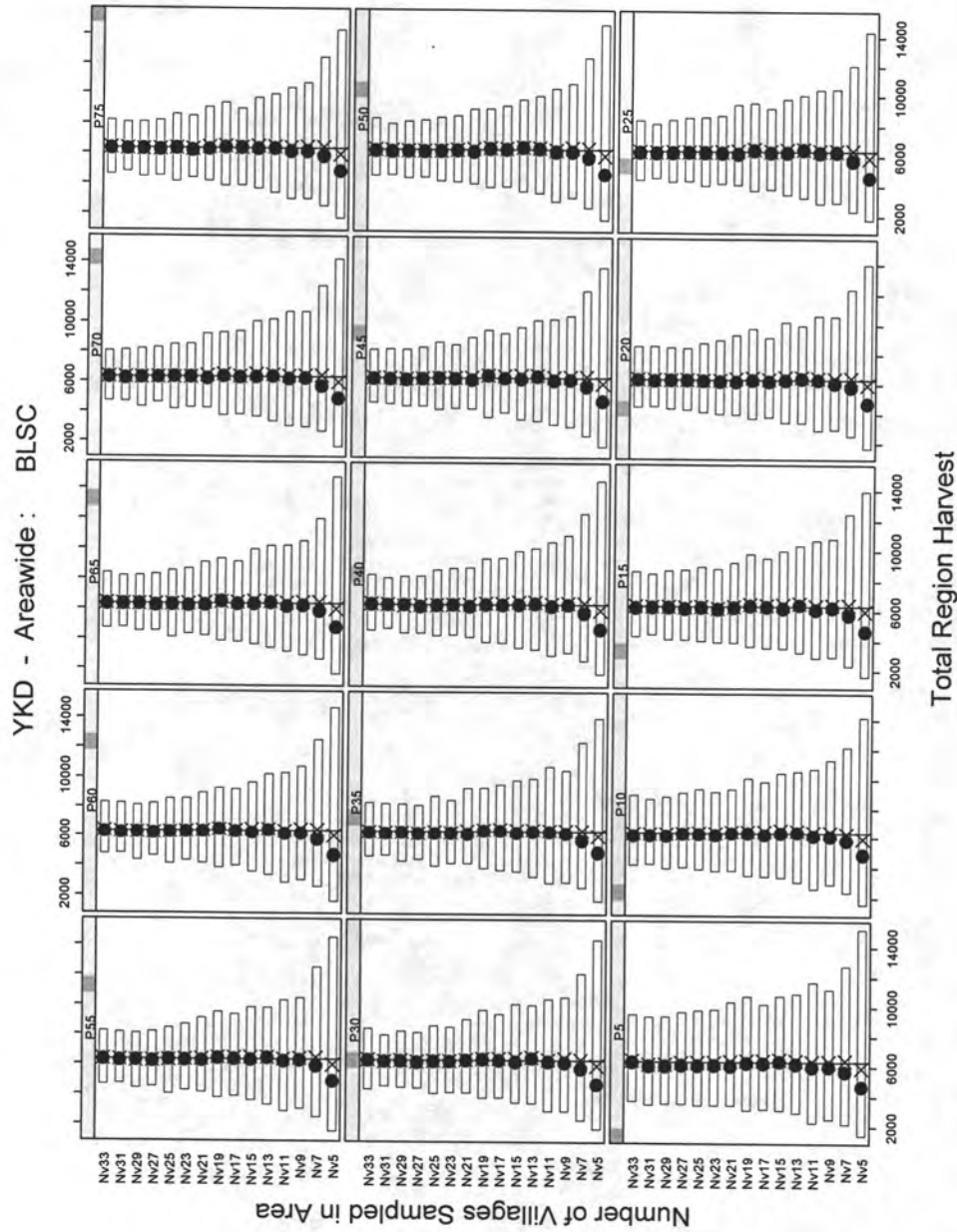


Figure 8. Simulated sampling distribution of Yukon-Kuskokwim Delta area total annual harvest estimates for Emperor Goose. There is little gain in precision from sampling more than either 19 or 23 or 27 villages in the area (+ Bethel), at a rate of more than 15-25% of the area households.

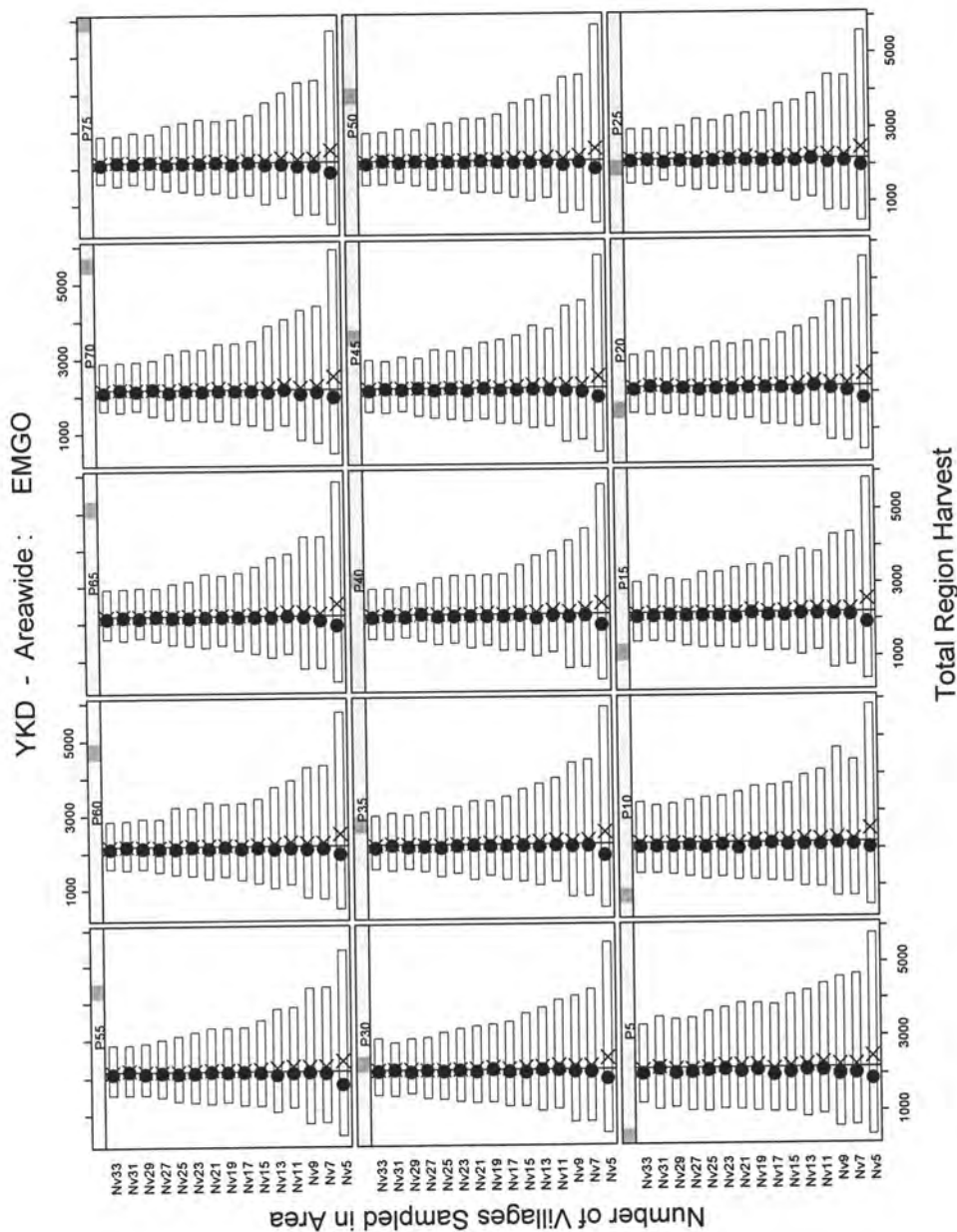


Figure 9. Simulated sampling distribution of Yukon-Kuskokwim Delta area total annual harvest estimates for White Fronted Goose. There is little gain in precision from sampling more than 23 villages in the area (+ Bethel), at a rate of more than 15-25% of the area households.

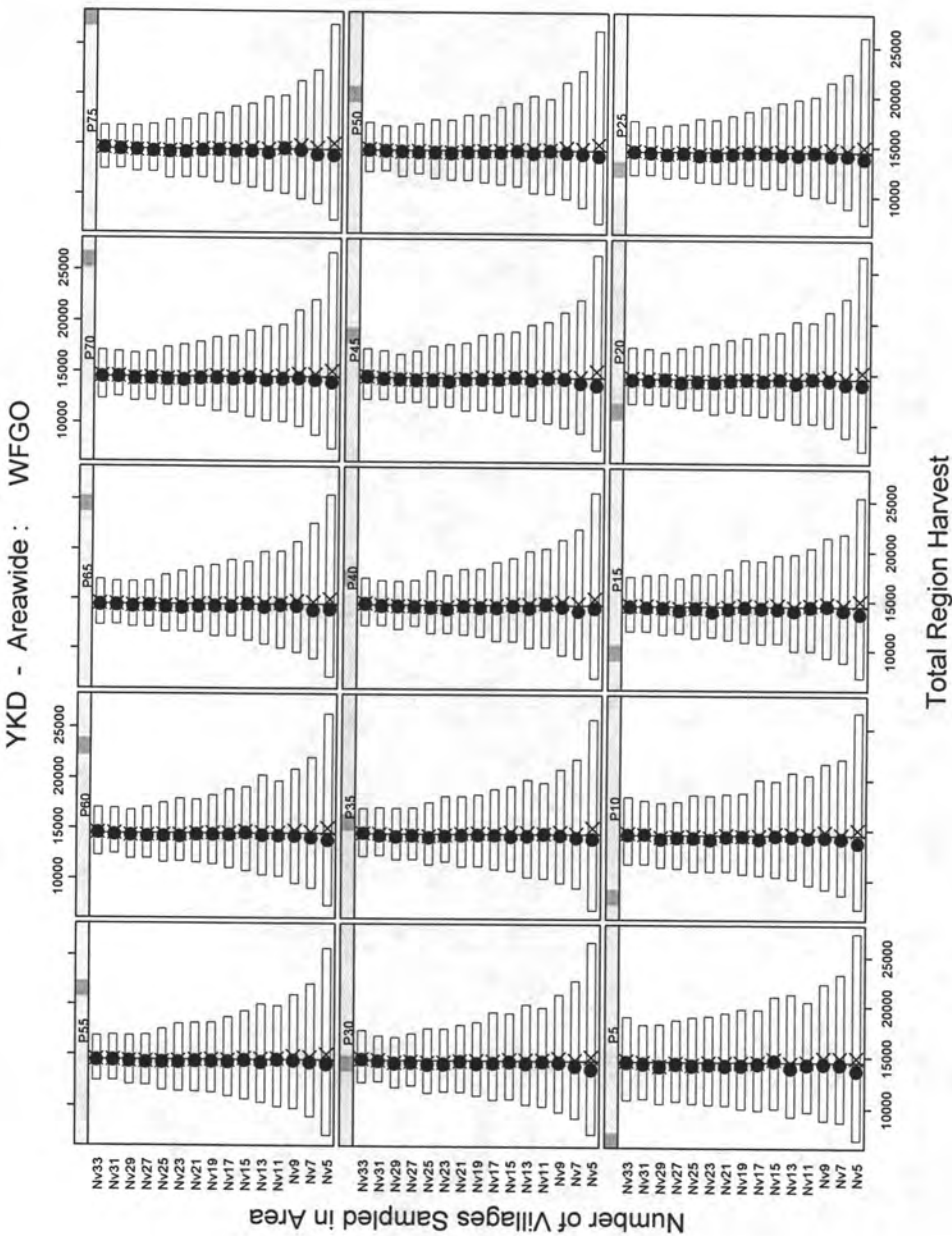


Figure 10. Simulated sampling distribution of Yukon-Kuskokwim Delta area total annual harvest estimates for Cackling Canada Goose. There is little gain in precision from sampling more than 23 villages in the area (+ Bethel), at a rate of more than 15-25% of the area households.

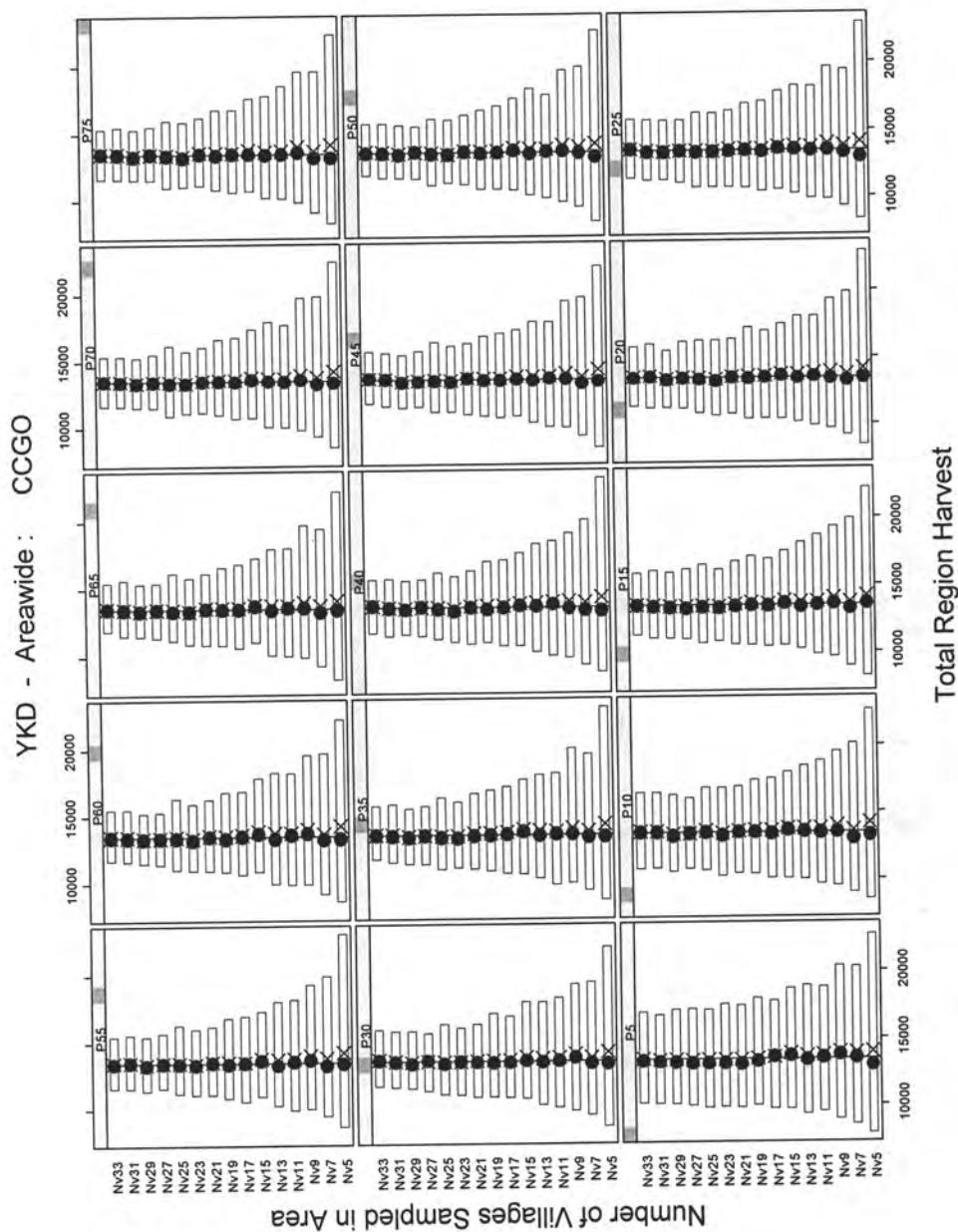


Figure 11. Simulated sampling distribution of Yukon-Kuskokwim Delta area total annual harvest estimates for Northern Pintail eggs. There is little gain in precision from sampling more than 17 to 23 villages in the area (+ Bethel), at a rate of more than 25-30% of the area households.

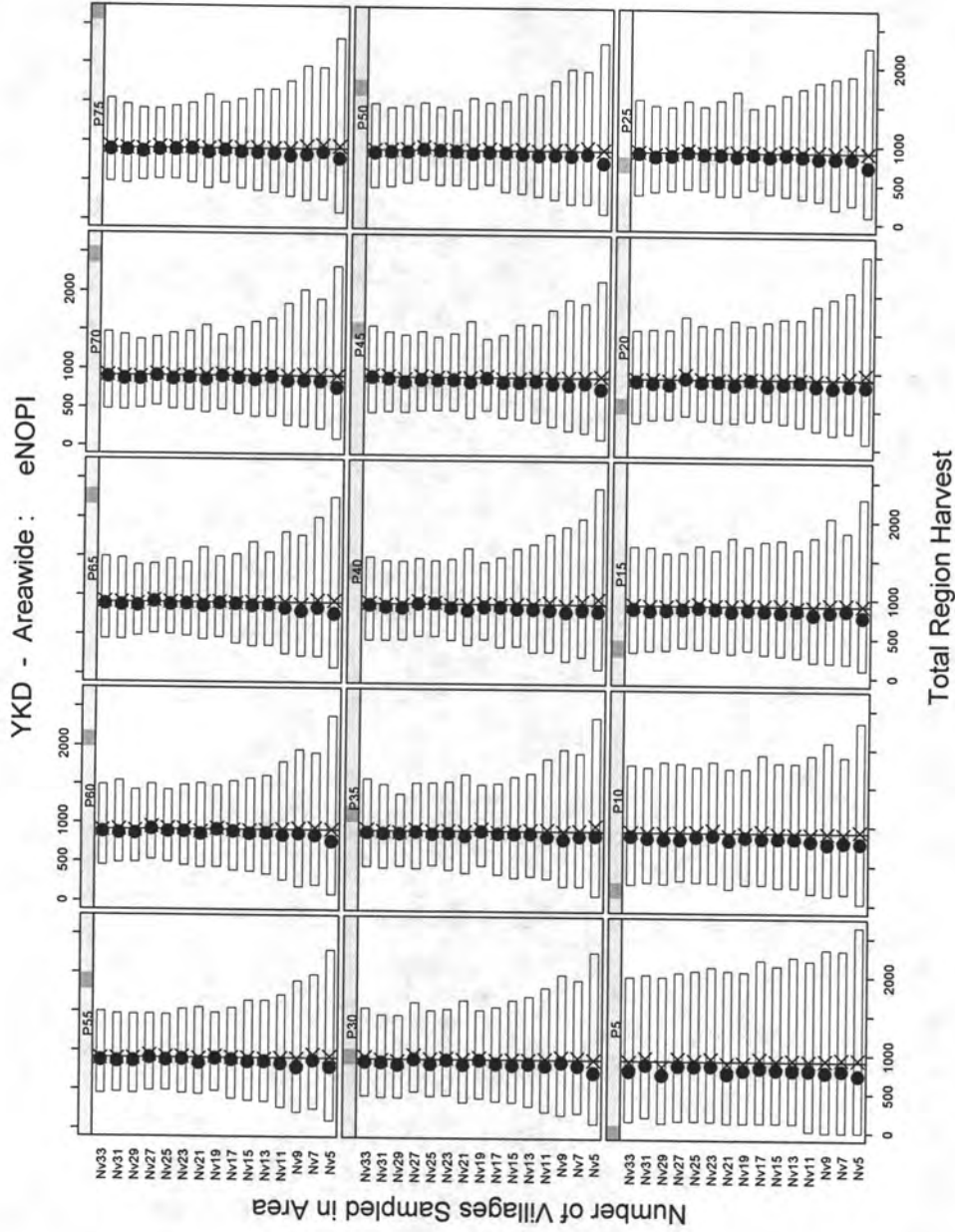


Figure 12. Simulated sampling distribution of Yukon-Kuskokwim Delta area total annual harvest estimates for Spectacled Eider eggs. There are too few non-zero harvests to produce a gain in precision by sampling more villages. Little precision is gained from sampling more than 15-20% of the area households. Many simulated sampling scenarios produced zero estimates for more than 95% of the simulations – hence for these scenarios the central 90% of the distribution is (0,0) and therefore produces no bar in the graph.

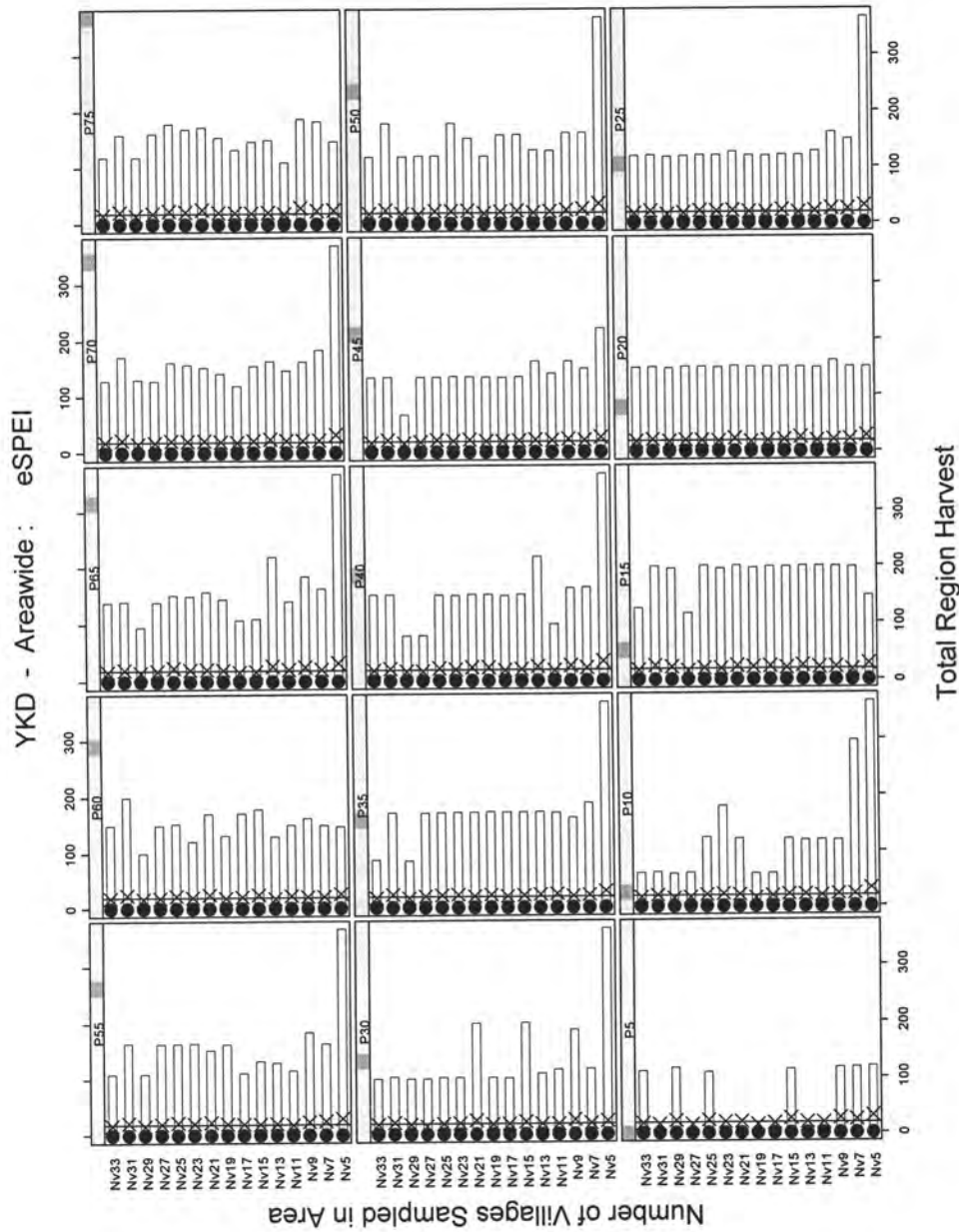


Figure 13. Simulated sampling distribution of Yukon-Kuskokwim Delta area total annual harvest estimates for Black Scoter eggs. There are too few non-zero harvests to produce a gain in precision by sampling more villages.

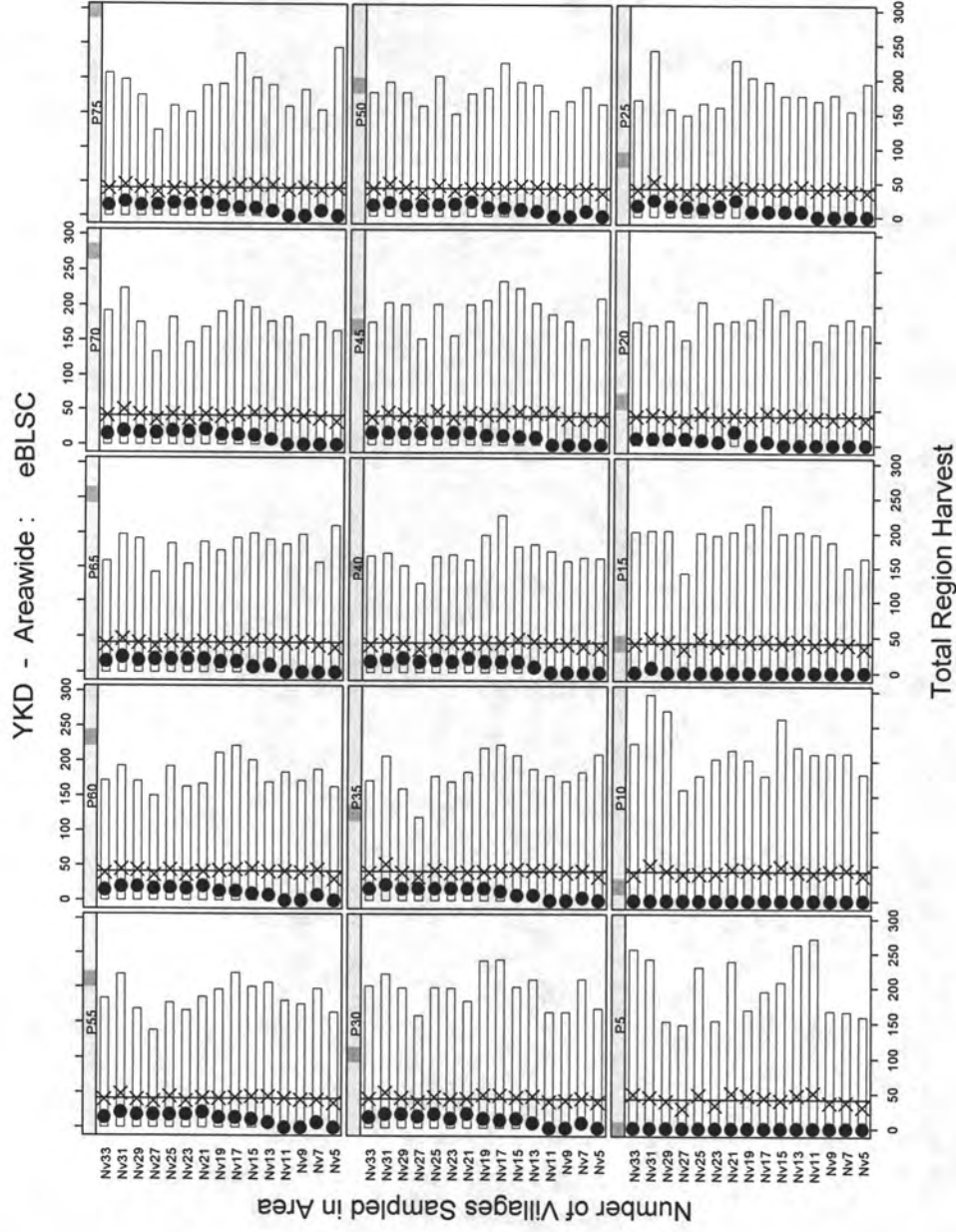


Figure 14. Simulated sampling distribution of Yukon-Kuskokwim Delta area total annual harvest estimates for Emperor Goose eggs. There is little gain in precision from sampling more than 19 or 23 villages in the area (+ Bethel), at a rate of more than 25-30% of the area households.

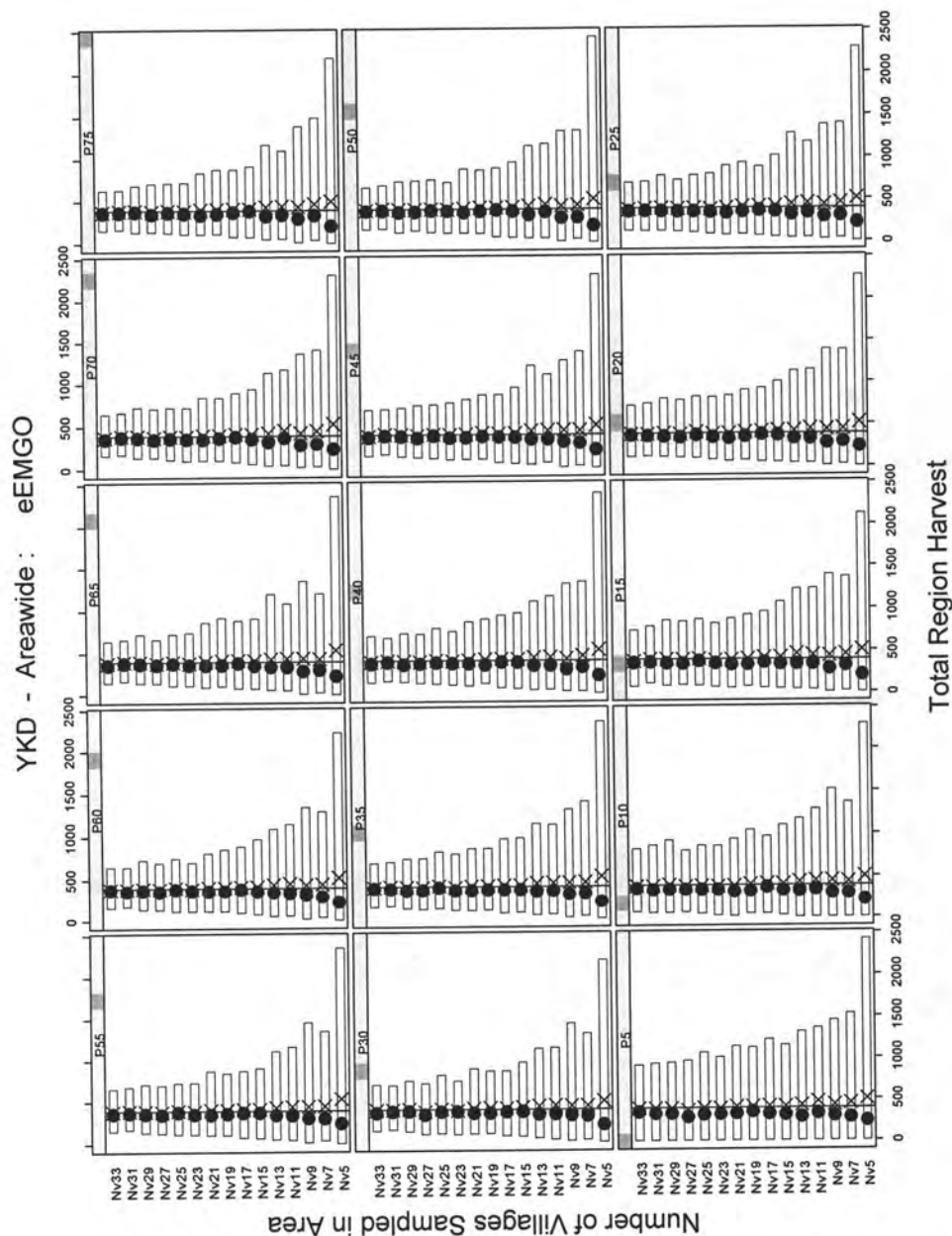


Figure 15. Simulated sampling distribution of Yukon-Kuskokwim Delta area total annual harvest estimates for White Fronted Goose eggs. There is little gain in precision from sampling more than 19 villages in the area (+ Bethel), at a rate of more than 20-30% of the area households.

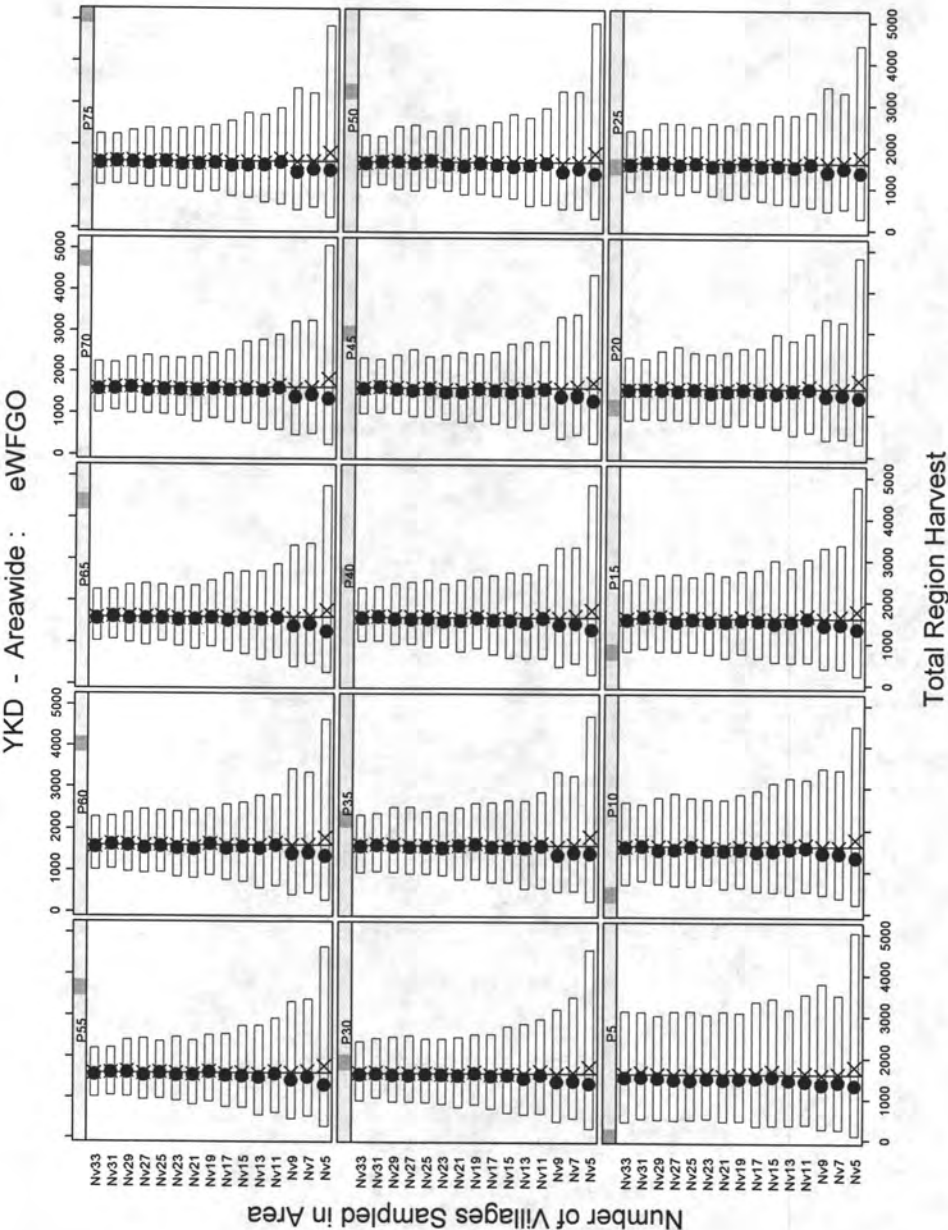


Figure 16. Simulated sampling distribution of Yukon-Kuskokwim Delta area total annual harvest estimates for Cackling Canada Goose eggs. There is little gain in precision from sampling more than 19 villages in the area (+ Bethel), at a rate of more than 20-30% of the area households.

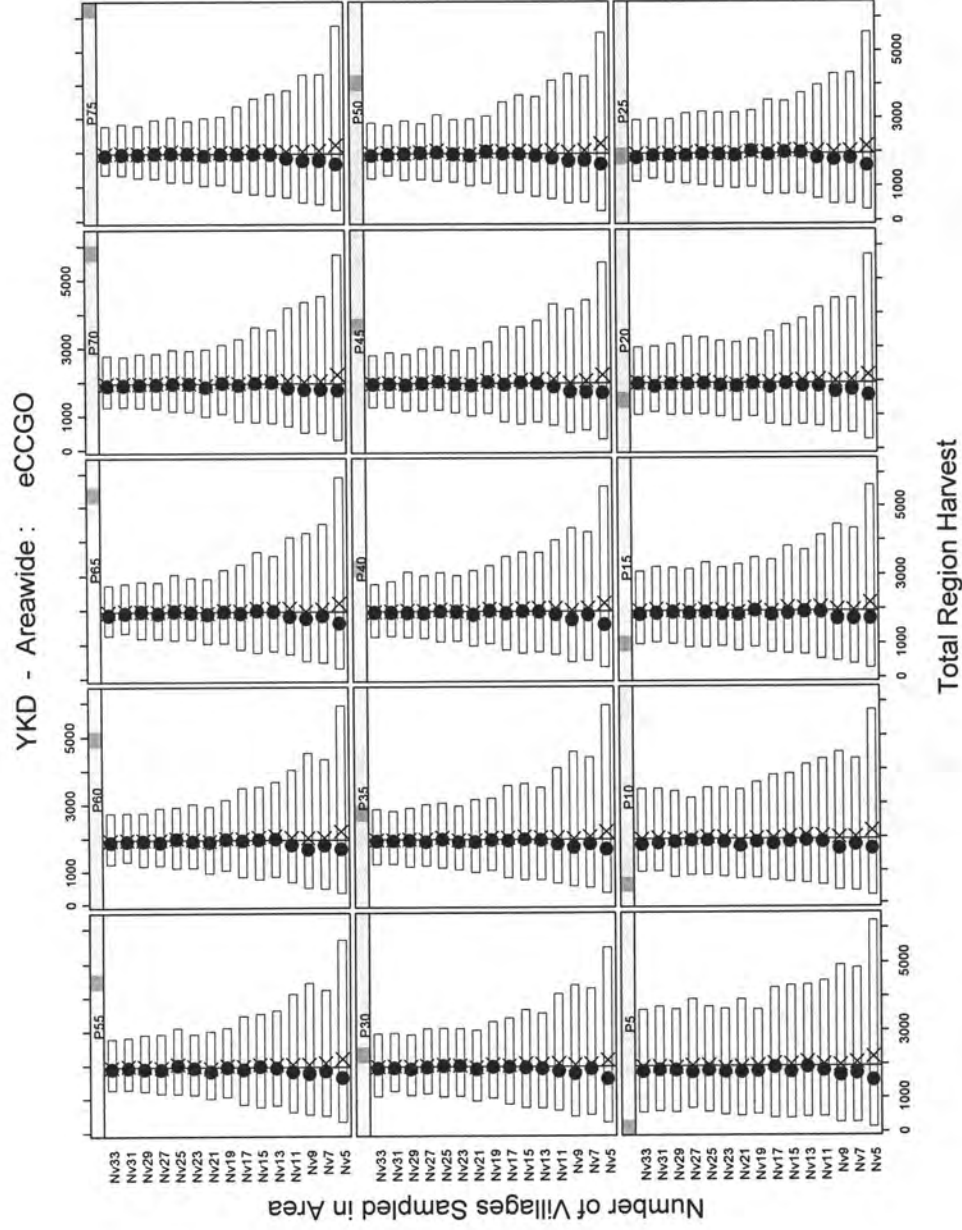


Figure 17. Summary display of sampling factor effects on precision for simulated Yukon-Kuskokwim Delta area total annual harvest estimates, all species and all responses (birds – left two columns; eggs – right two columns). Each panel contains 15 curves, one for each value of the ‘percentage of area households sampled’ factor: 5% – top curve, 10% – second to top curve, ..., 75% – bottom curve. Each curve displays the total width of the central 90% of the simulated sampling distribution, i.e., the length of the ‘rectangular box’ in the respective previous display, for the number of villages sampled given on the x-axis. For example, the width of the central 90% of the sampling distribution for estimated total annual harvest of Northern Pintails when sampling 5 villages (+ Bethel) and 5% of the area households is, from the legend of Figure 5, 18289 – 3025 = 15264 birds. This is the leftmost point on the top curve in the top left panel, labeled ‘NOPI’. Note that in all cases, there is little gain in precision from sampling more than around 23 villages in the area (+ Bethel), at a rate of more than 25-30% of the area households. Zero ‘widths’ arise when 95% or more of the harvest estimates under a given sampling scenario were 0.

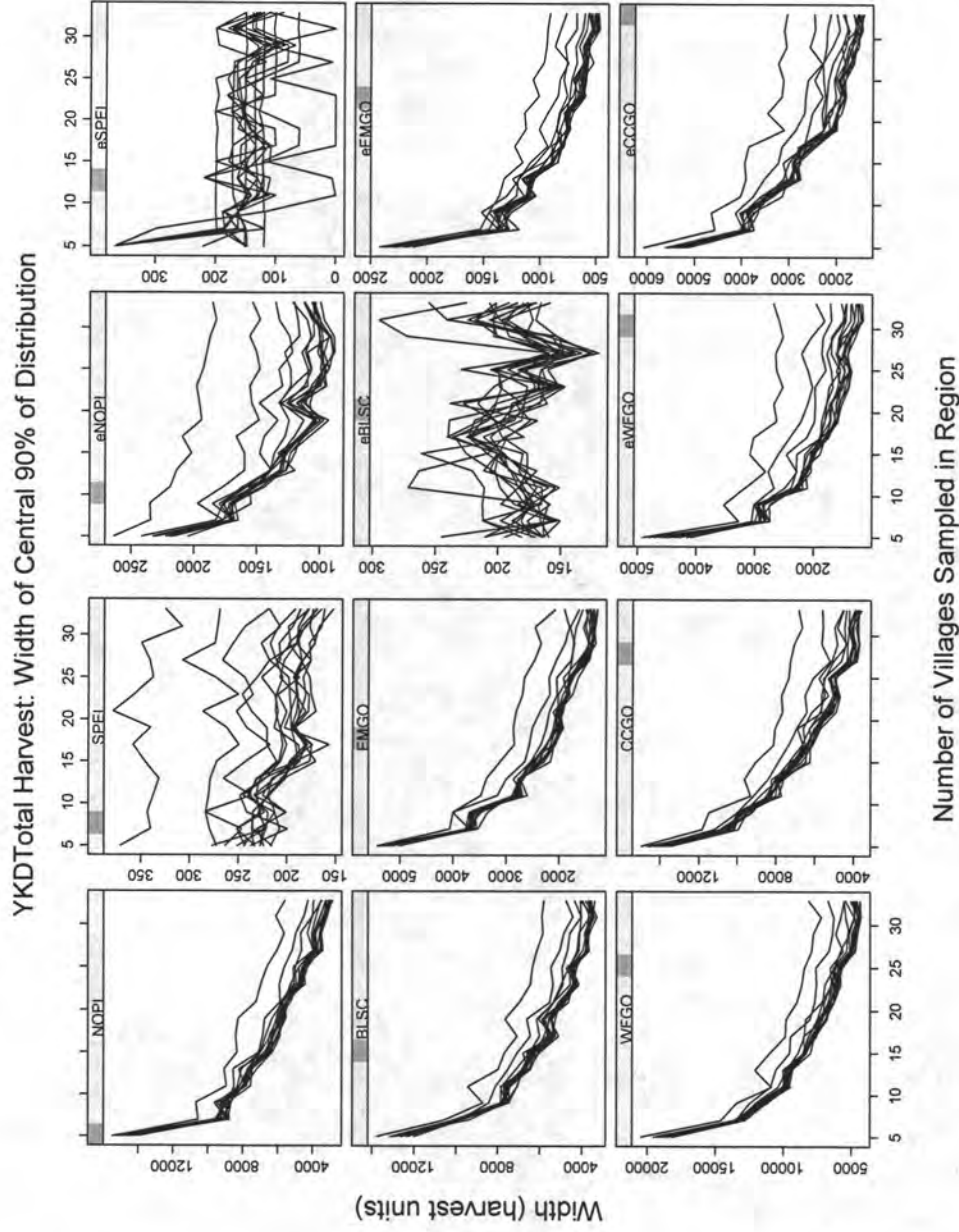


Figure 18. Simulated sampling distribution of Bristol Bay area total annual harvest estimates for Northern Pintails. There is little gain in precision from sampling more than 21 villages in the area (+ Dillingham), at a rate of more than 30% of the area households.

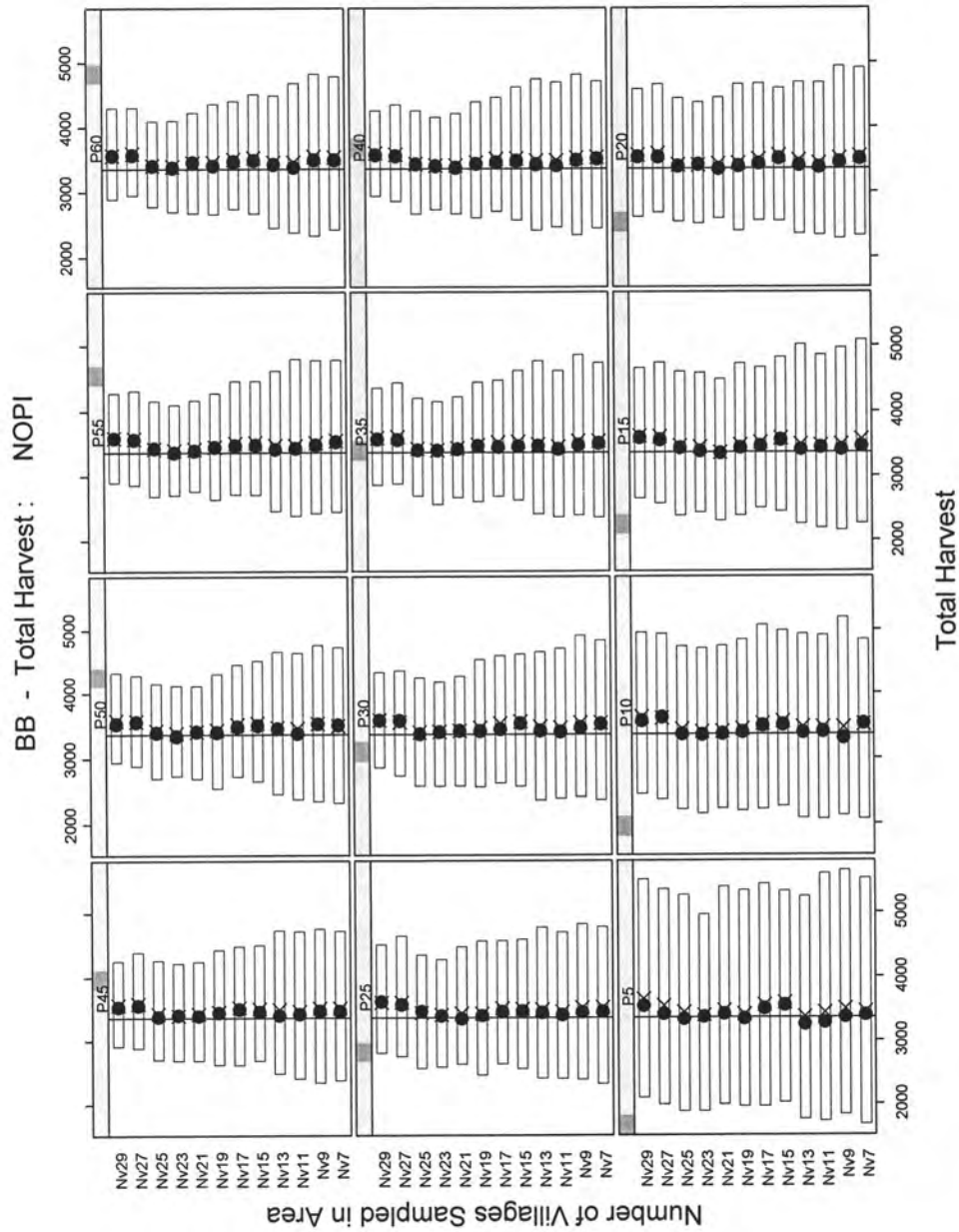


Figure 19. Simulated sampling distribution of Bristol Bay area total annual harvest estimates for Spectacled Eiders. There are too few non-zero harvests to produce a gain in precision by sampling more villages. There is little gain in precision from sampling more than 25% of the area households.

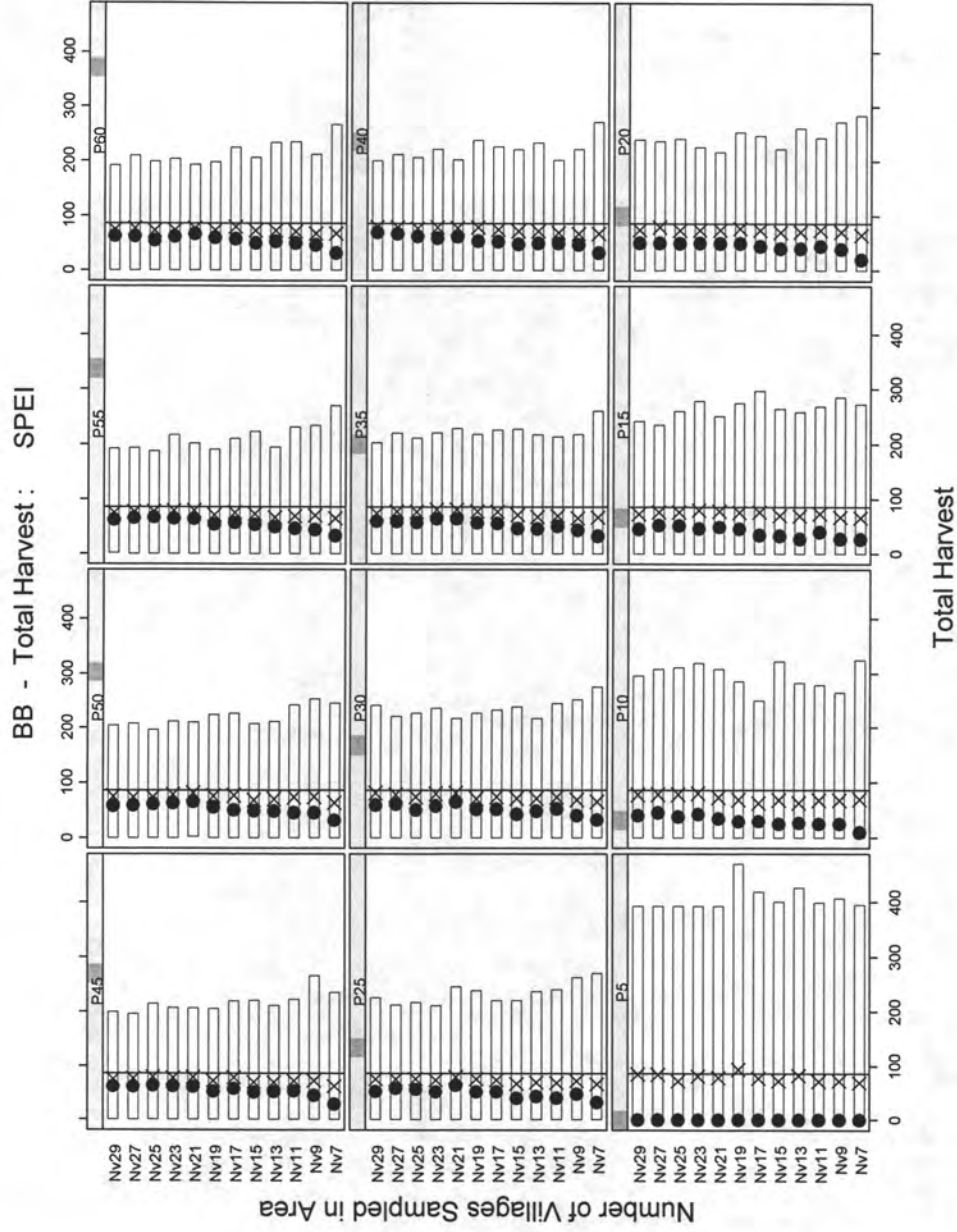


Figure 20. Simulated sampling distribution of Bristol Bay area total annual harvest estimates for Black Scoters. There is little gain in precision from sampling more than 21 villages in the area (+Dillingham), at a rate of more than 25% of the area households.

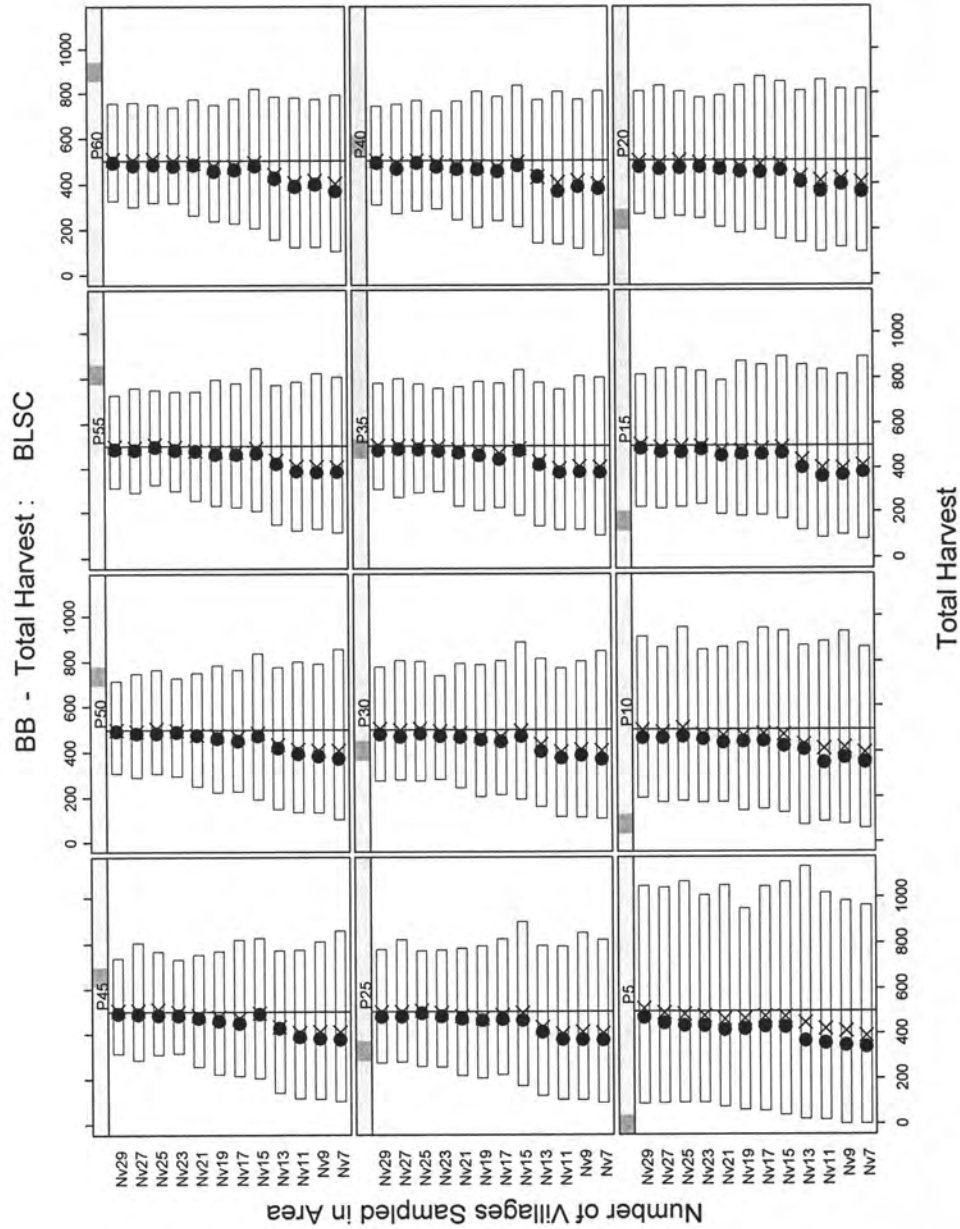


Figure 21. Simulated sampling distribution of Bristol Bay area total annual harvest estimates for Emperor Goose. There are relative few nonzero harvests of Emperor Geese in the BB area; a sampling effort of at least 21 villages (+ Dillingham) is required to adequately represent this sparse harvest. There is little gain in precision from sampling more than 21 villages in the area (+Dillingham), at a rate of more than 25-30% of the area households.

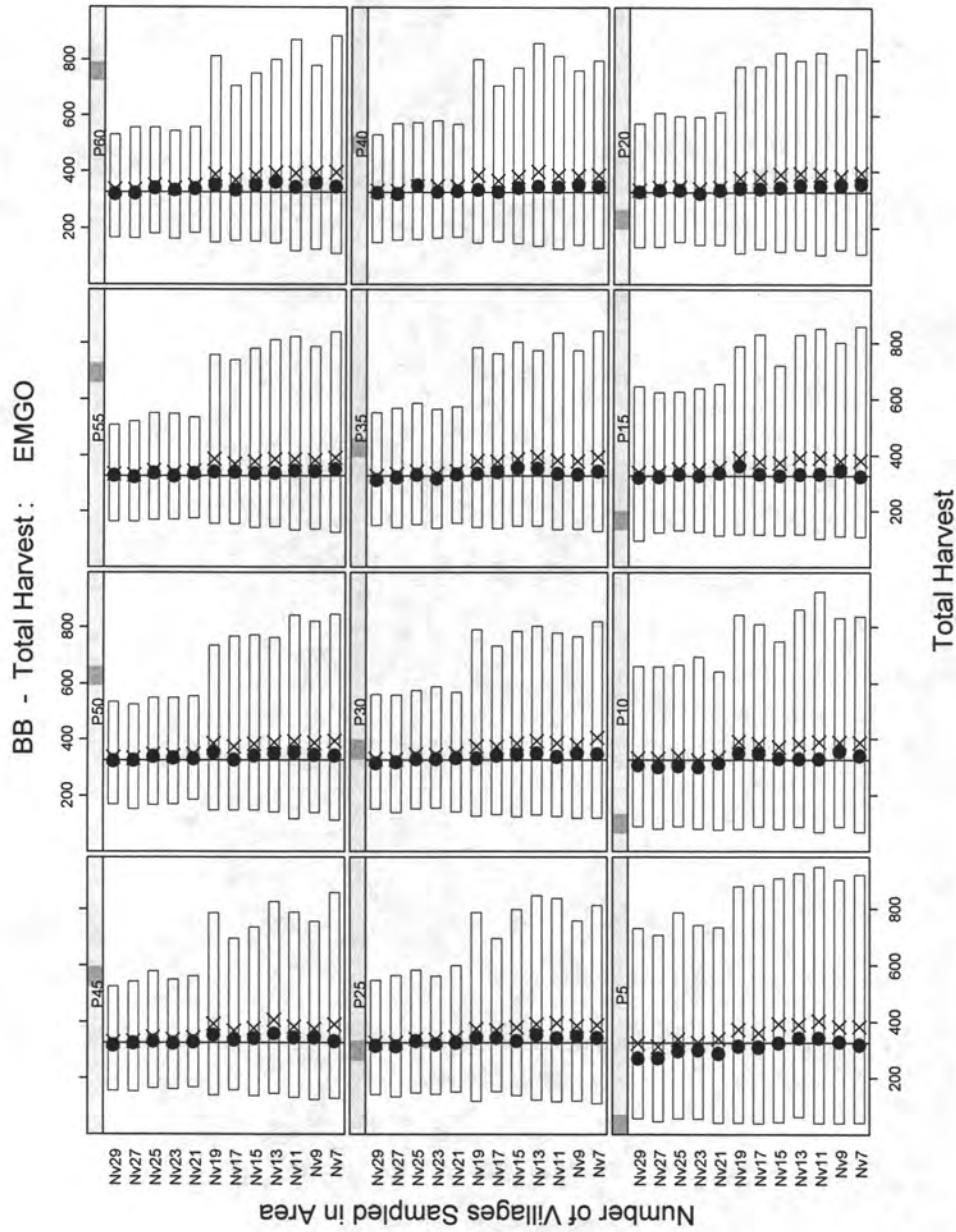


Figure 22. Simulated sampling distribution of Bristol Bay area total annual harvest estimates for White Fronted Goose. There is little gain in precision from sampling more than 19 villages in the area (+Dillingham), at a rate of more than 25% of the area households.

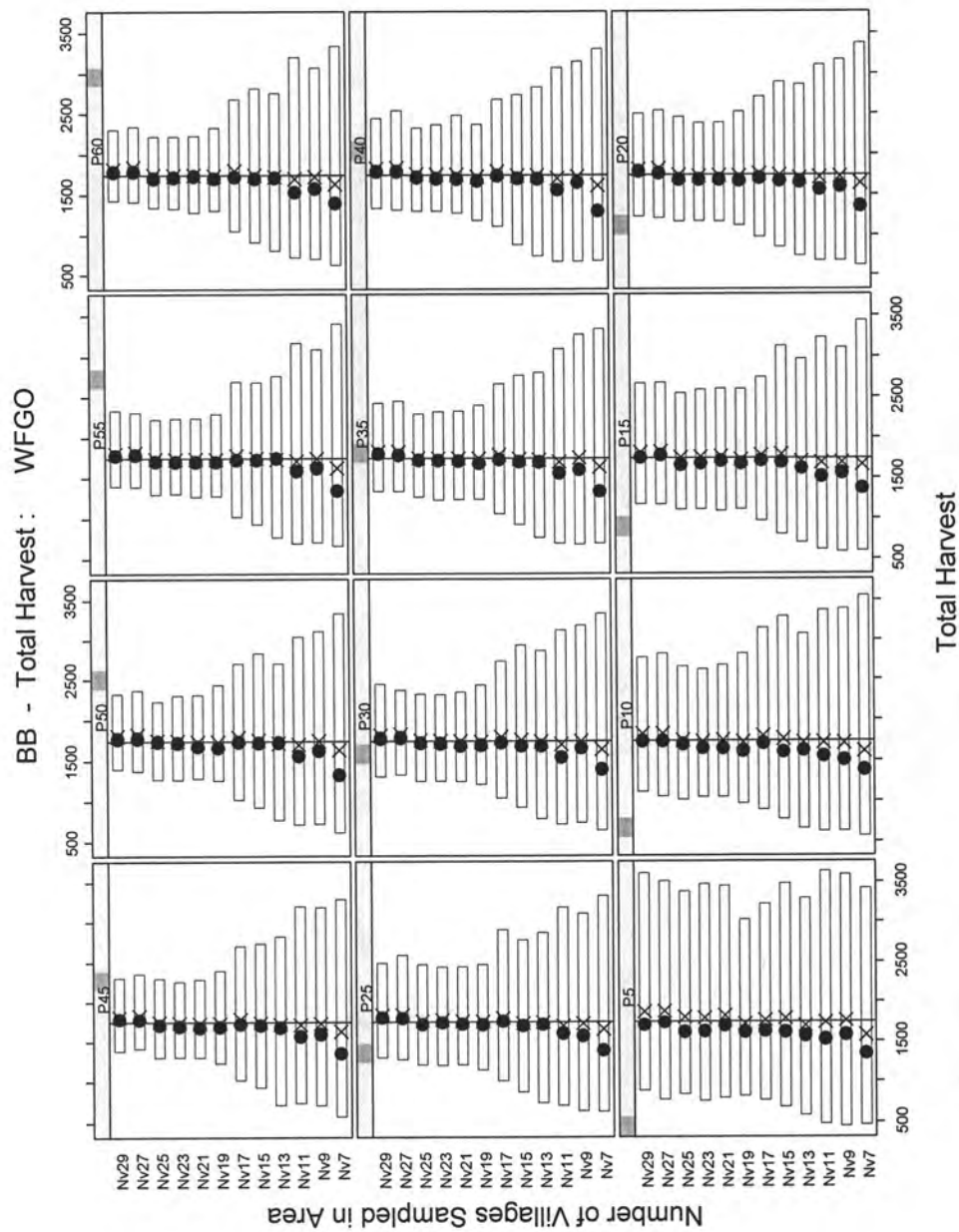


Figure 23. Simulated sampling distribution of Bristol Bay area total annual harvest estimates for Cackling Canada Goose. There is little gain in precision from sampling more than 19 villages in the area (+Dillingham), at a rate of more than 25% of the area households.

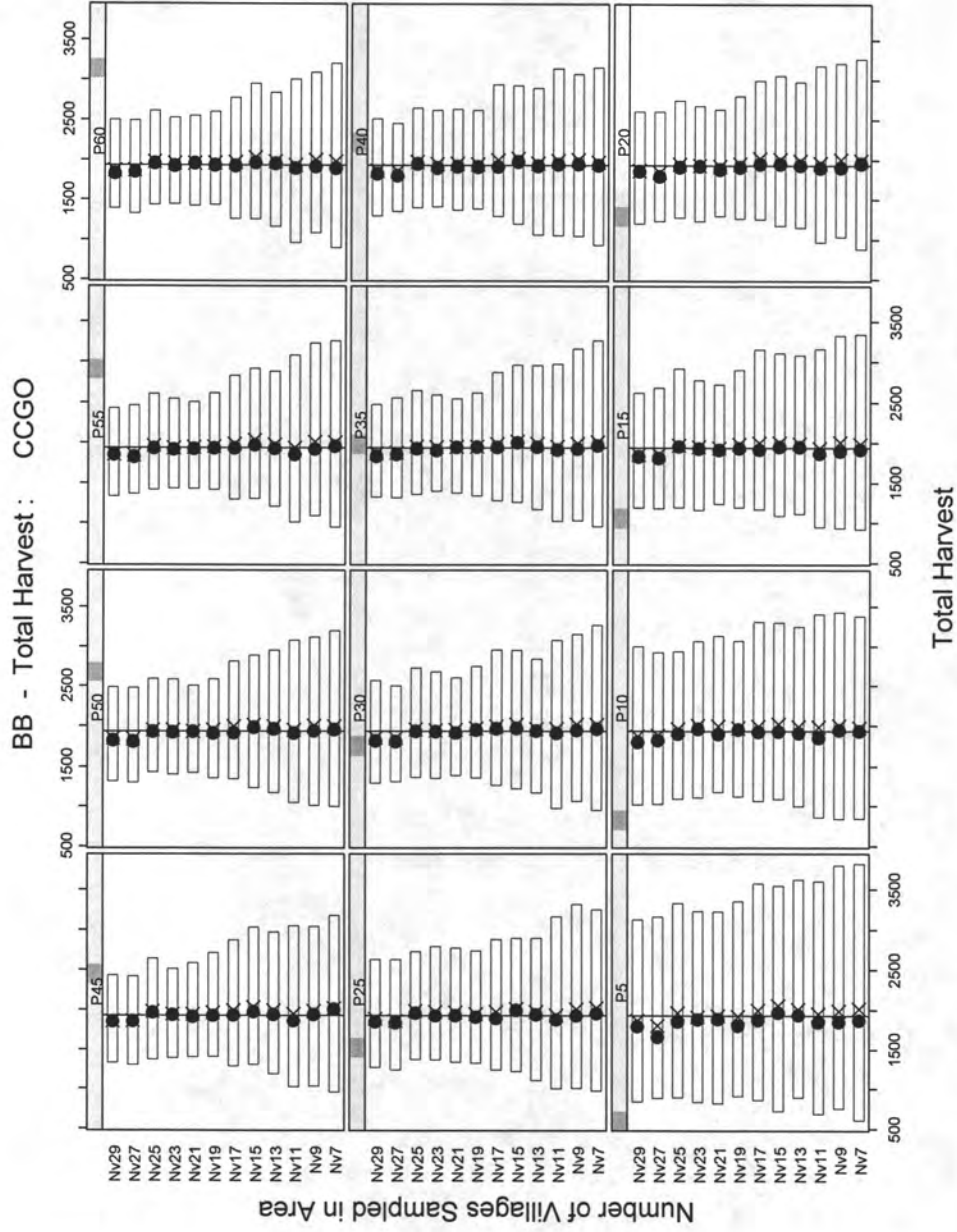


Figure 24. Simulated sampling distribution of Bristol Bay area total annual harvest estimates for Northern Pintail eggs. There are too few non-zero harvests to produce a gain in precision by sampling more than 13 villages (+ Dillingham) at a rate of more than 30% of the area households.

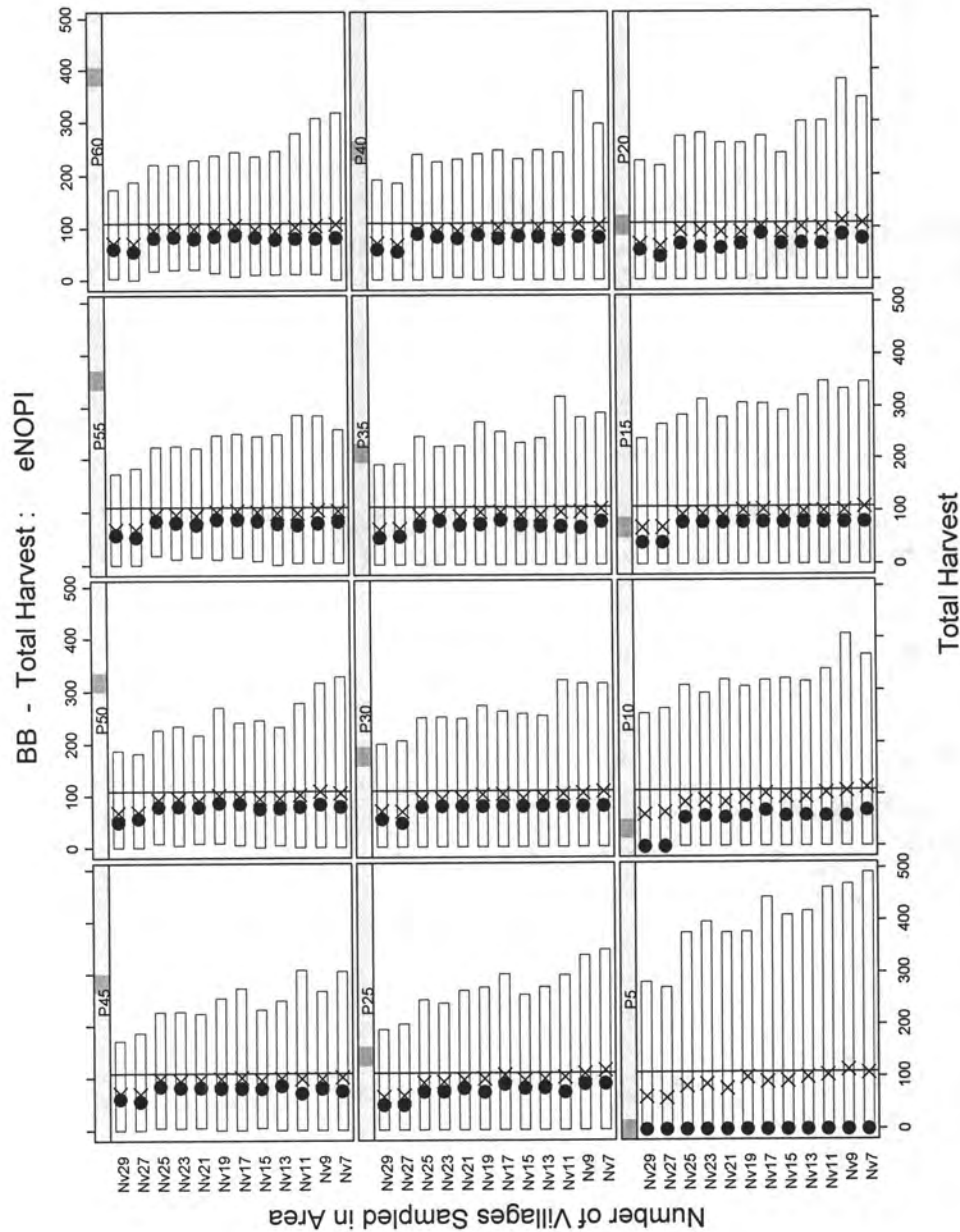


Figure 25. Simulated sampling distribution of Bristol Bay area total annual harvest estimates for Spectacled Eider eggs. There are too few non-zero harvests to produce a gain in precision by sampling more villages. There is little gain in precision from sampling more than 25% of the area households.

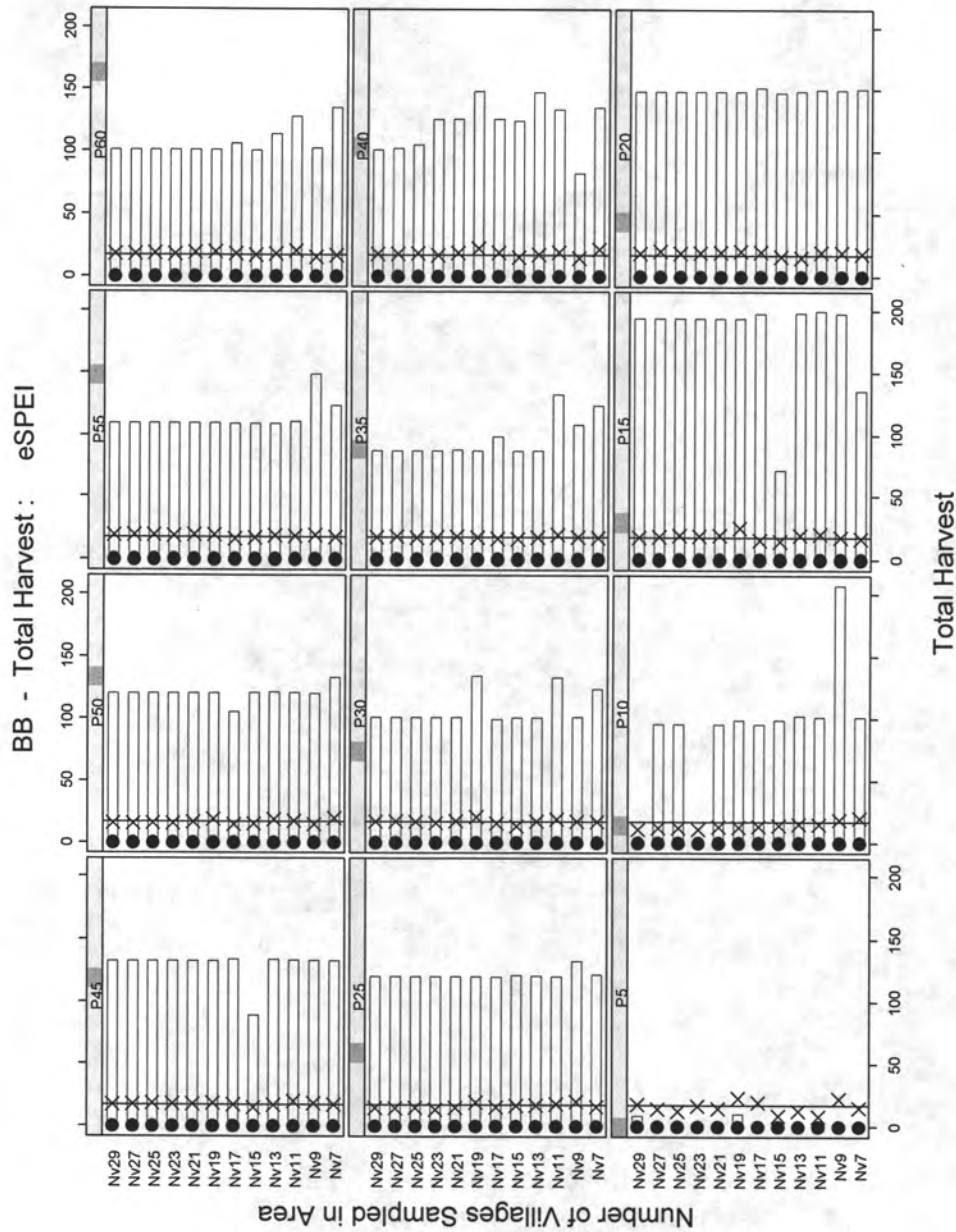


Figure 26. Simulated sampling distribution of Bristol Bay area total annual harvest estimates for Black Scoter eggs. There are too few non-zero harvests to display an improved precision as a function of either sampling factor. See legend of Figure 12 for why some bars appear to be missing.

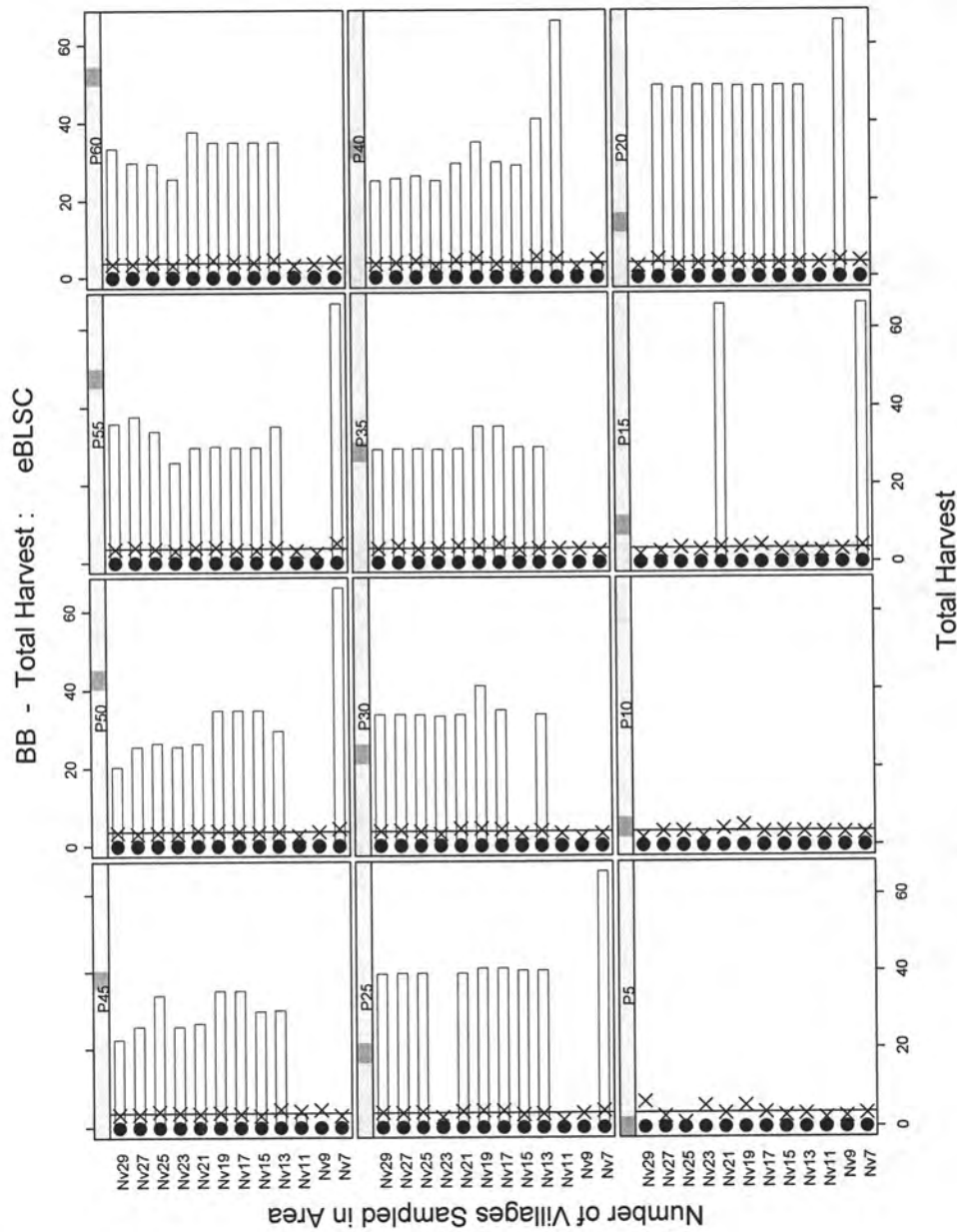


Figure 27. Simulated sampling distribution of Bristol Bay area total annual harvest estimates for Emperor Goose eggs. There are too few non-zero harvests to display an improved precision as a function of either sampling factor. See legend of Figure 12 for why some bars appear to be missing.

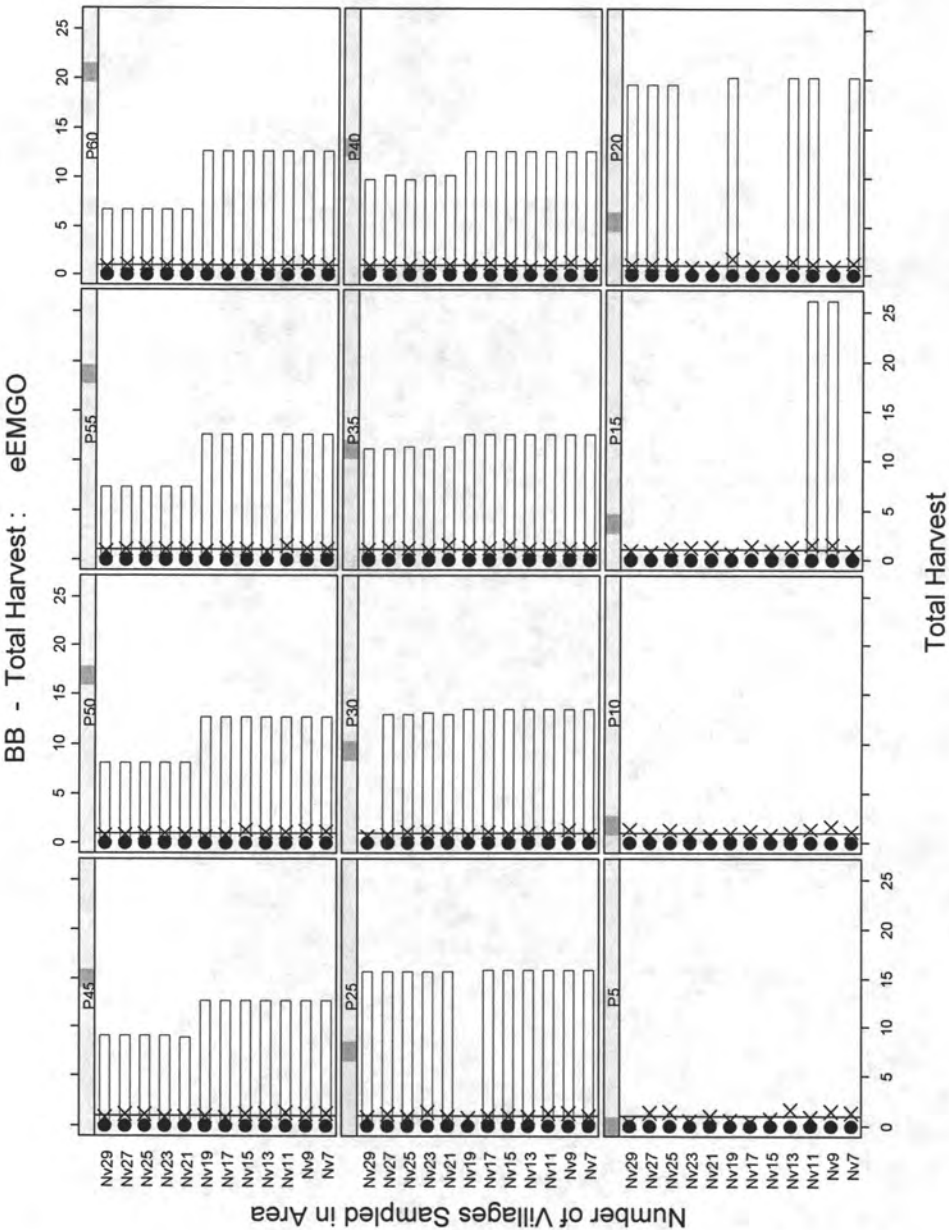


Figure 28. Simulated sampling distribution of Bristol Bay area total annual harvest estimates for White Fronted Goose eggs. There are too few non-zero harvests to display an improved precision as a function of sampling more villages. There is little gain in precision from sampling more than 25% of the area households.

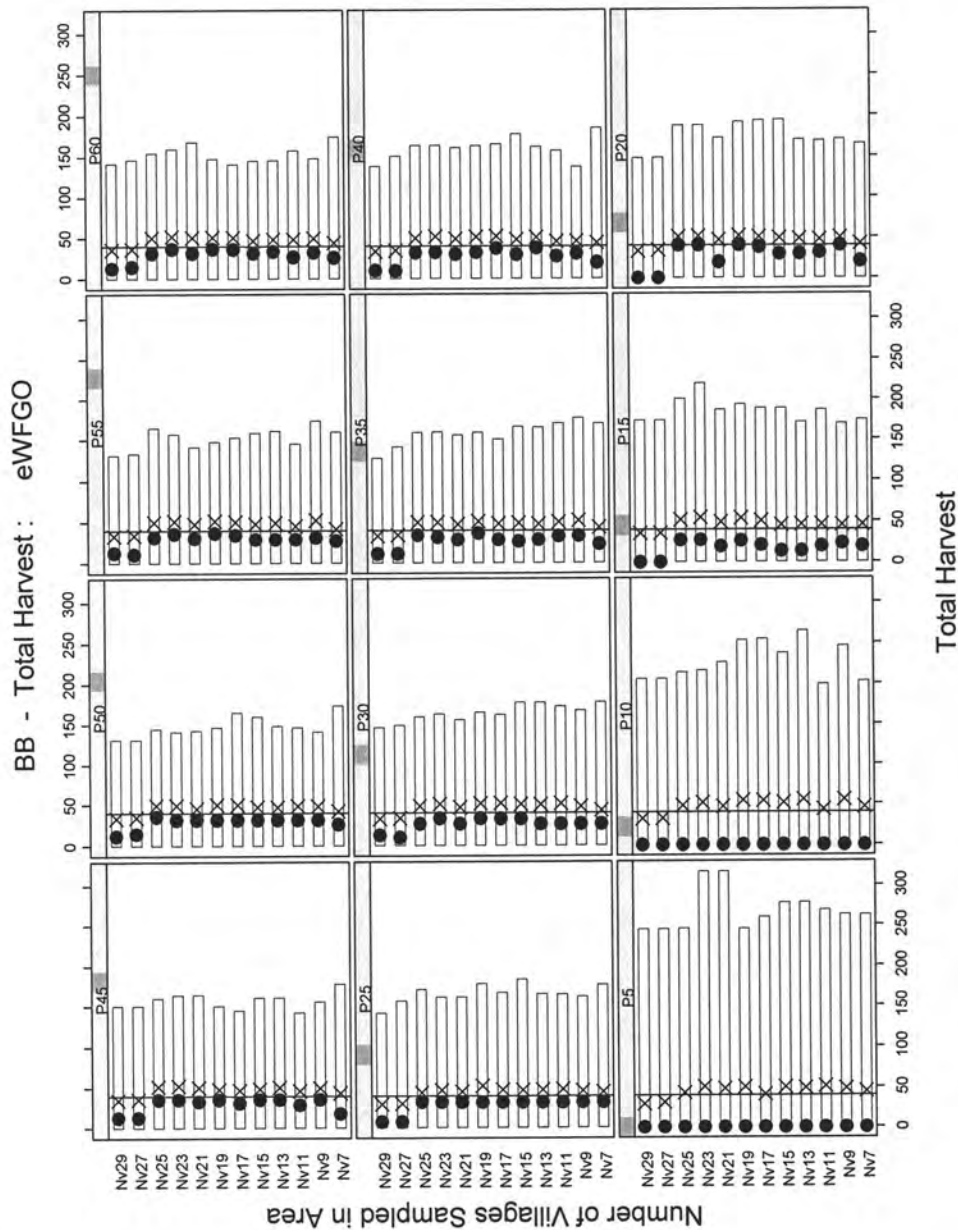


Figure 29. Simulated sampling distribution of Bristol Bay area total annual harvest estimates for Cackling Canada Goose eggs. There are too few non-zero harvests to display an improved precision as a function of sampling more villages. There is little gain in precision from sampling more than 20% of the area households.

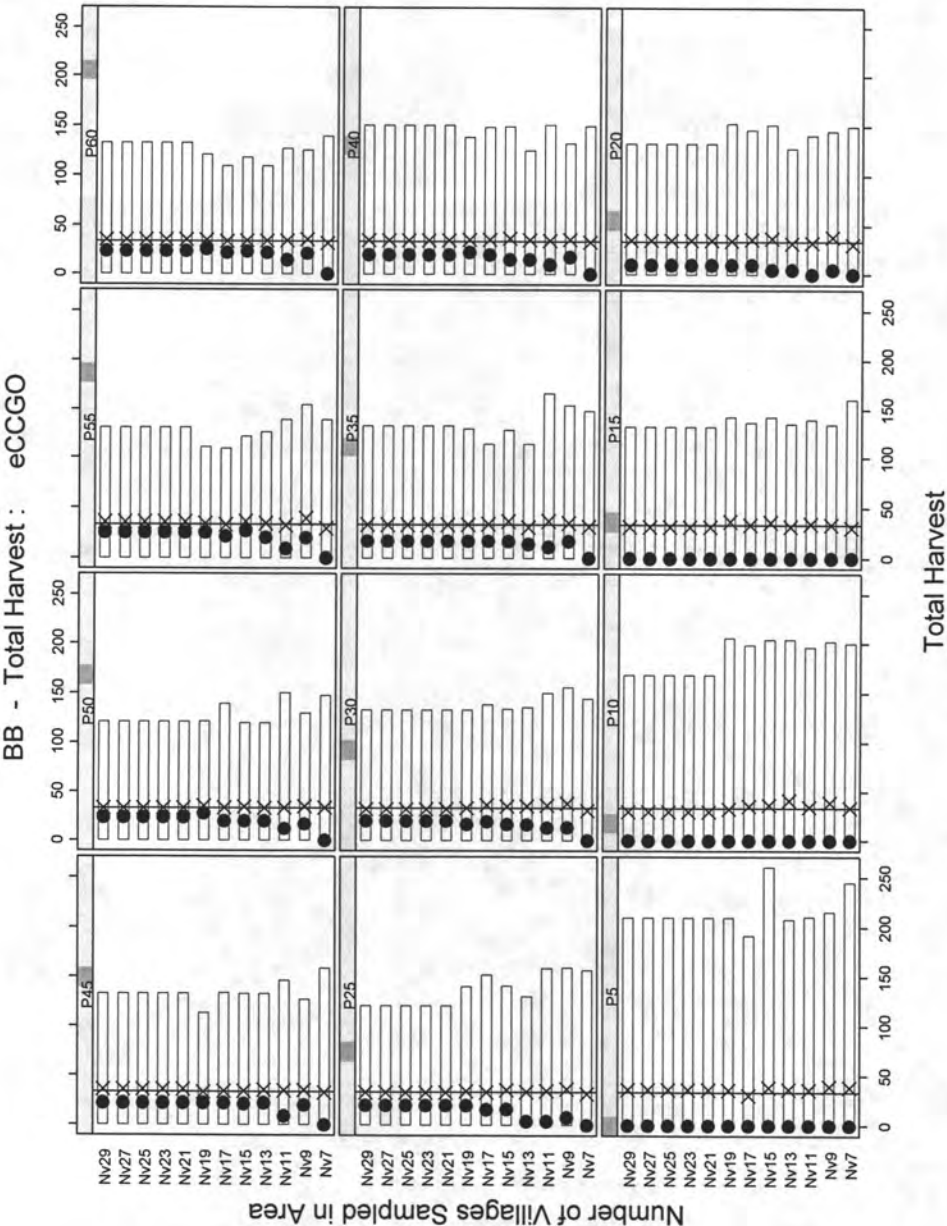


Figure 30. Summary display of sampling factor effects on precision for simulated Bristol Bay area total annual harvest estimates, all species and all responses (birds – left two columns; eggs – right two columns). See legend of Figure 17 for detailed explanation. The parallel lines on the far right of the curves arise because of the cap on the number of villages that can be sampled in a given region (this is described in the Discussion: *Simulation cap on number of villages sampled in a region*).

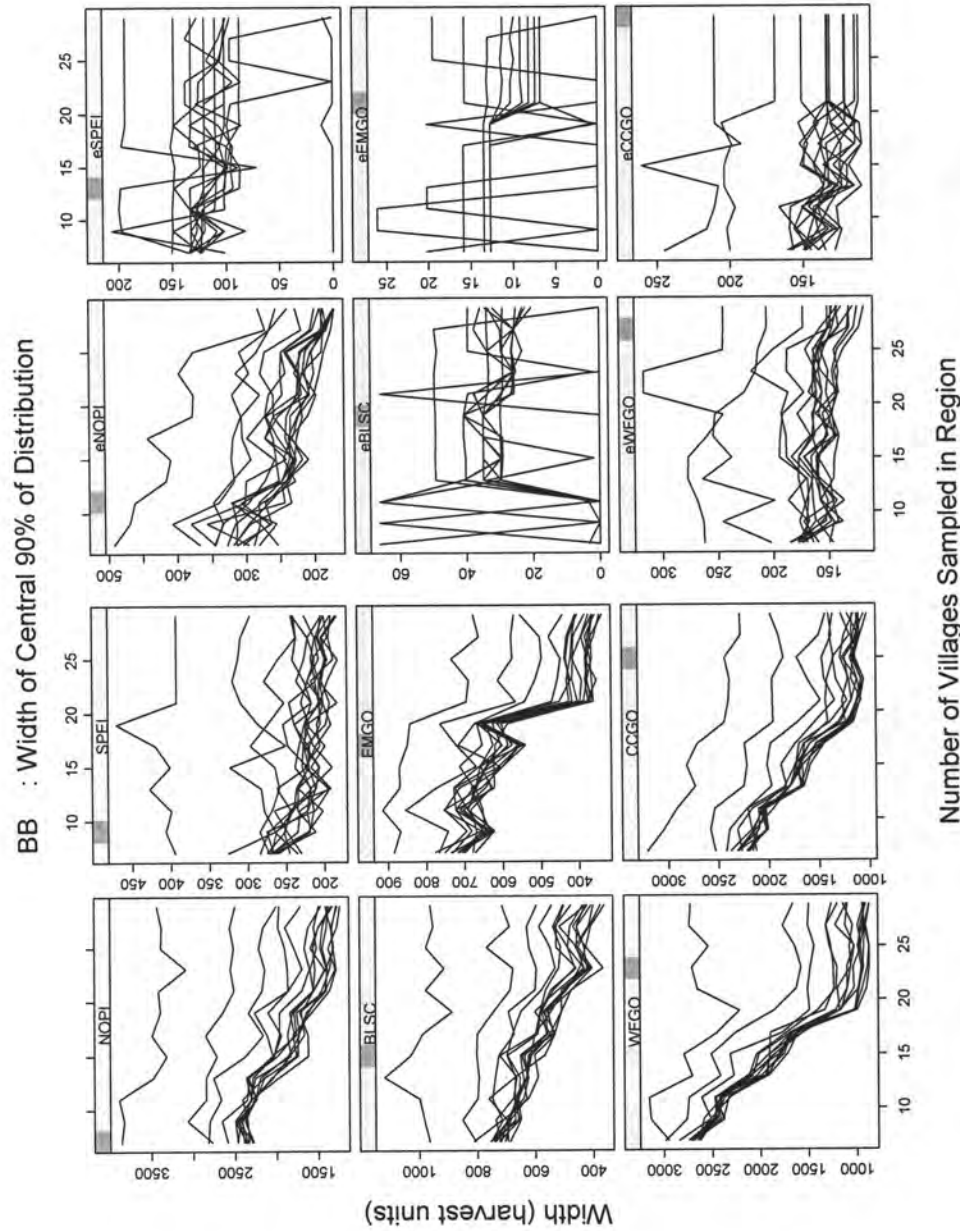


Figure 31. Simulated sampling distribution of approximate statewide total annual harvest estimates for Northern Pintails. There is little gain in precision from sampling more than 27 villages in an area (+ hub), at a rate of more than 25% of the area households.

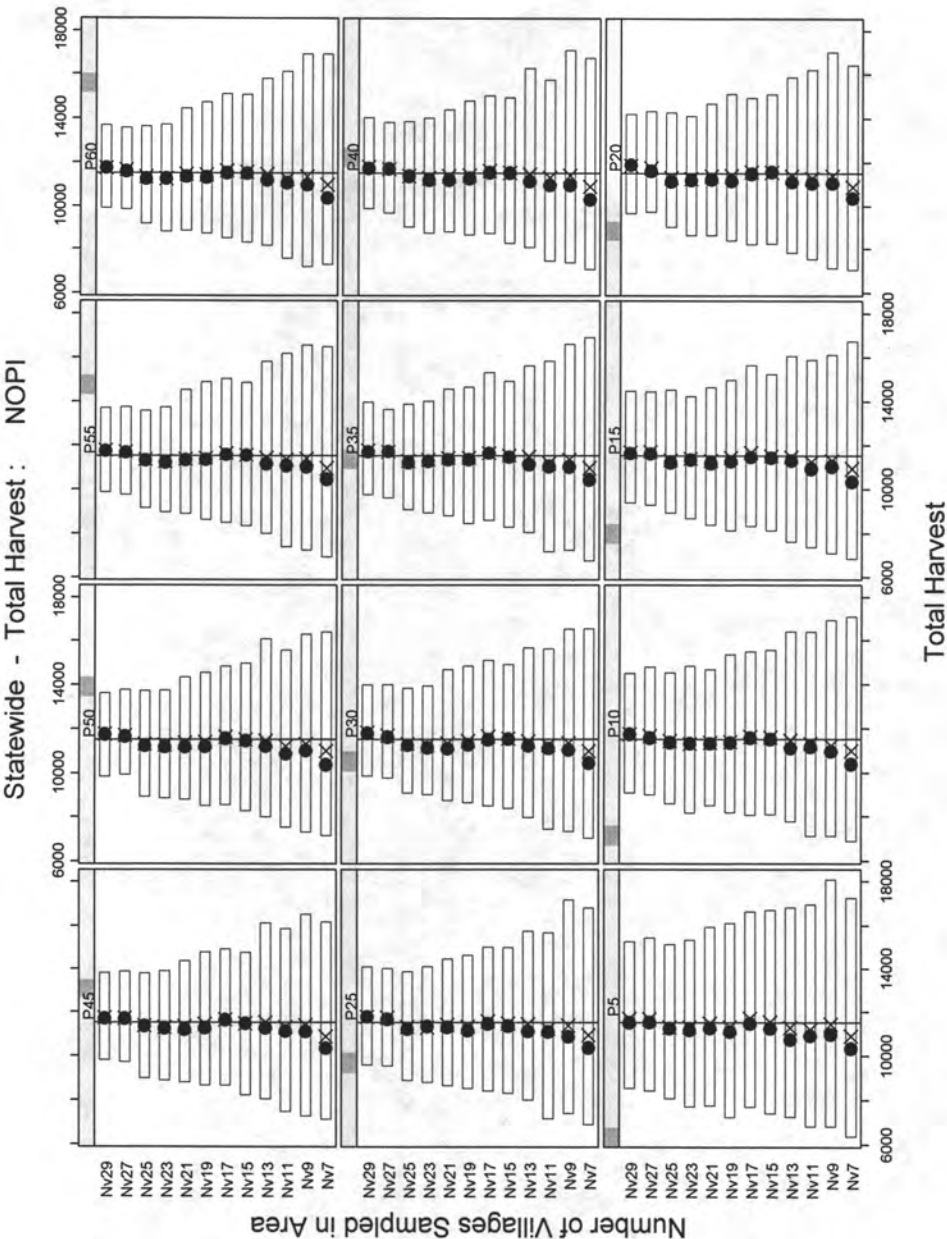


Figure 32. Simulated sampling distribution of approximate statewide total annual harvest estimates for Spectacled Eiders. There are too few non-zero harvests to produce a gain in precision by sampling more villages. There is little gain in precision from sampling more than 25% of the area households.

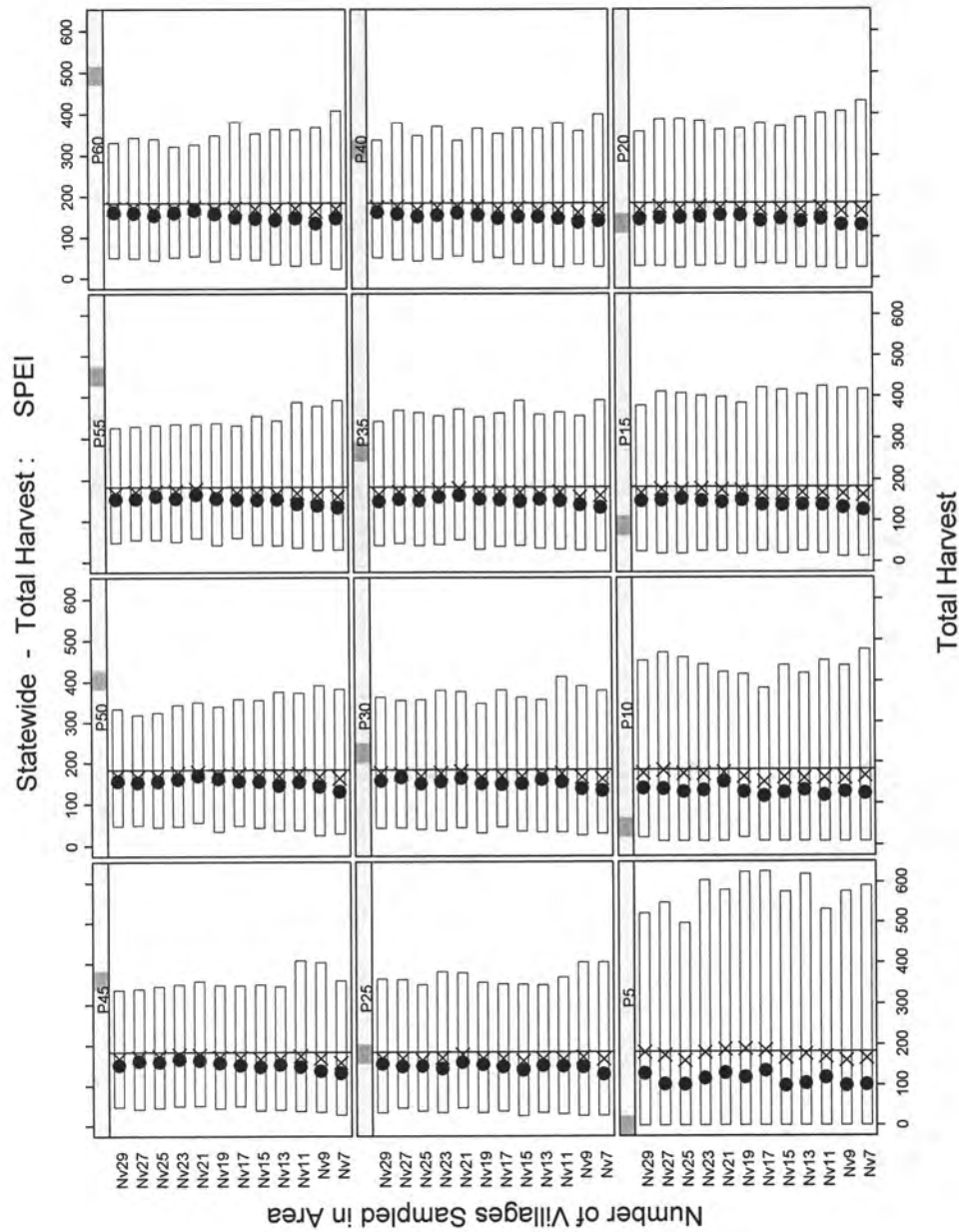


Figure 33. Simulated sampling distribution of approximate statewide total annual harvest estimates for Black Scoters. There is little gain in precision from sampling more than 23 villages in an area (+hub), at a rate of more than 25% of the area households.

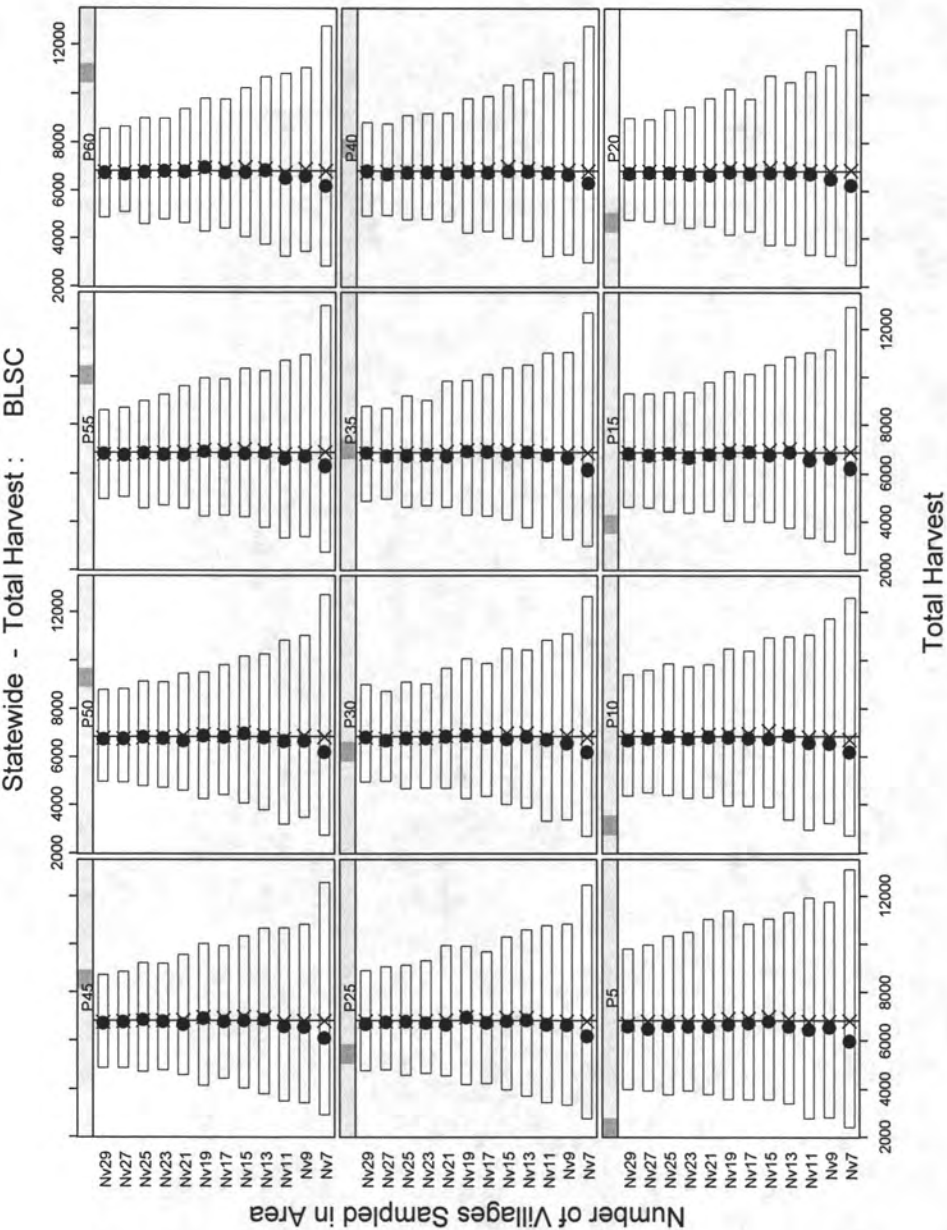


Figure 34. Simulated sampling distribution of approximate statewide total annual harvest estimates for Emperor Goose. There is little gain in precision from sampling more than 15 villages in an area (+ hub), at a rate of more than 25% of the area households.

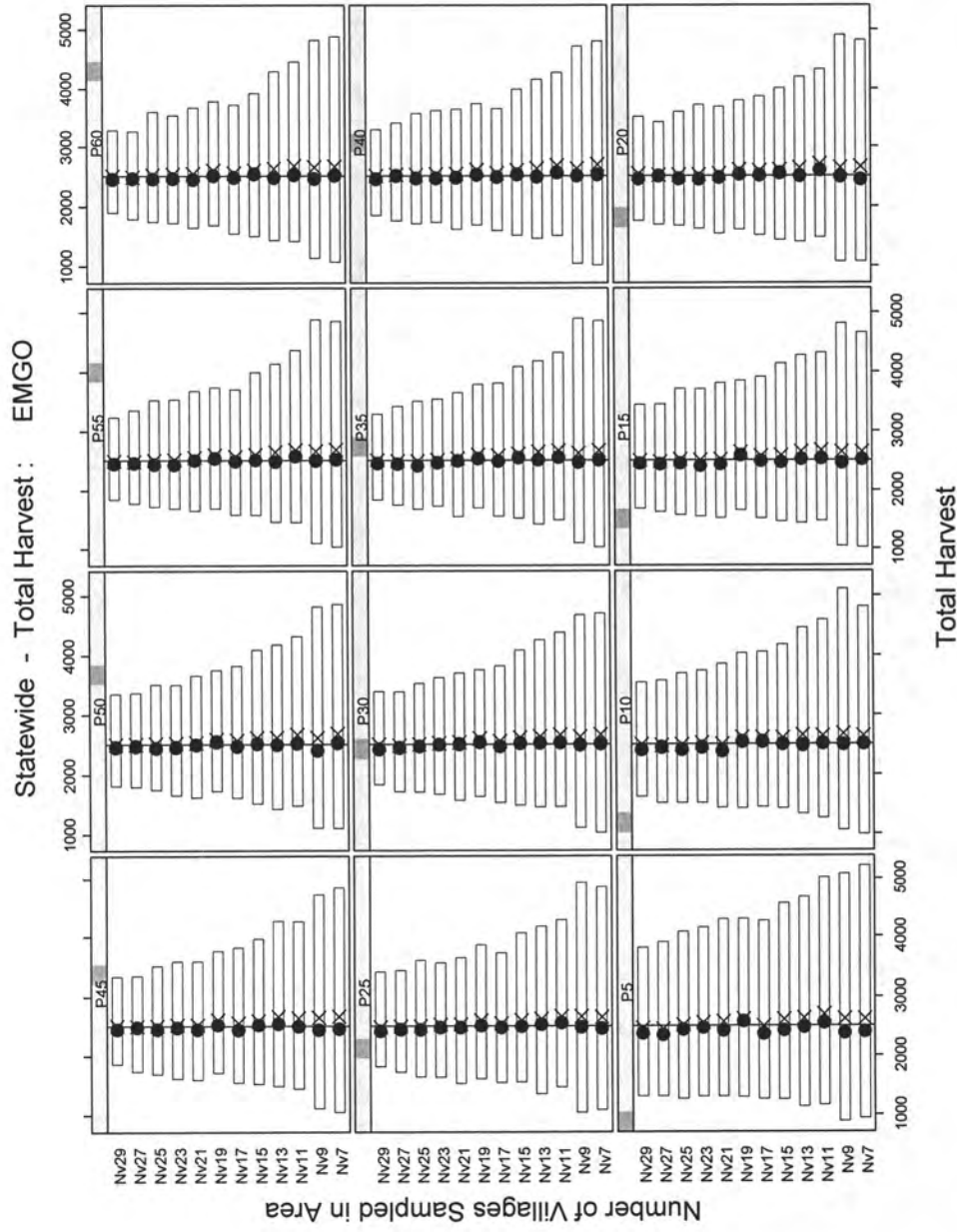


Figure 35. Simulated sampling distribution of approximate statewide total annual harvest estimates for White Fronted Goose. There is little gain in precision from sampling more than 27 villages in an area (+hub), at a rate of more than 20% of the area households.

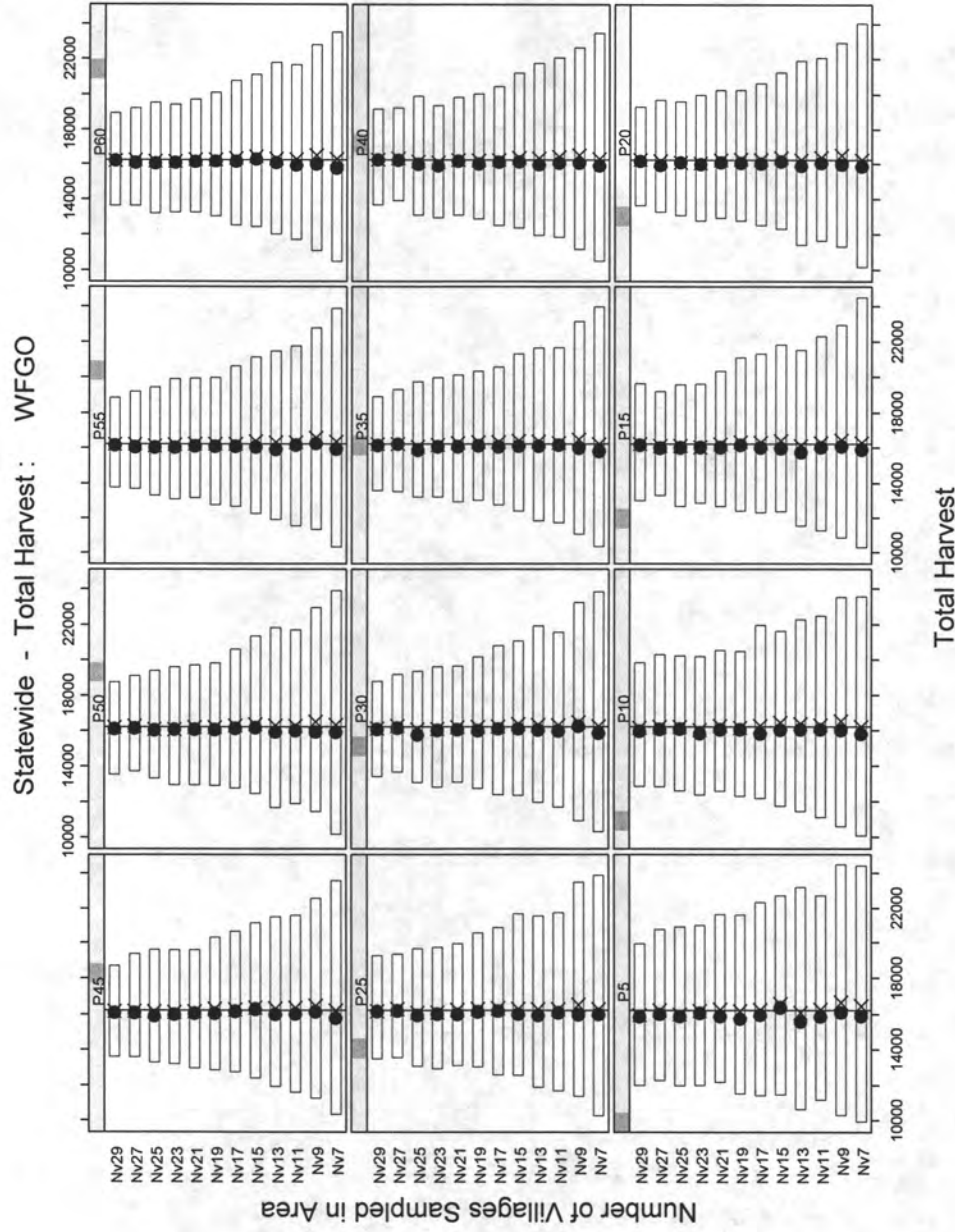


Figure 36. Simulated sampling distribution of approximate statewide total annual harvest estimates for Cackling Canada Goose. There is little gain in precision from sampling more than 21 villages in an area (+hum), at a rate of more than 25% of the area households.

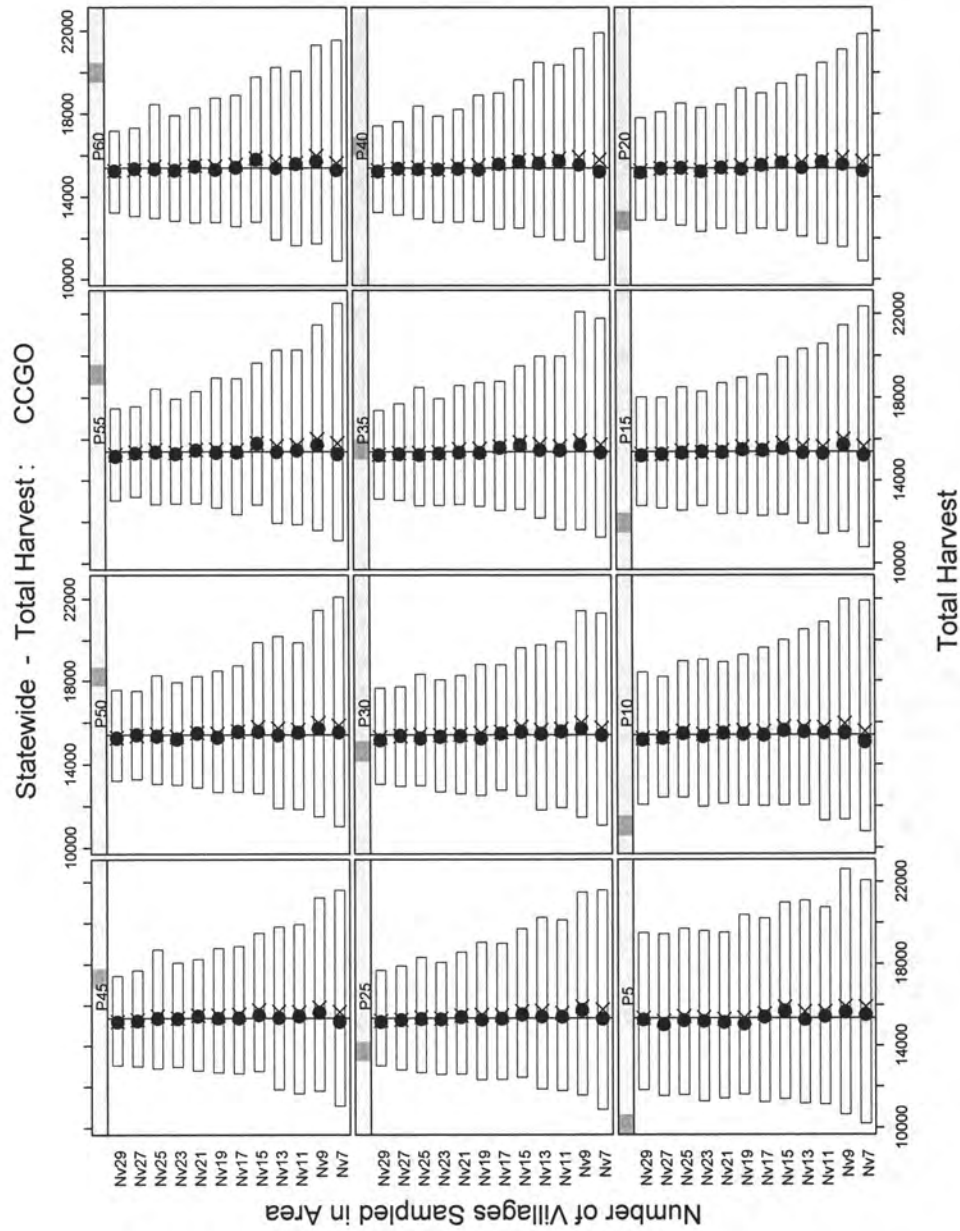


Figure 37. Simulated sampling distribution of approximate statewide total annual harvest estimates for Northern Pintail eggs. There is little gain in precision by sampling more than 17 villages in an area (+ hub) at a rate of more than 30% of the area households.

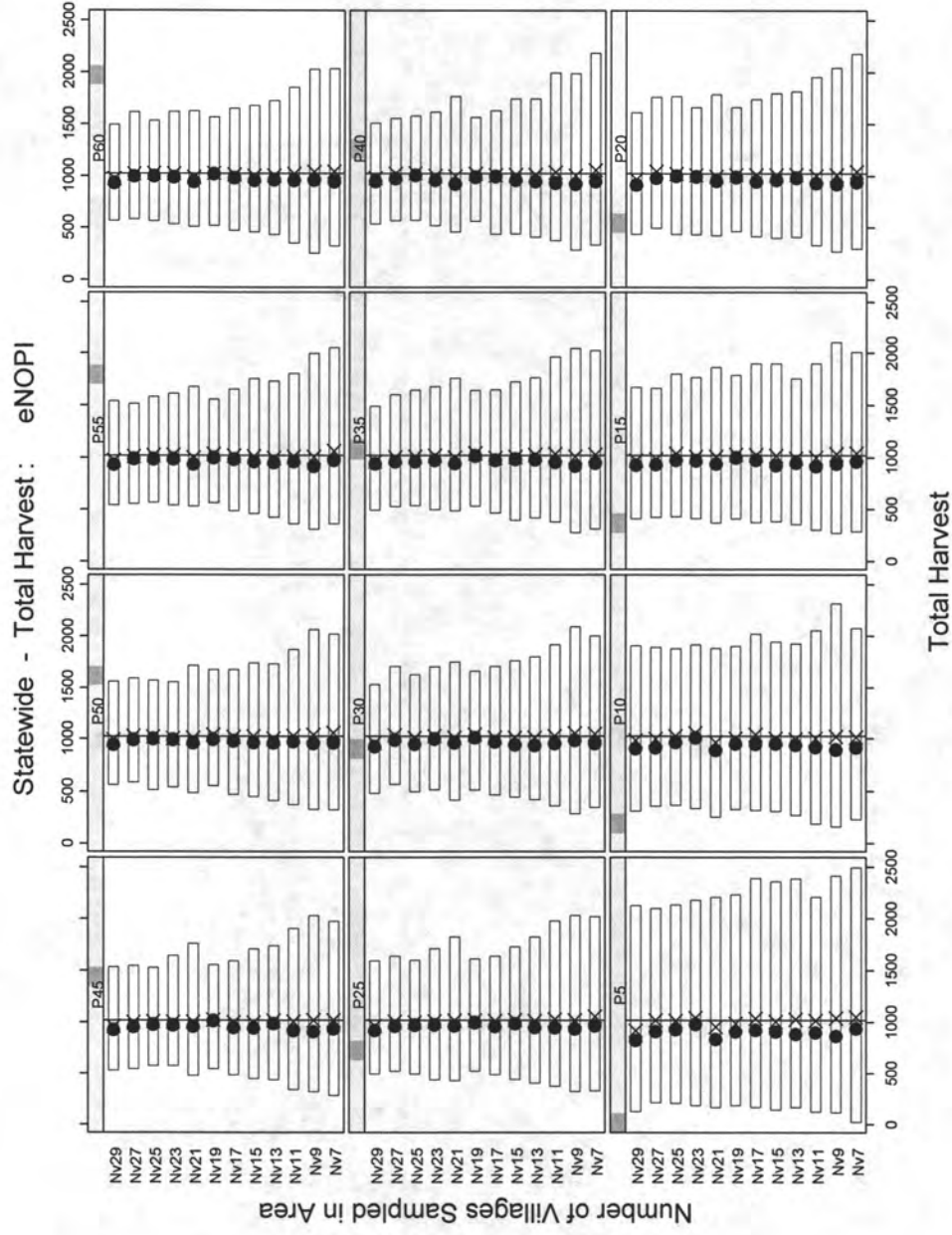


Figure 38. Simulated sampling distribution of approximate statewide total annual harvest estimates for Spectacled Eider eggs. There are too few non-zero harvests to produce a gain in precision by sampling more villages. There is little gain in precision from sampling more than 25% of the area households.

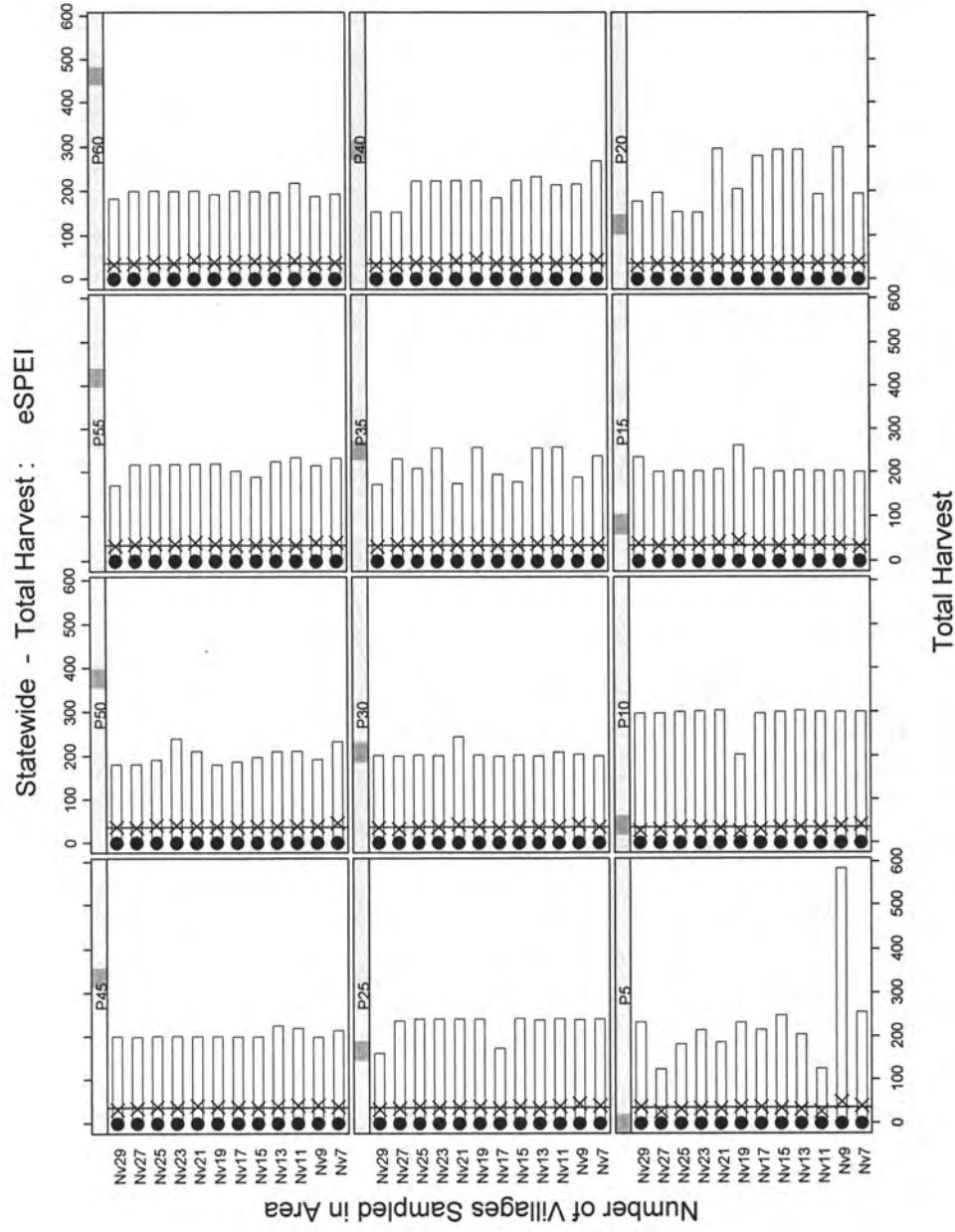


Figure 39. Simulated sampling distribution of approximate statewide total annual harvest estimates for Black Scoter eggs. There are too few non-zero harvests to display an improved precision as a function of either sampling factor.

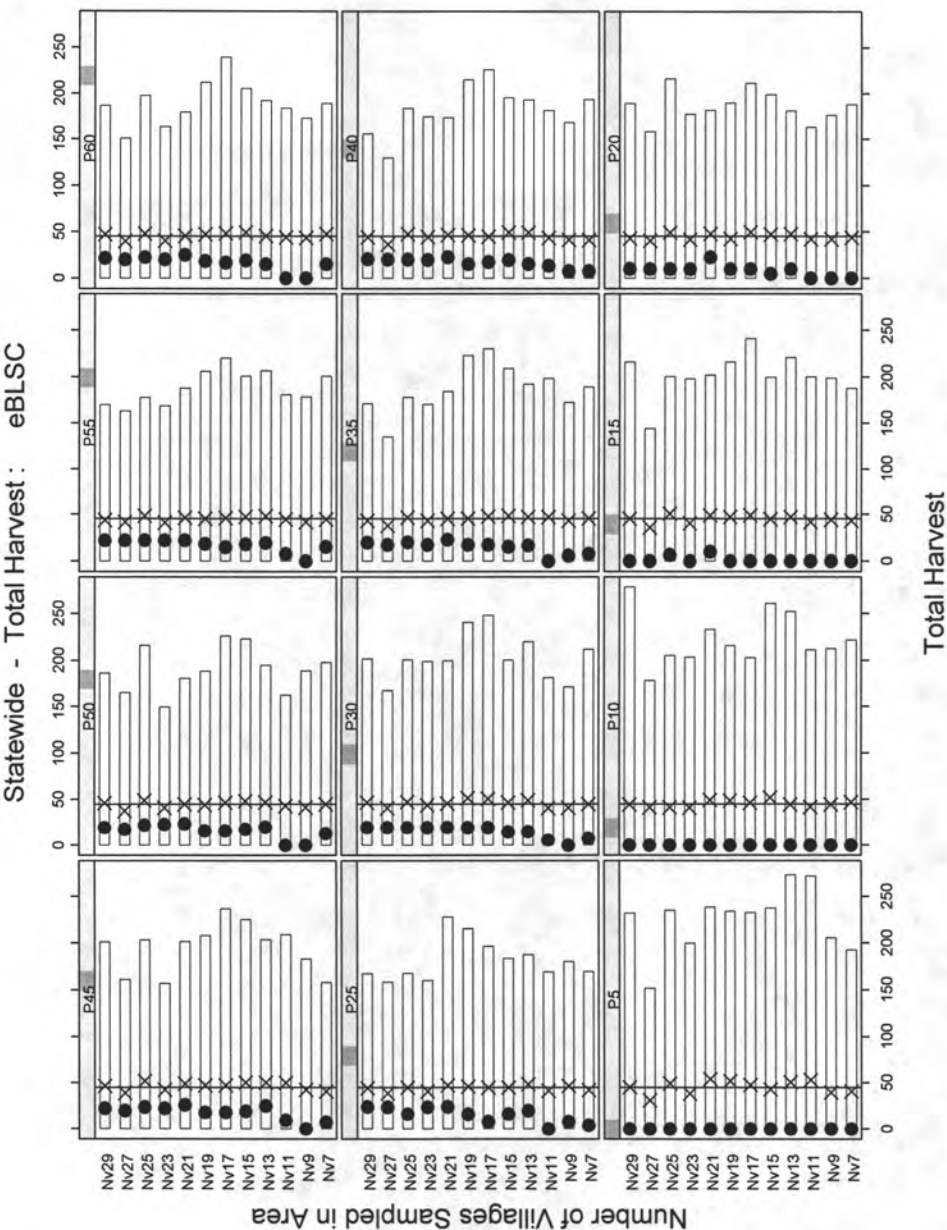


Figure 40. Simulated sampling distribution of approximate statewide total annual harvest estimates for Emperor Goose eggs. There is little gain in precision from sampling more than 21 villages (+ hub) in an area, at a rate of more than 25% of the area households.

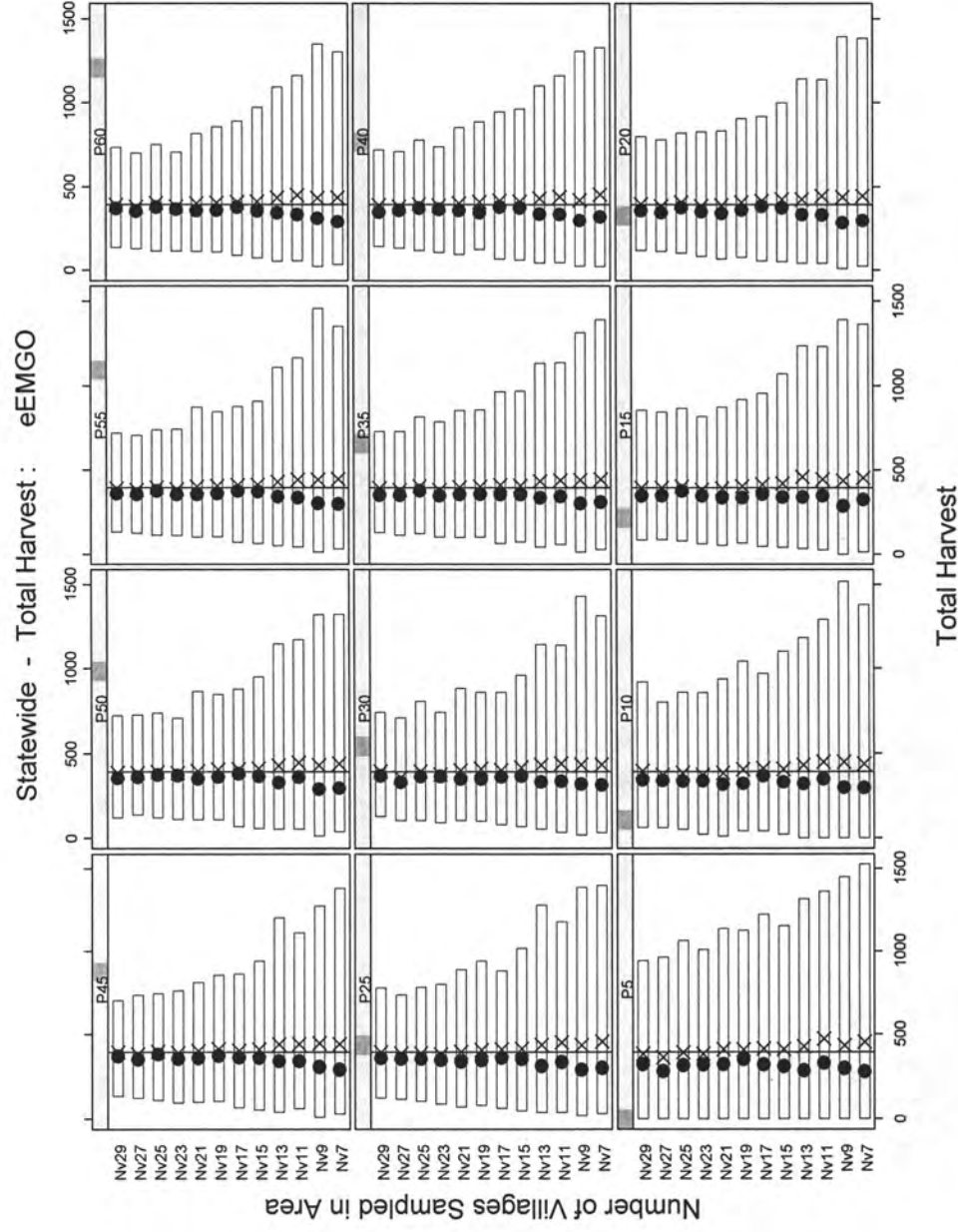


Figure 41. Simulated sampling distribution of approximate statewide total annual harvest estimates for White Fronted Goose eggs. There is little gain in precision from sampling more than 19 villages in an area (+ hub) at a rate of more than 25% of the area households.

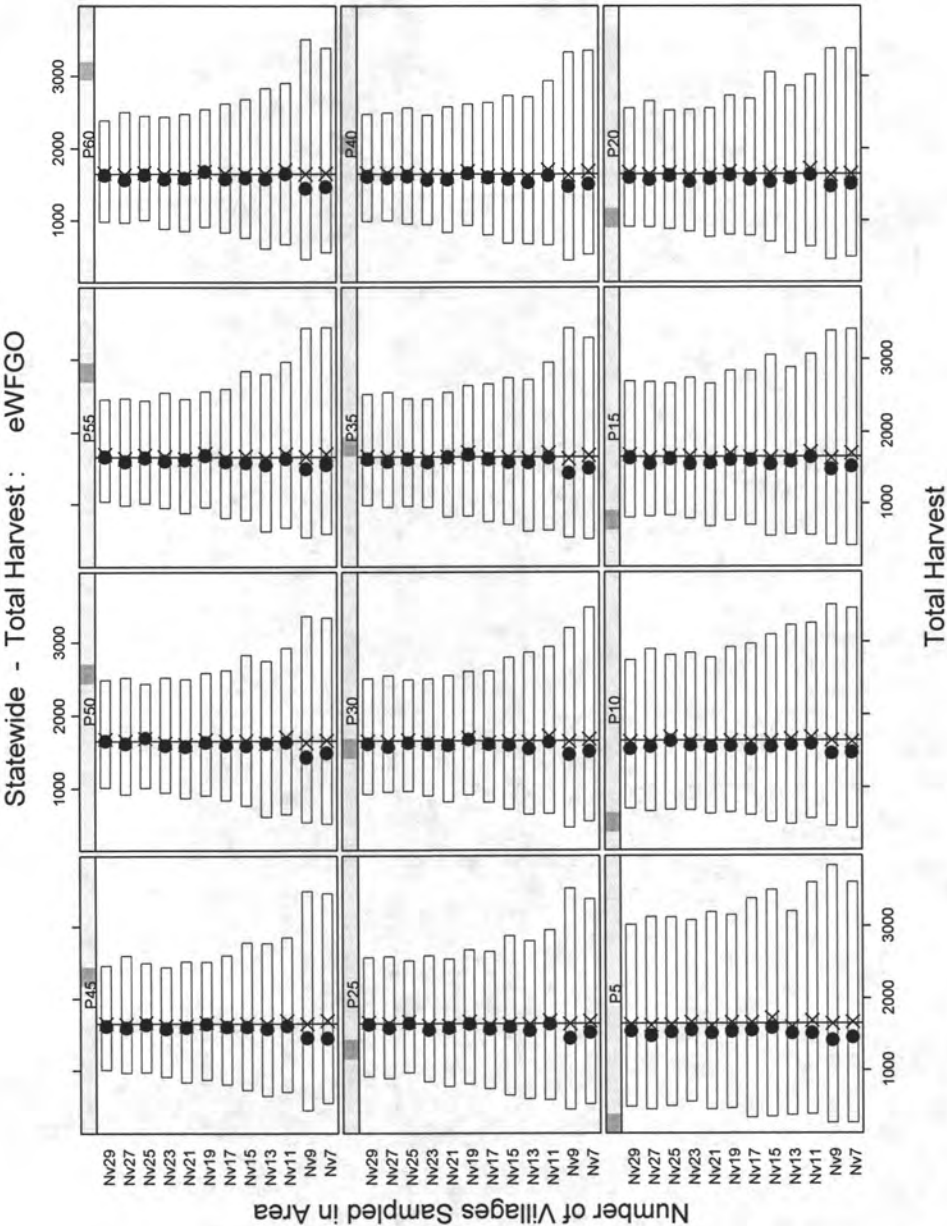


Figure 42. Simulated sampling distribution of approximate statewide total annual harvest estimates for Cackling Canada Goose eggs. There is little gain in precision from sampling more than 19 villages in an area (+hub) at a rate of more than 20% of the area households.

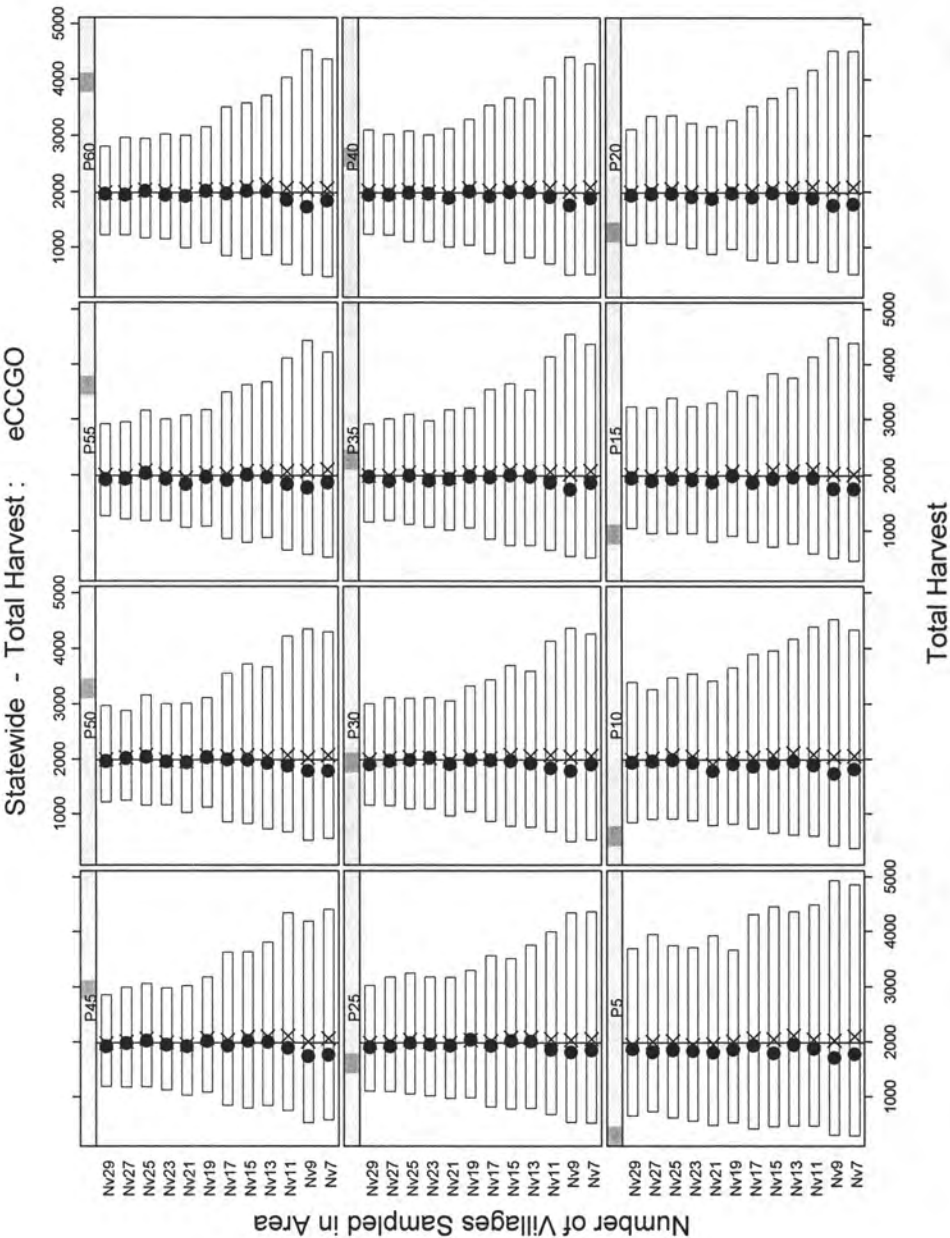
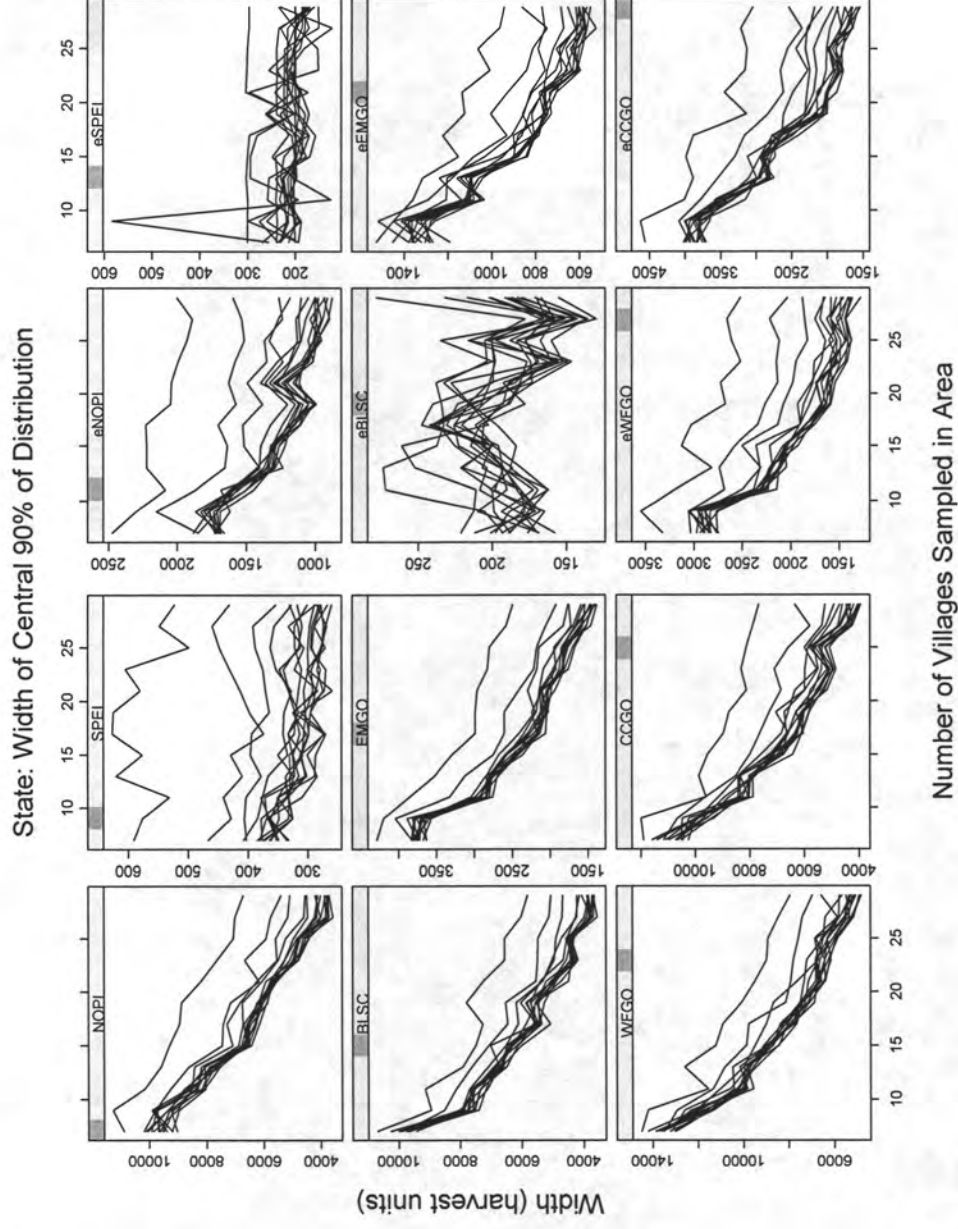


Figure 43. Summary display of sampling factor effects on precision for simulated approximate statewide total annual harvest estimates, all species and all responses (birds – left two columns; eggs – right two columns). See legend of Figure 17 for detailed explanation.



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APPENDIX 1. SELECTION OF SIMULATION APPROACH & HISTORIC DATA FOR ANALYSIS

The proposal (Reynolds 2002a) set forth the statistical issues associated with the analysis, presented a series of approaches to the analysis, and listed a series of decisions and data required from the ad hoc subsistence harvest committee (the 'Committee') for the analysis to begin.

The Committee chose an analysis built upon the recently adopted stratified random sampling design. Given the limited amount of stratified data available, the Committee selected to fit a standard parametric model for each village by strata by season combination, with the power analysis simulating observations from these fitted models. Given its completeness, the Bristol Bay area data was used in an initial investigation of the feasibility of the parametric modeling approach for the harvest survey data.

The Bristol Bay area data were very poorly fit by the most plausible standard models (Poisson and Zero-Inflated Poisson), eliminating the parametric modeling approach (Progress Report, Reynolds 2002b). The very low sample sizes for each village by season by strata combination eliminated the use of the nonparametric bootstrap approach for the stratified random sample data, the only other approach available for simulating stratified sampling. The analysis was forced to proceed using the nonparametric bootstrap approach with the simple random sample data from 1995 – 2001 (those years were readily available). Note the poor fit of standard models for the strata-specific data implies an equally poor fit, if not worse, for the simple random sample data.

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APPENDIX 2. SAMPLE SIMULATION CODE

The following S-Plus code generates the Monte Carlo simulations for the Kuskokwim River region of the YKD area. The two main data objects called in the code are:

YKDSRSAnnualSubsetdf -

an S-Plus data frame containing the following columns:

```
[1] "year"      "vcode"      "viln"      "villagename" "area"
[6] "rn"        "region"     "hhn"       "NOPI"       "SPEI"
[11] "BLSC"      "EMGO"       "WFGO"      "CCGO"       "eNOPI"
[16] "eSPEI"     "eBLSC"      "eEMGO"     "eWFGO"      "eCCGO"
```

This object contains all the complete household survey results (already summed to an annual harvest result for each household) for all species and responses of interest (columns 9 - 14 contain the bird takes, 15 - 20 contain the egg takes).

VillageTotalHH-

An S-Plus data frame containing the following columns:

```
[1] "vi"         "village.name" "area"       "rn"
[5] "region"     "All"
```

This object contains current number of households in each village.

```
#####

# YKD - Region 2 - KuskR
# unique(YKDSRSAnnualSubsetdf$region)
# [1] "northC" " KuskR" "southC" "LYukon" " midC" "Bethel"
#####
## Area total harvest is weighted sum of total region harvest estimates, which
## are independent.
#####
##Region-Specific Simulations
#####
## YKD: Dec 02, Jan 20- ,2003
## Number of villages to sample in each area:
## (1 per region or # regions) to total # villages in area
## Always include Area hub (Bethel, Dillingham, etc.)
##
## FOR YKD : seq(5,34,2) + Bethel
#as per 20 Jan 2003, based on Stehn's 9 Dec 02 request (# regions -35) and time
issues.

NV <- seq(5,34,2)

## Create Empty Data Structures - save memory costs
#####
####
TempRegion_YKDRegionNames[2]
Temparea_"YKD"
TempVillageRegionName_"KuskoR"
TempRegionHHCost_92 #YKD regions

NumberSims <- 500
#info(file="C:\\JOEL\\PROJECT\\USFWS\\BtchlInfo",append=F)

## Figure out what % of the HH in the area (excepting area Hub) occur in this
Region.
##
```

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```
RegionPercTotalHH<-
  sum(VillageTotalHH[VillageTotalHH$region==TempVillageRegionName,]$All[-
    c(2,7)]) /
    (sum(VillageTotalHH[VillageTotalHH$area==Temparea,]$All[-
      c(2,13)])-VillageTotalHH[VillageTotalHH$region=="Bethel",]$All)

TempRegionResults<-vector("list",13) # 12 = number of outcomes, + Cost
TempRegionResults<-
  lapply(seq(length(TempRegionResults)),function(Index,TempRegionResults,NV,NumberSims)
  {
    ### 20 Jan 03 - TEST RUN USING SMALLER NUMBER TRIALS.
    ### REAL DEAL? -> RESET CALL TO SIMINDEX - 10 to 1000
    # Note 15 = number of P values to explore, P = % households in each
    village.
    # 10 = number of sims per setting

    if (Index < 13)
      TempRegionResults[[Index]]<-
        list("Mean"=array(NA,dim=c(length(NV),15,NumberSims),
          dimnames=list(paste("Nv",NV,sep=""),
            paste("P",seq(5,75,5),sep=""),seq(NumberSims))),
          "WeightedMean"=array(NA,dim=c(length(NV),15,NumberSims),
            dimnames=list(paste("Nv",NV,sep=""),
              paste("P",seq(5,75,5),sep=""),seq(NumberSims))))
    else #(Index == 13)
      TempRegionResults[[Index]]<-array(NA,dim=c(length(NV),15,NumberSims),
        dimnames=list(paste("Nv",NV,sep=""),
          paste("P",seq(5,75,5),sep=""),seq(NumberSims)))
  },TempRegionResults=TempRegionResults,NV=NV,NumberSims=NumberSims)
names(TempRegionResults)<-c(ResponseNames,"Cost")

cat(paste("Structures made ",date()))

### NOW FILL IN THE RESULTS!!!
### loop over NV
### 20 Jan 03 - TEST RUN USING SMALLER NUMBER TRIALS.
### REAL DEAL? -> RESET CALL TO SIMINDEX - 10 to 500

#DataObjects

TempData_YKDSRSAnnualSubsetdf[YKDSRSAnnualSubsetdf$region==TempRegion,]
TempVillageHH_VillageTotalHH[VillageTotalHH$region==TempVillageRegionName,]
# Drop Akiak & Kasigluk - no observations.
#
TempVillageHH<-TempVillageHH[-c(2,7),]

##### WORK #####

NVindex <- 1
cat(paste("\n",NVindex,date()),"\n"))

# How many villages to sample in this region
NVThisRegion <- round(NV[NVindex]*RegionPercTotalHH)
# make sure sample at least one village per region
if (NVThisRegion < 1) NVThisRegion <- 1

# if sufficient villages from this region...
if (length(unique(TempData$villagename)) >= NVThisRegion)
{ # sample 'em

  for (SimIndex in seq(NumberSims))
```

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```
{ # screen marker...status
  if (SimIndex%%50==0) cat(SimIndex)
  else if (SimIndex%%10==0) cat(".")

  # pick villages
  SampleVillages<-sample(unique(TempData$vilagename),
NVThisRegion,replace=F)

  # For each P%, figure out PSample for selected villages
  # Want to get, say 75% all HH in region, so what % of HH in the chosen
  villages?
  # Note that equal % HH each sampled village (equal effort, in some sense,
  per village).
  PSample<-
seq(.05,.75,.05)*sum(TempVillageHH$All)/sum(TempVillageHH$All[match(SampleVi
llages,TempVillageHH$village.name)])

  # Depending on the number of HH in the village, PSample could be > 100%.
  # If so, reset to 100%
  # REALLY, in this case, you'd want to pull in households from past or other
  villages?
  PSample[PSample>1] <- 1.0

  # calculate annual region estimate, each response, each PSample - array
  RegionEst <-CalcRegionEst.f(PSample,SampleVillages,TempVillageHH,

  TempData[TempData$vilagename==levels(SampleVillages)[SampleVillages],],
  Weighted="Both")
#cat("RegionEst")
  # Since Weighted=="Both", RegionEst is List w/ two components
  for (i in seq(12)) # each outcome
  {
    TempRegionResults[[i]]$Mean[NVindex,,SimIndex]<-RegionEst$Mean[,i]
    TempRegionResults[[i]]$WeightedMean[NVindex,,SimIndex]<-
    RegionEst$WeightedMean[,i]
  }

  # Calculate and save Cost info
  if (T) { # just save cost
    trash<-
    round(outer(TempVillageHH$All[match(SampleVillages,TempVillageHH$village.nam
e)],PSample,"*"))
    TempRegionResults[[13]][NVindex,,SimIndex] <-
    apply(trash,2,sum)*TempRegionHHCost
  }

  } # End SimIndex loop
} # if sufficient villages loop
```

Repeat for NV = 2,...,15. Then repeat for all other regions.

The above code calls the following function to calculate the sample mean harvest rate for each of the sampled villages for each species and response:

```
##### Last Edit 20 Jan 03
CalcRegionEst.f<-
  function(PSample,SampleVillages,TempVillageHH,NPBootData,Weighted=F)
{
  ## Takes sampled total annual household harvest for a set of responses
  ## for a village,
```


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```
## samples a range of portions PSample (turned into absolute # vi
TempVillageHH)
## calculates total sample harvest, each response, for each village
## expand to total village harvest, each response, each village
## expand to total region harvest estimate, each response

OldOptions<-options()
options(warn=-1)

TempVillageMeanEsts<-
lapply(seq(length(SampleVillages)),function(VN,TempVillageHH,NPBootData,PSam
ple,SampleVillages)
{ # For each Sample village, sample and estimate mean
  #
  # calculate how big a sample (vector)
  TempSampleSize<-
round(PSample*TempVillageHH$All[TempVillageHH$village.name==as.character(Sam
pleVillages[VN])),0)
  # Pull out Village data.
  TempVillageData<-
NPBootData[NPBootData$villagename==levels(SampleVillages)[SampleVillages[VN]
],]

  #Sample - result is matrix length(TempSampleSize) by #
Responses
  # this assumes a single summary statistic per sample
  SampleVillageMean<-
t(sapply(TempSampleSize,function(Nsize,TempVillageData)
{
  SampleIndex<-
sample(seq(dim(TempVillageData)[1]),Nsize,replace=T)
  # get sample mean, each response
  trash2<-apply(TempVillageData[SampleIndex,9:20],2,mean)
},TempVillageData=TempVillageData))

  # Want regional mean * total # households, so return Village
Estimate
  return(SampleVillageMean)

},TempVillageHH=TempVillageHH,NPBootData=NPBootData,PSample=PSample,Saml
eVillages=SampleVillages)

##### Turn village mean estimates into Regional Estimates

if (Weighted!="Both")
{
  # define weighting scheme
  # WEIGHTED:
  # regional estimate via sample village means weighted by their relative
% total region households
  if (Weighted)
    Weights<-
TempVillageHH$All[match(SampleVillages,TempVillageHH$village.name)]/sum(Temp
VillageHH$All[match(SampleVillages,TempVillageHH$village.name)])
  # UNWEIGHTED:
  # regional estimate via mean sample village means
  else Weights<-rep(1,length(SampleVillages))/length(SampleVillages)

  # Calculate Result
  RegionMeanEst<-Weights[1]*TempVillageMeanEsts[[1]]
  for (i in seq(length(SampleVillages))[-1]) RegionMeanEst <-
RegionMeanEst+Weights[i]*TempVillageMeanEsts[[i]]
}
```


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```
dimnames(RMeanEst)_list(NULL,dimnames(NPBootData)[[2]][9:20])
# Expand to get Region Total Harvest Estimate
RegionEst<-RegionMeanEst*sum(TempVillageHH$All)
options(warn=OldOptions$warn)
return(RegionEst)
}
else
{ # Give both means - weighted and unweighted.
  # Weighted Calculations
  Weights<-
TempVillageHH$All[match(SampleVillages,TempVillageHH$village.name)]/sum(Temp
VillageHH$All[match(SampleVillages,TempVillageHH$village.name)])
  RegionWMeanEst<-Weights[1]*TempVillageMeanEsts[[1]]
  for (i in seq(length(SampleVillages))[-1]) RegionWMeanEst <-
RegionWMeanEst+Weights[i]*TempVillageMeanEsts[[i]]
  dimnames(RegionWMeanEst)_list(NULL,dimnames(NPBootData)[[2]][9:20])
  # Expand to get Region Total Harvest Estimate
  RegionWEst<-RegionWMeanEst*sum(TempVillageHH$All)

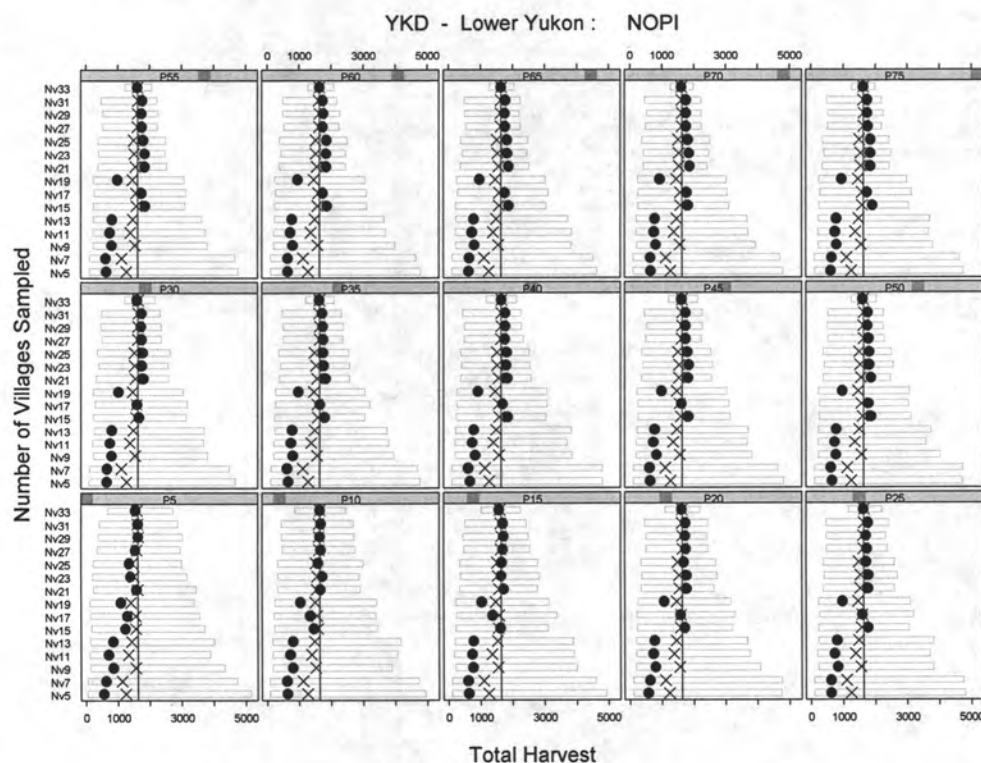
  # Now unweighted
  # Weighted Calculations
  Weights<-rep(1,length(SampleVillages))/length(SampleVillages)
  RegionMeanEst<-Weights[1]*TempVillageMeanEsts[[1]]
  for (i in seq(length(SampleVillages))[-1]) RegionMeanEst <-
RegionMeanEst+Weights[i]*TempVillageMeanEsts[[i]]
  dimnames(RegionMeanEst)_list(NULL,dimnames(NPBootData)[[2]][9:20])
  # Expand to get Region Total Harvest Estimate
  RegionEst<-RegionMeanEst*sum(TempVillageHH$All)

  # Return results
  options(warn=OldOptions$warn)
  return(list("Mean"=RegionEst,"WeightedMean"=RegionWEst))
}
```

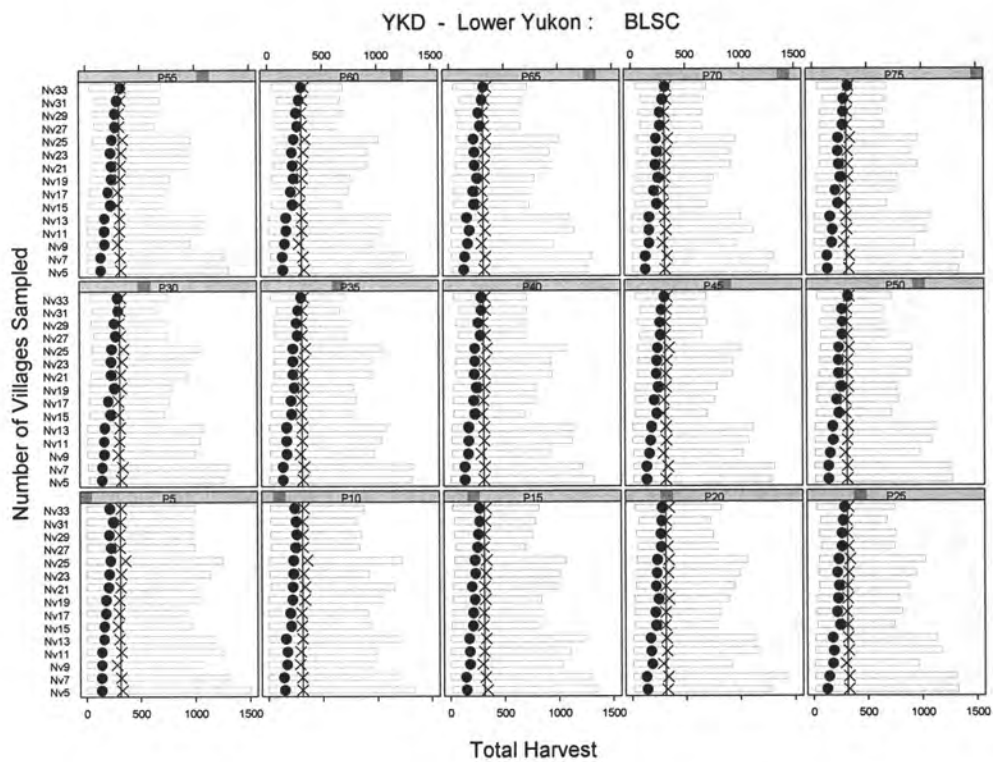
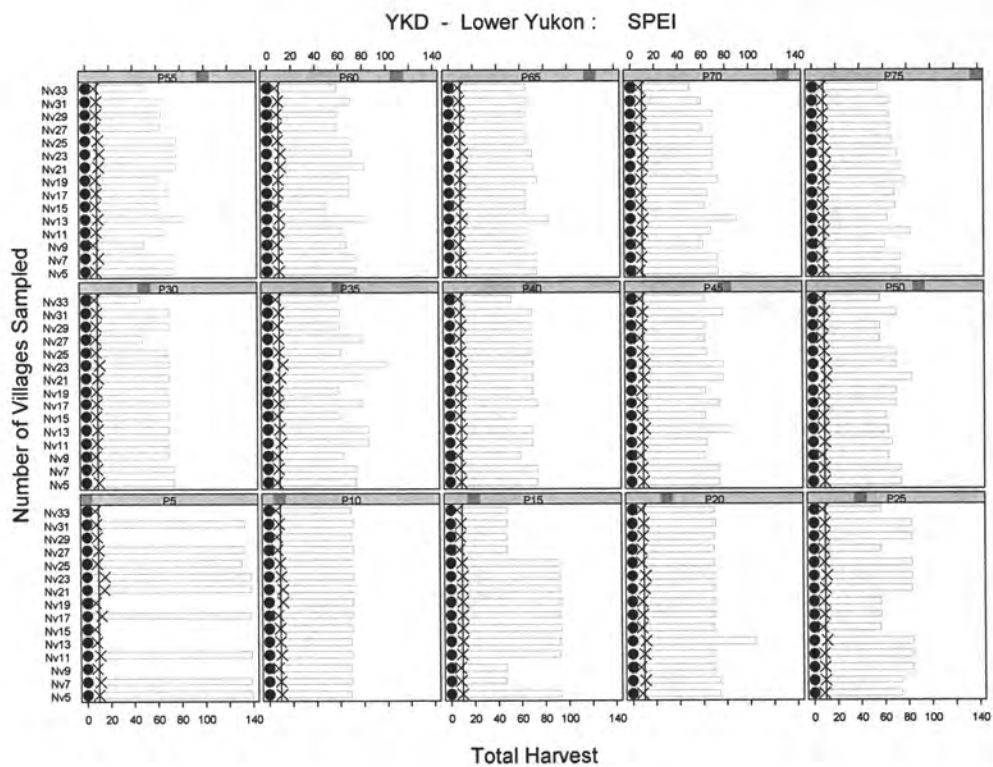
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APPENDIX 3. YUKON-KUSKOKWIM AREA REGION RESULTS

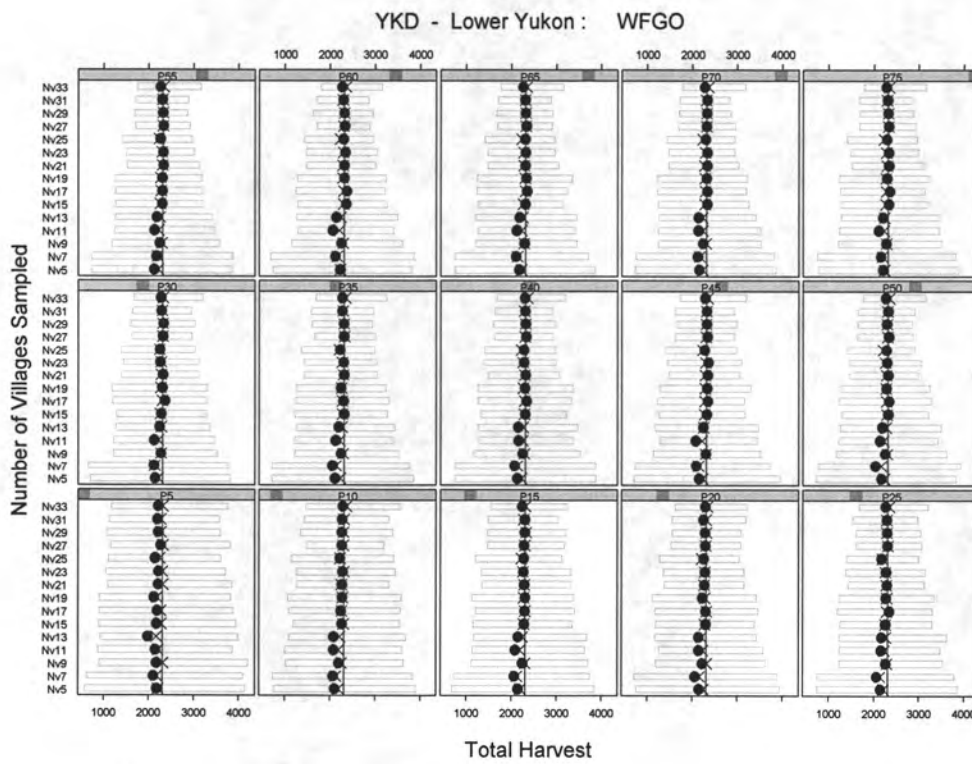
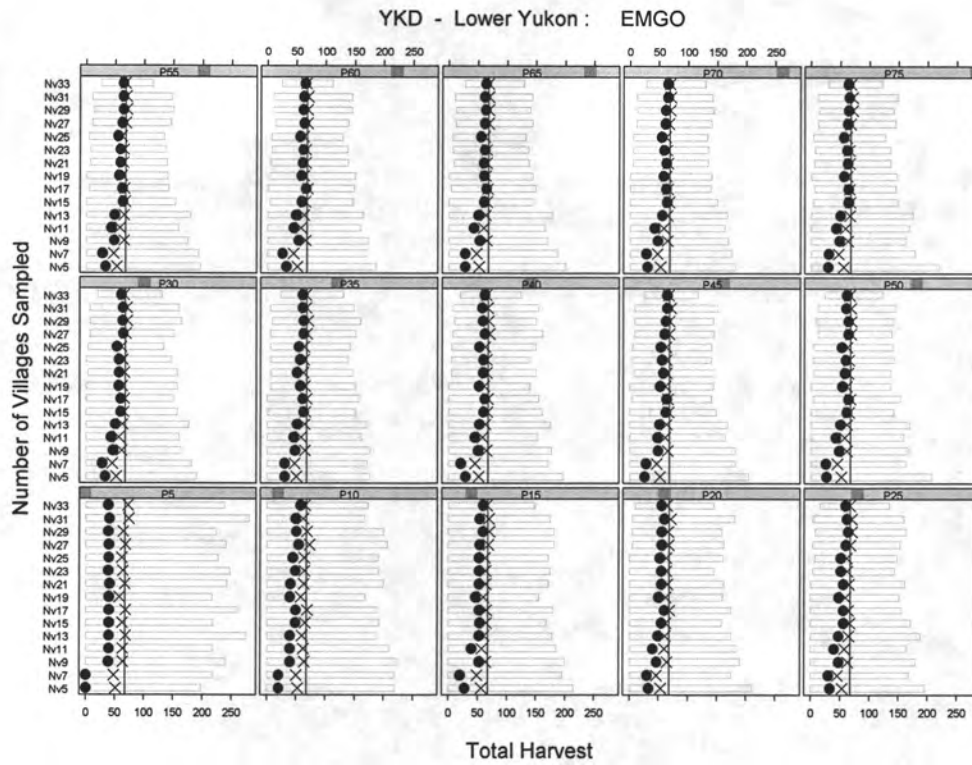
The species- and response-specific simulation results are given for each region in the YKD area, in the following order: Yukon River, North Coast, Mid Coast, South Coast, Bethel, Kuskokwim River. The figures are described in the legend of Figure 5.



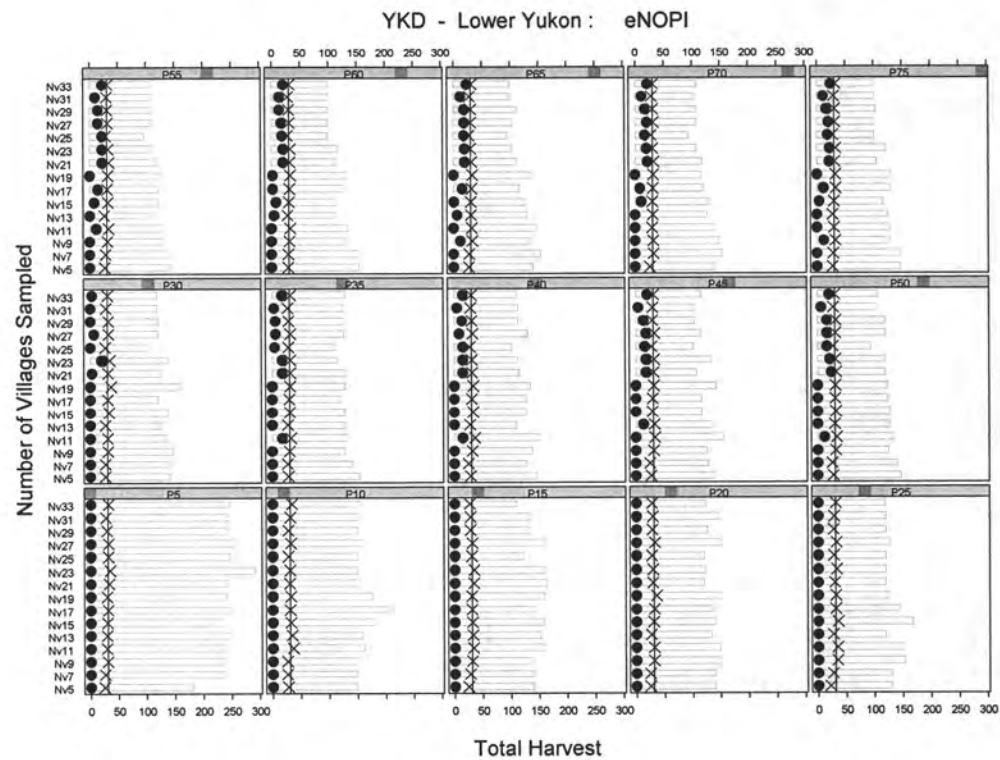
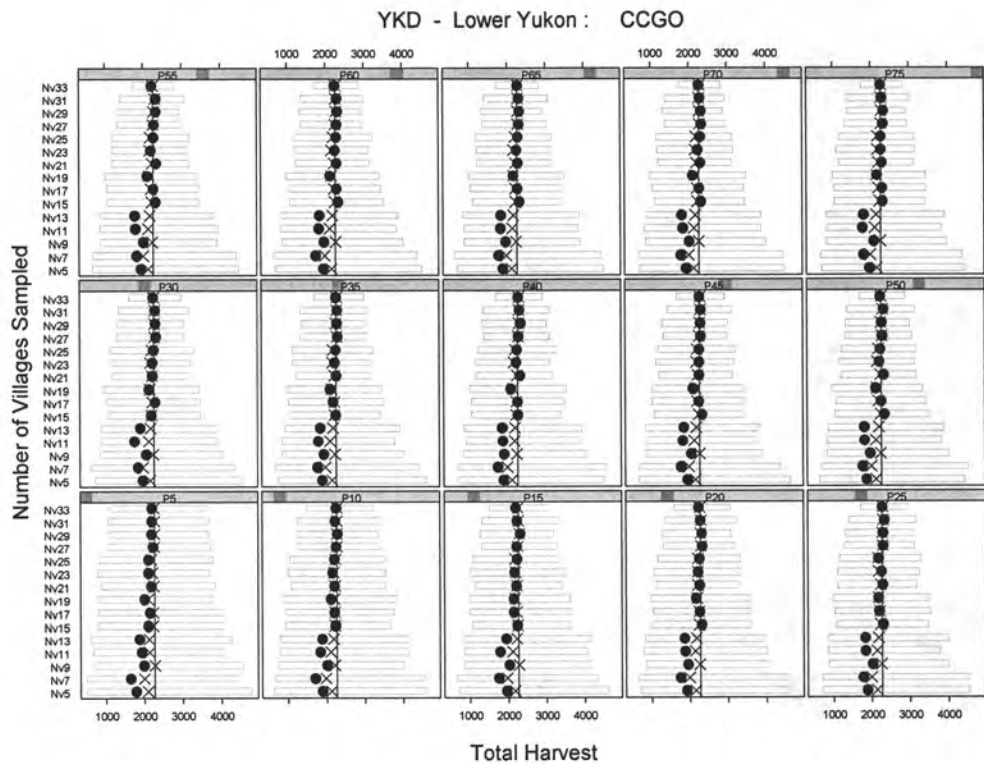
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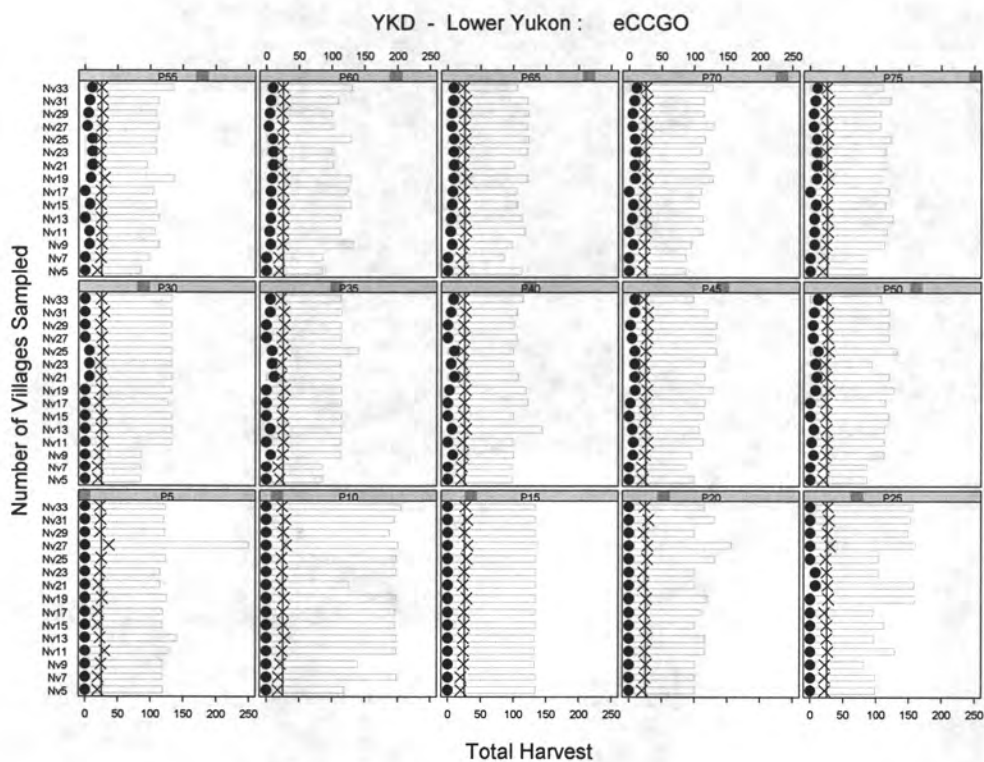
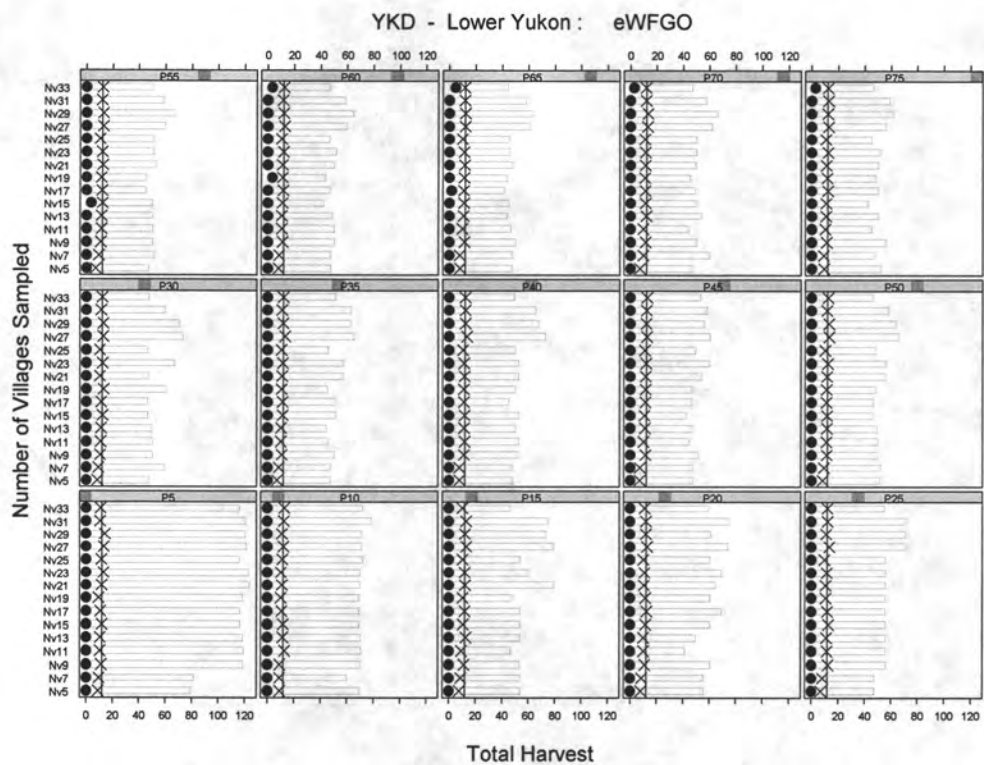
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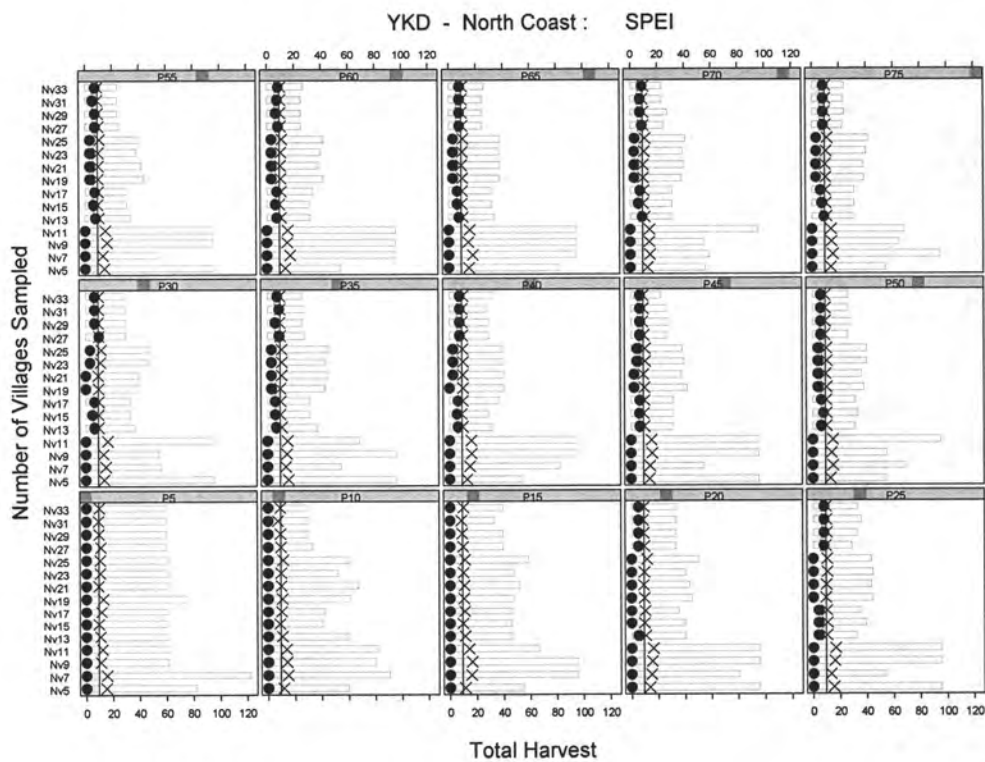
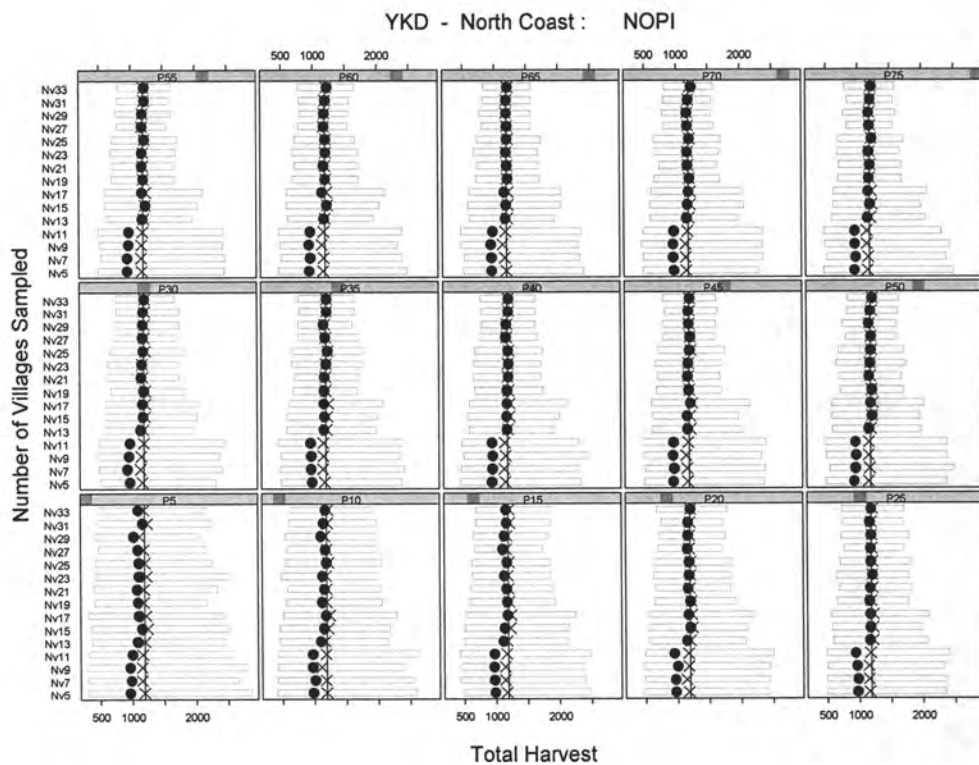
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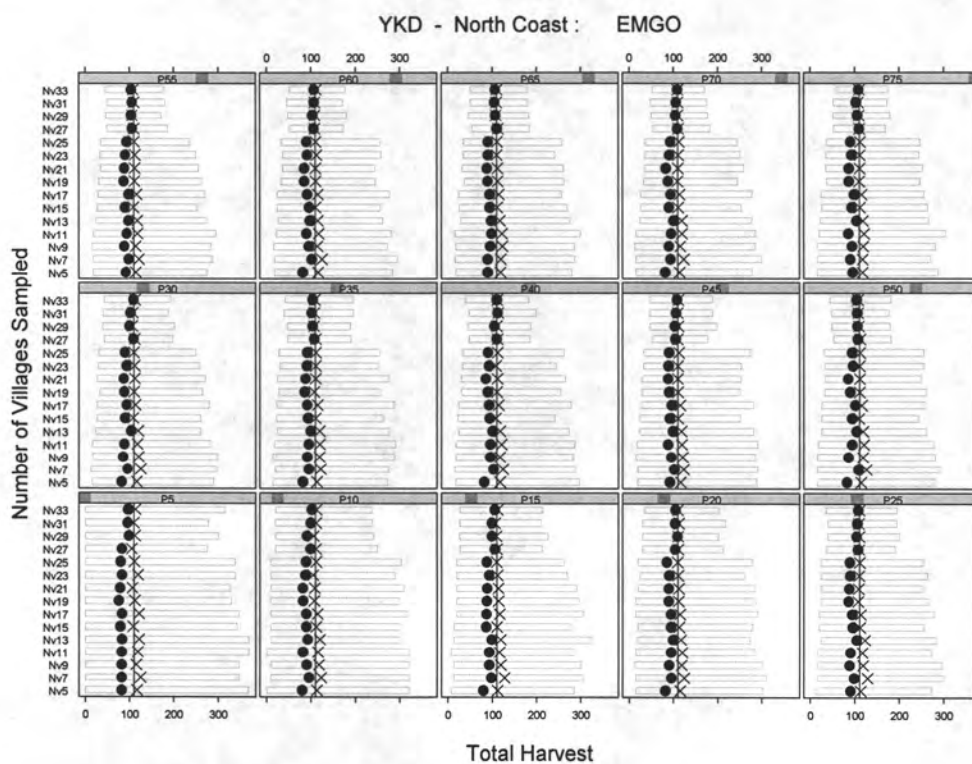
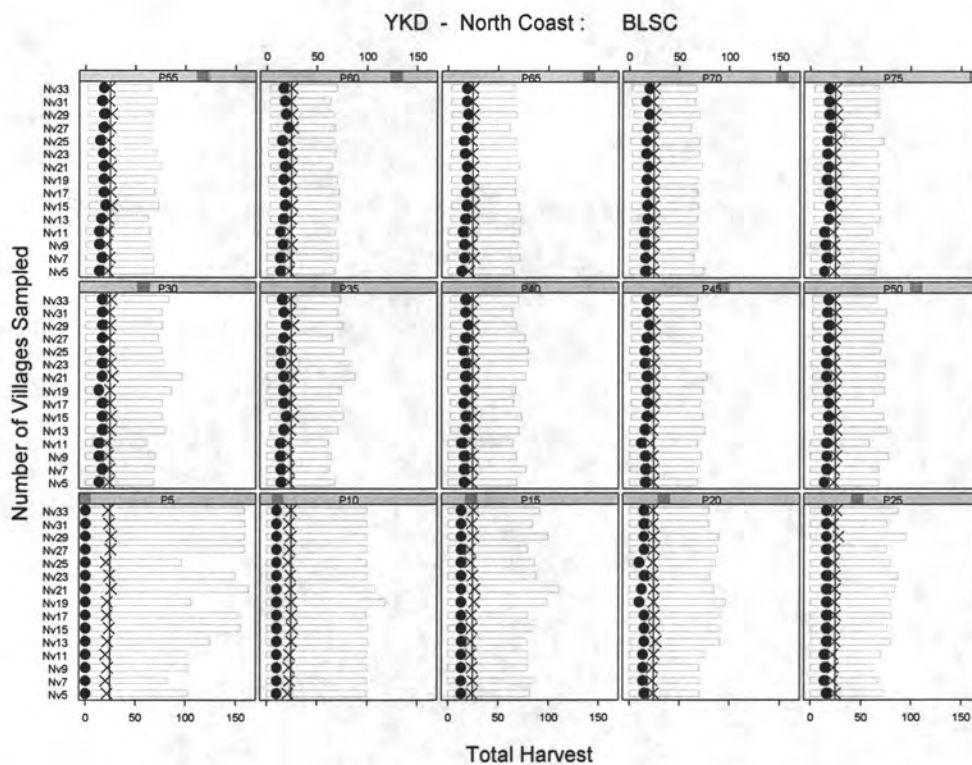
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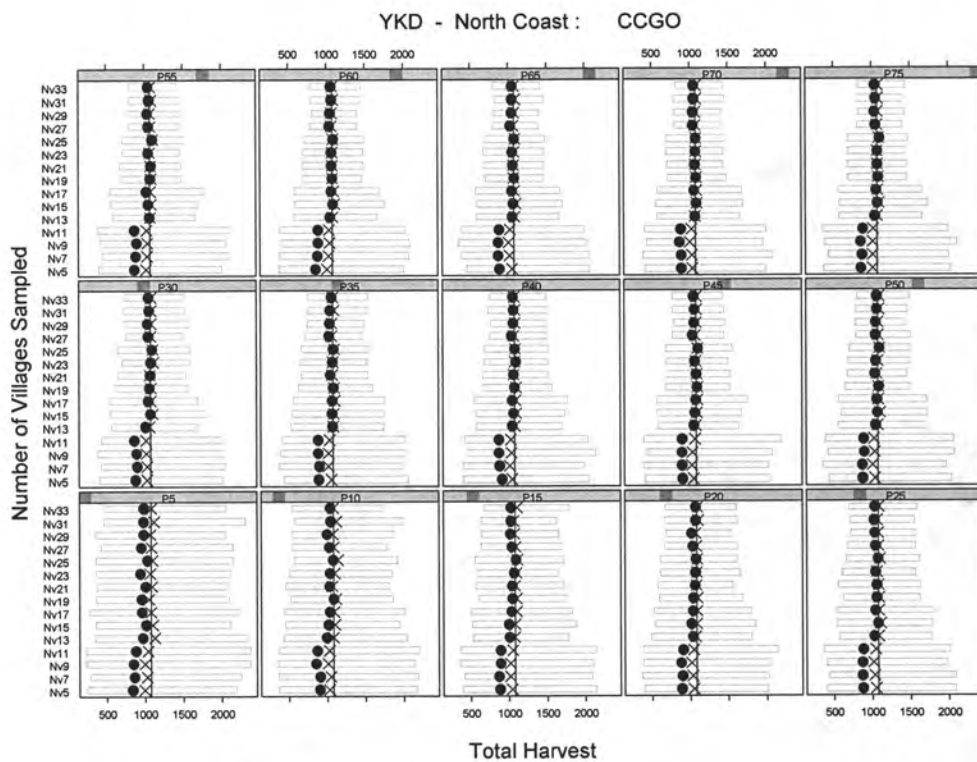
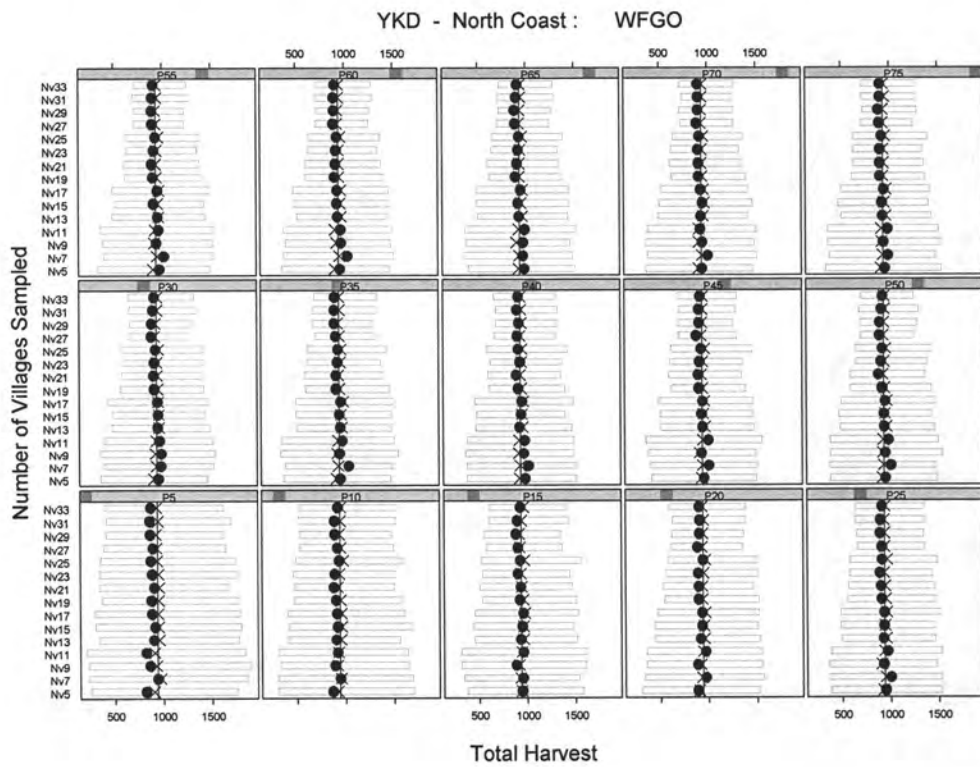
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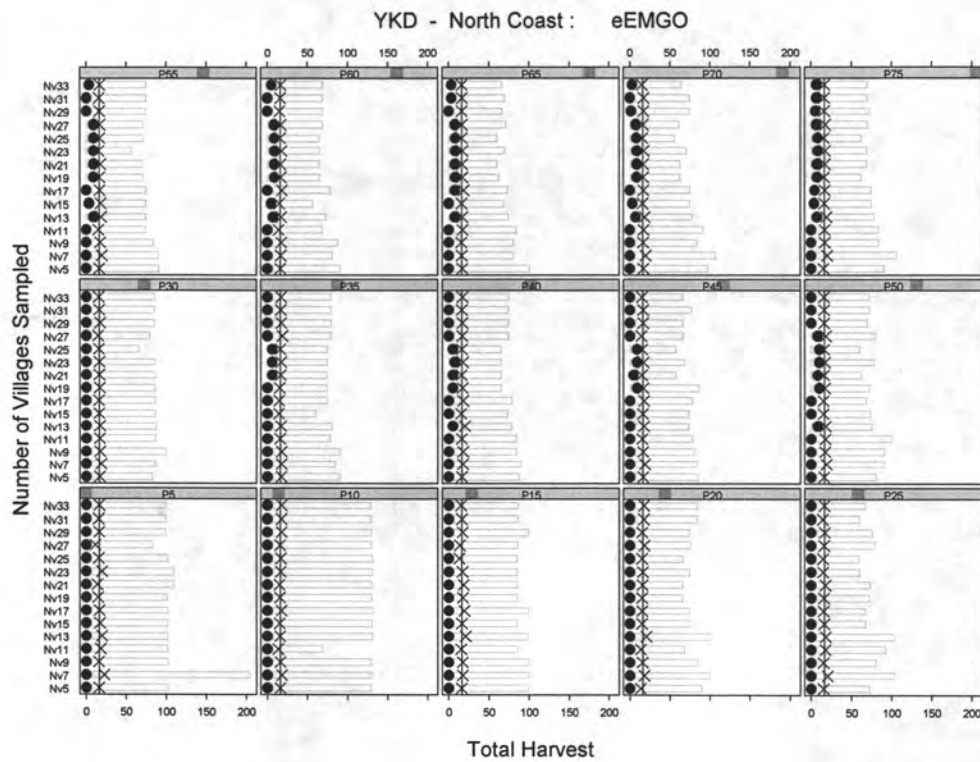
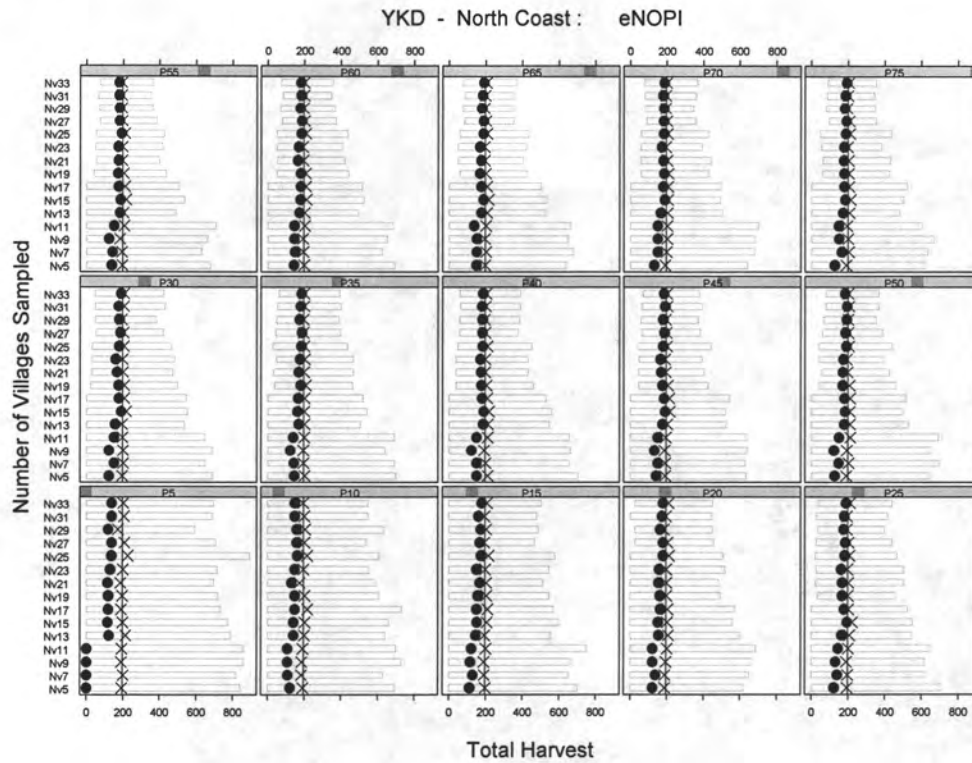
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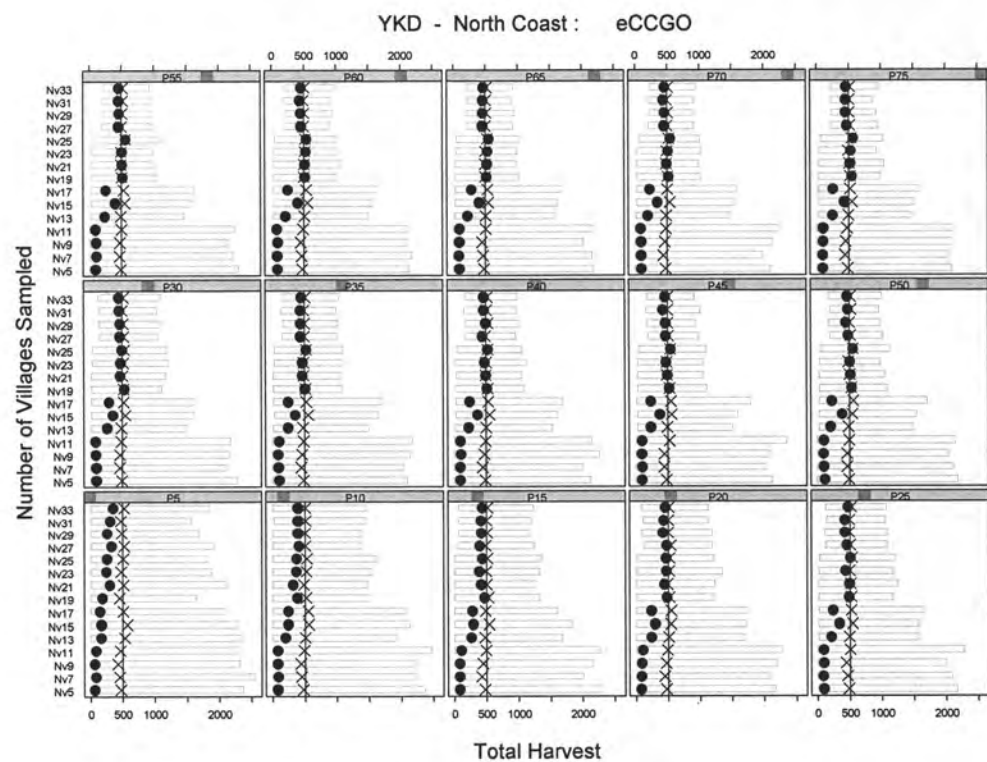
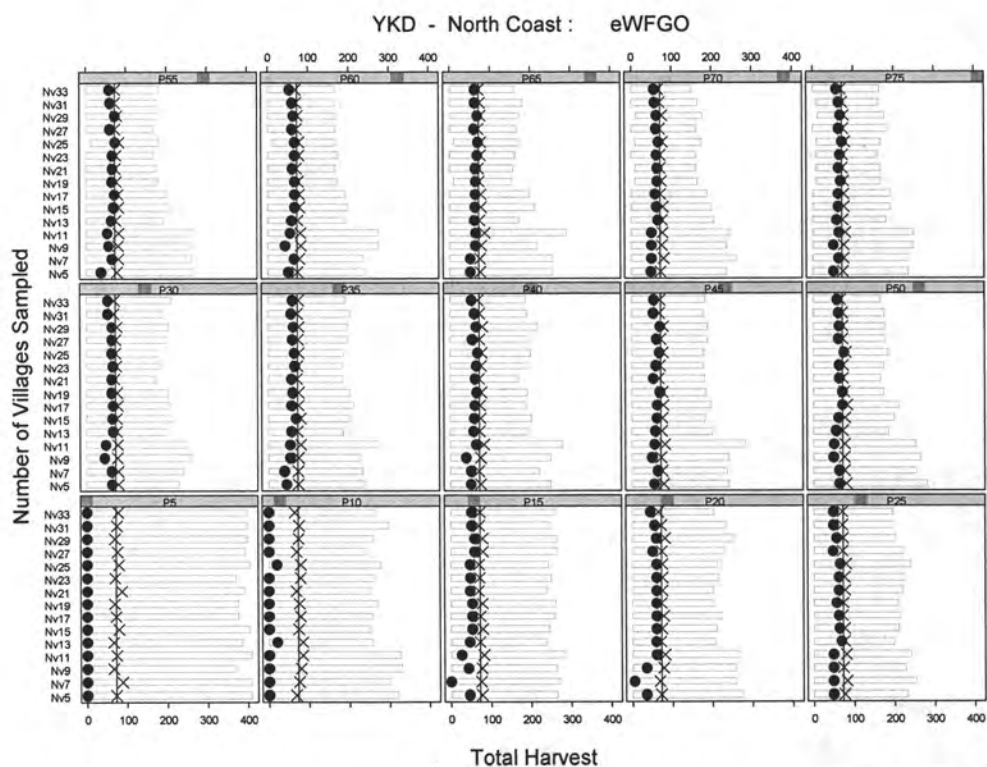
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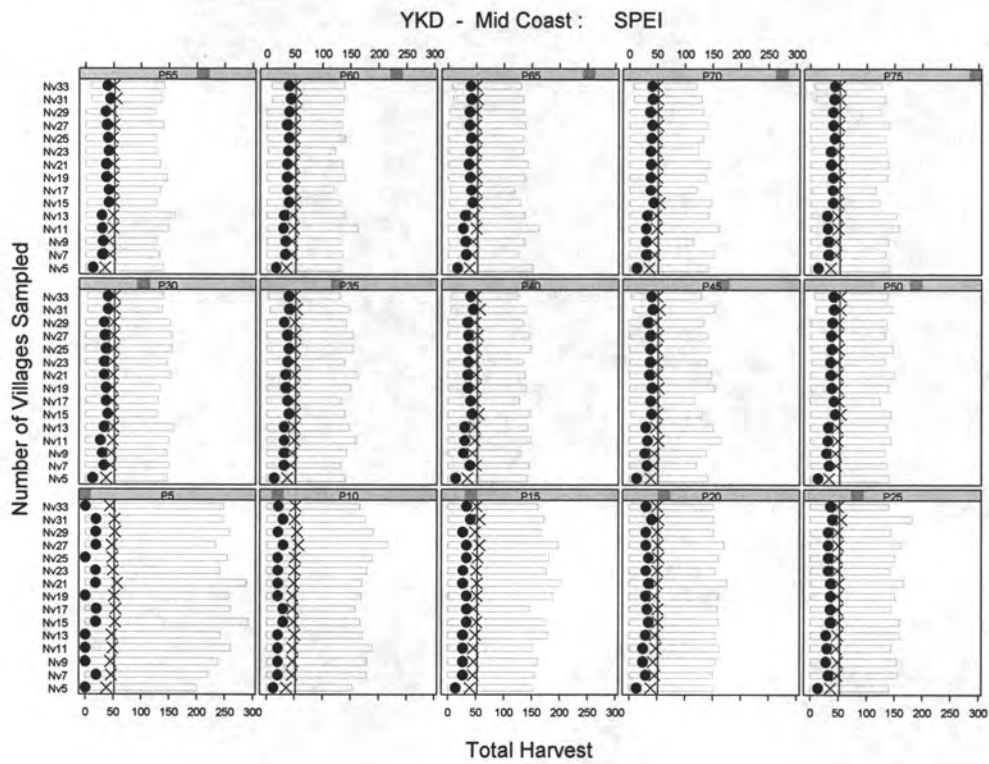
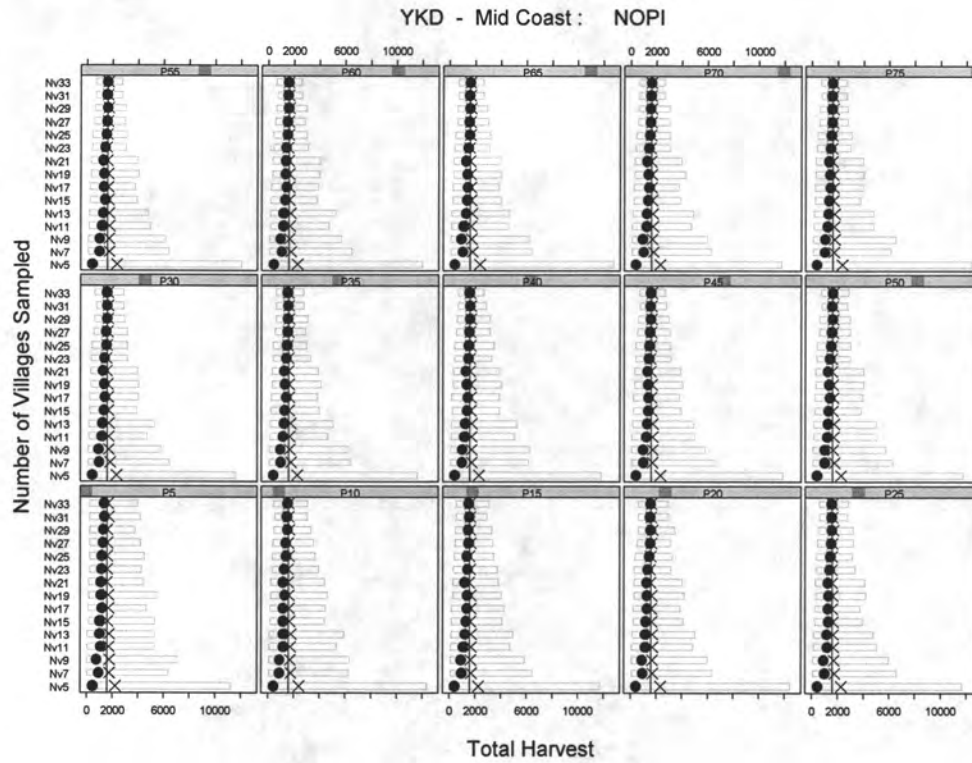
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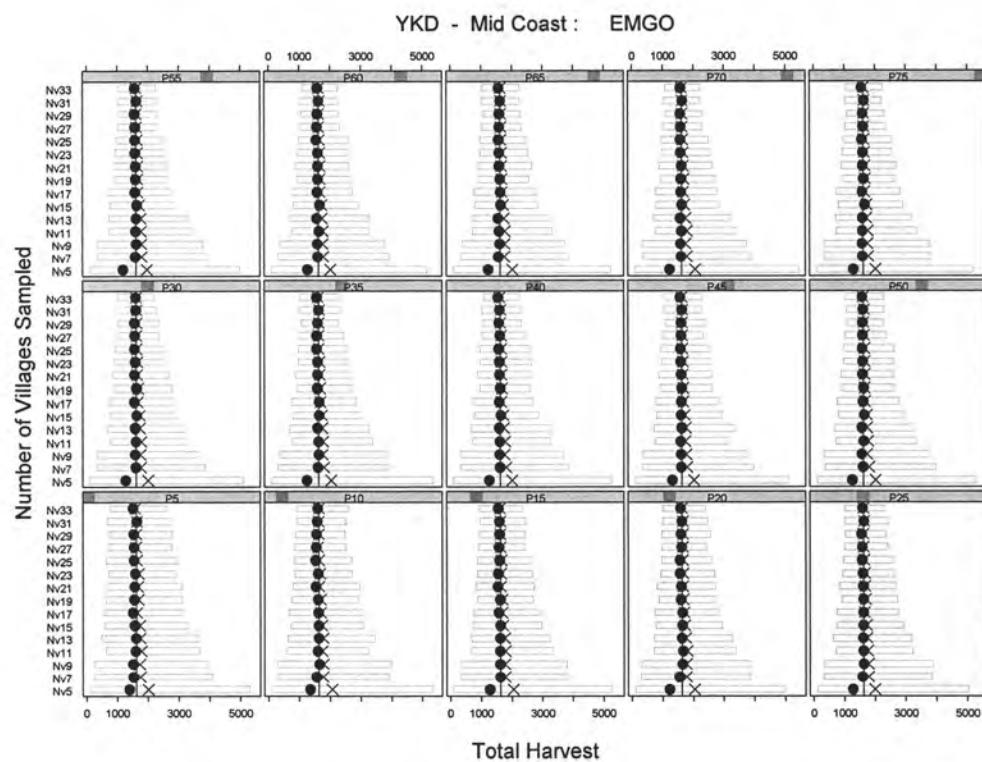
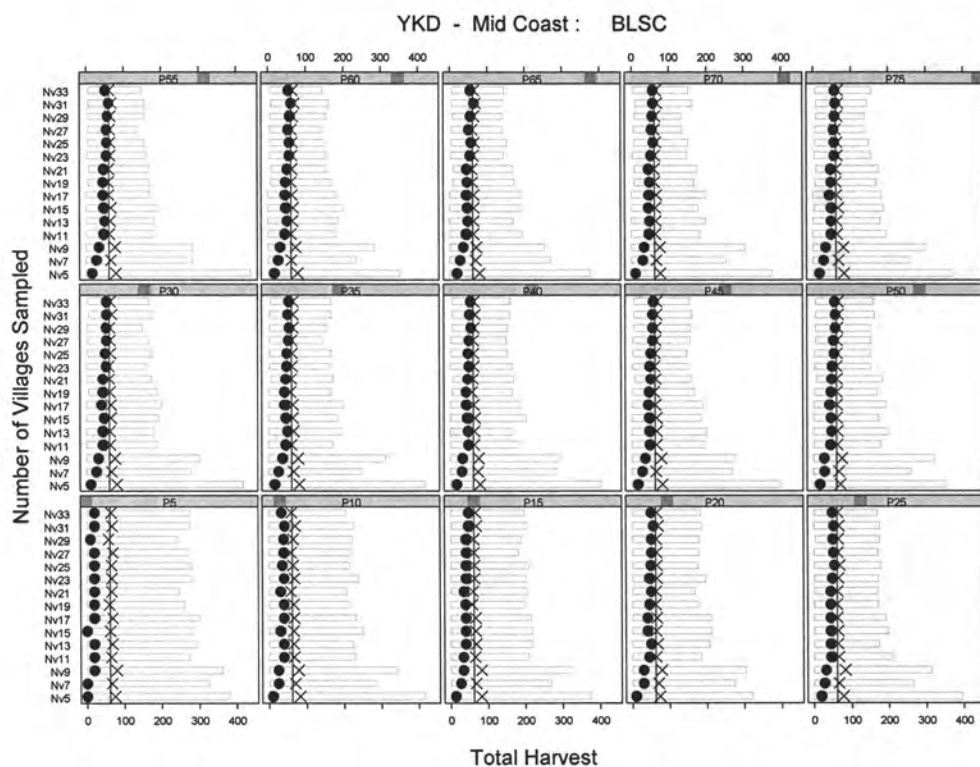
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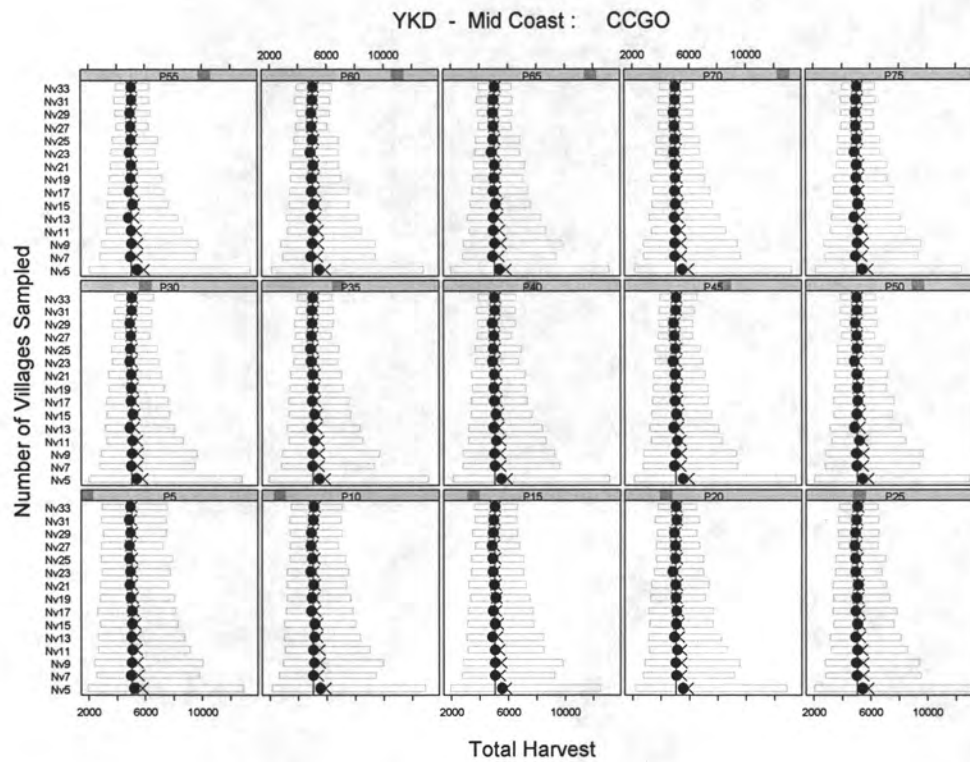
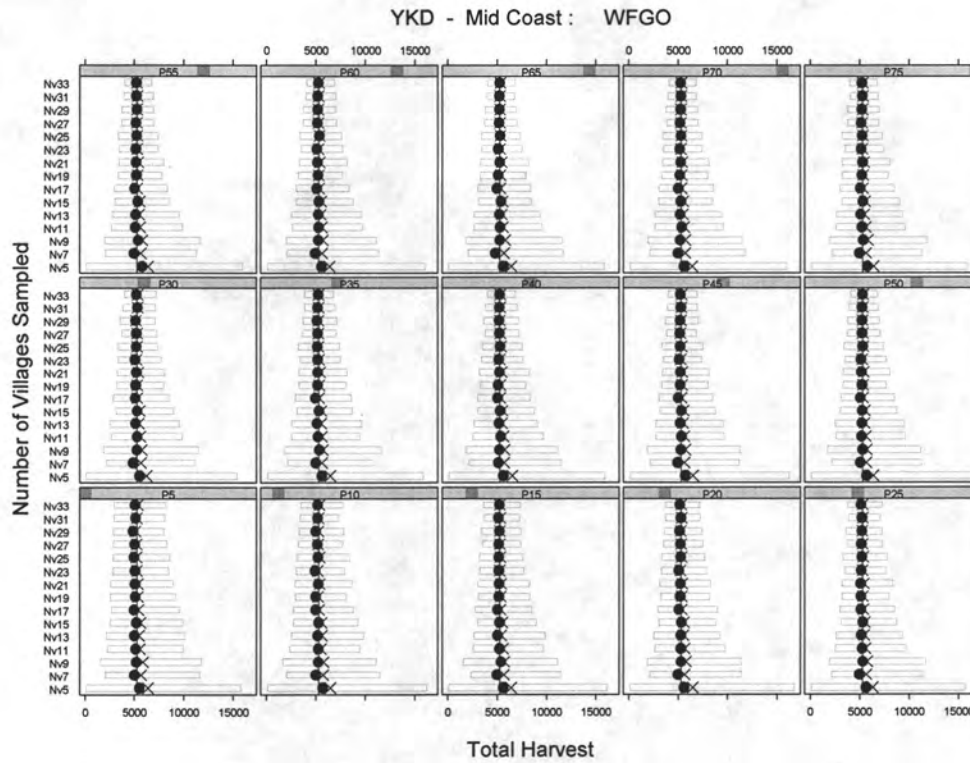
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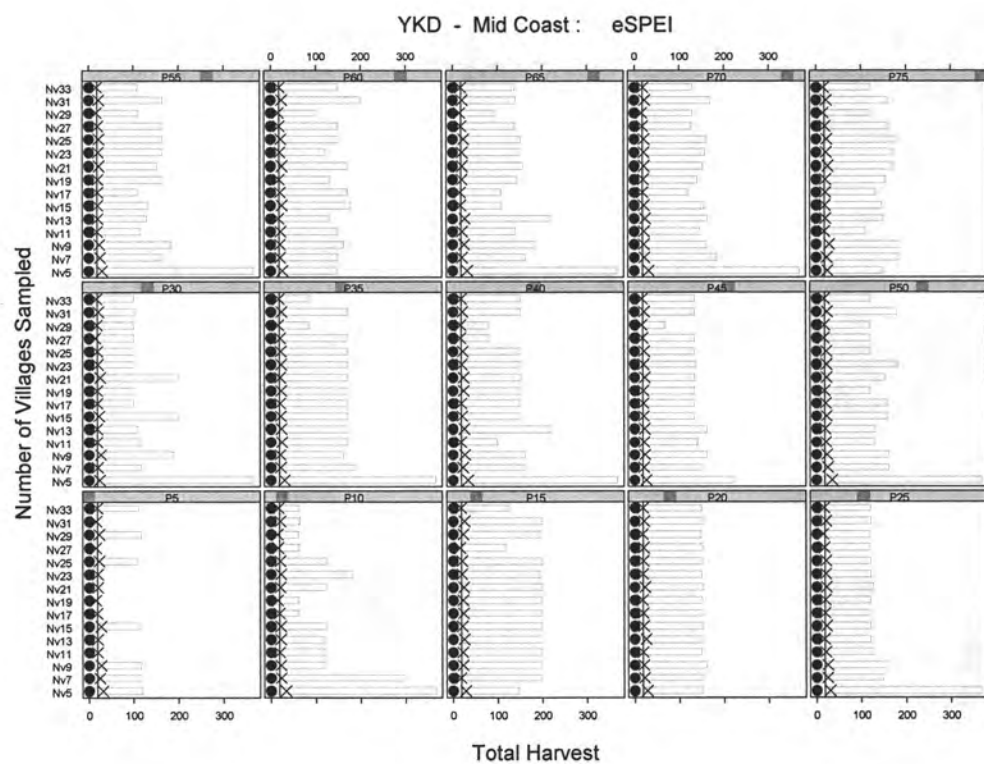
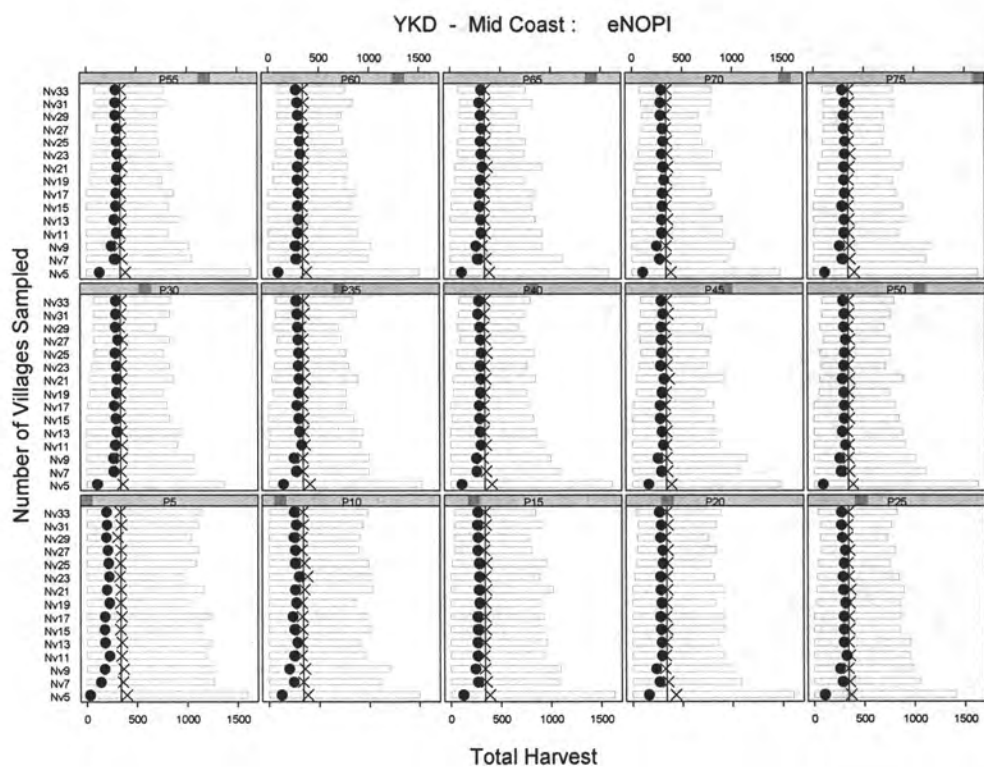
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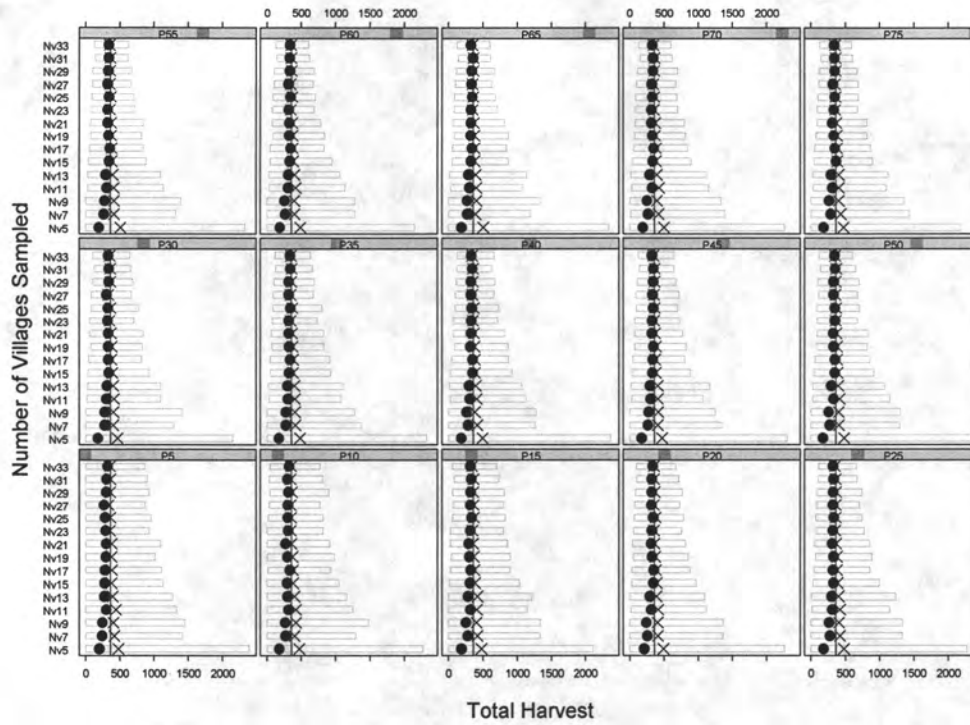


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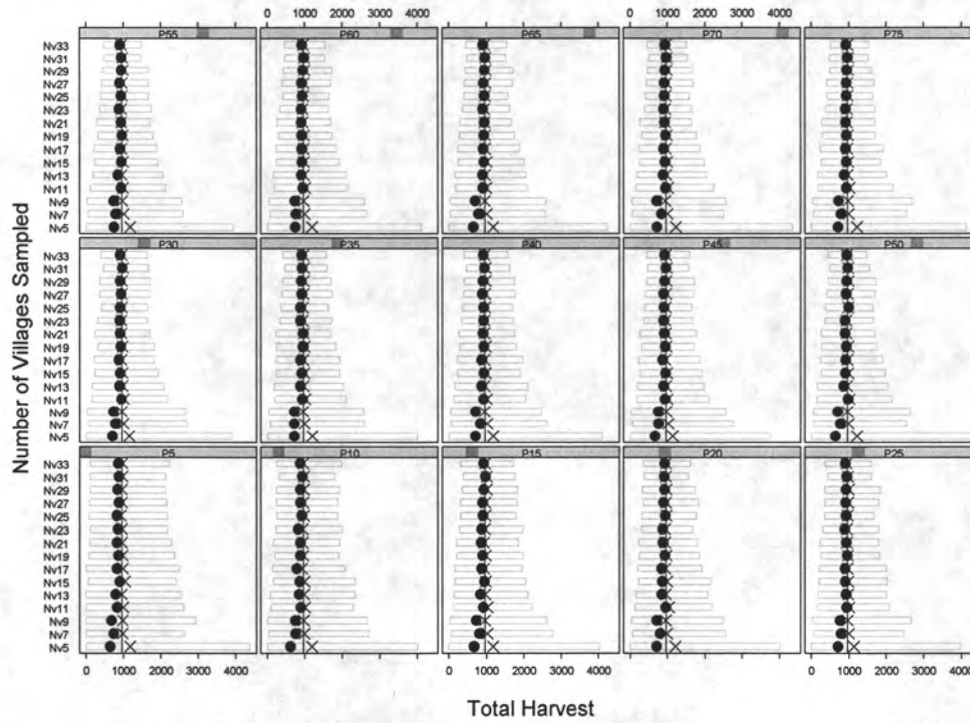


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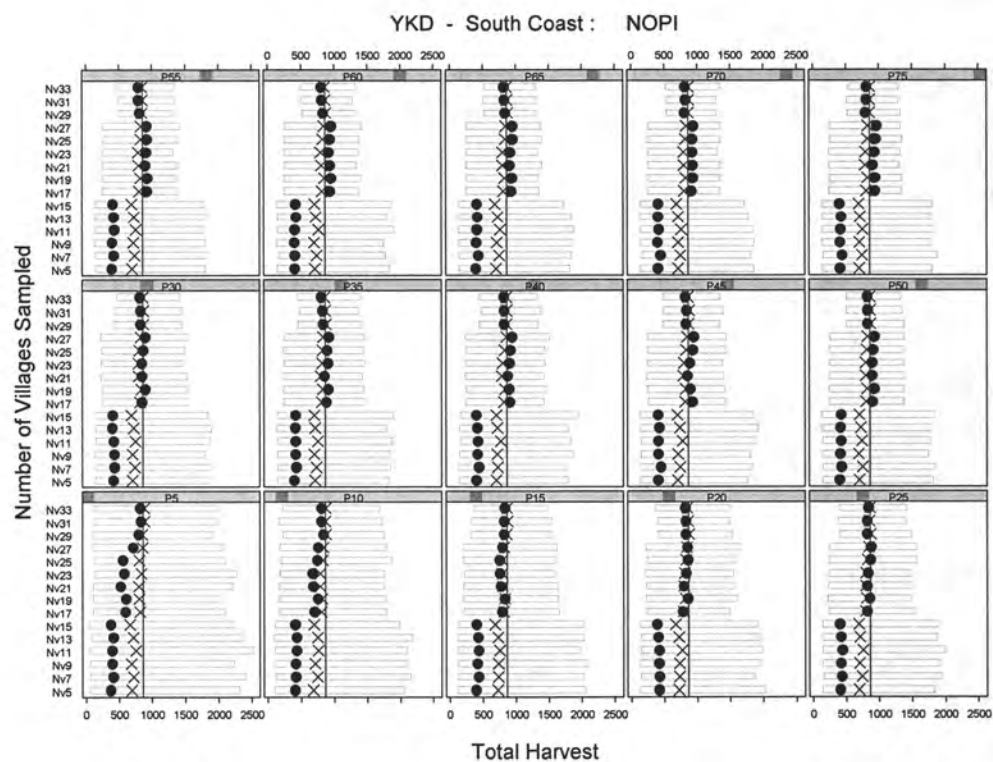
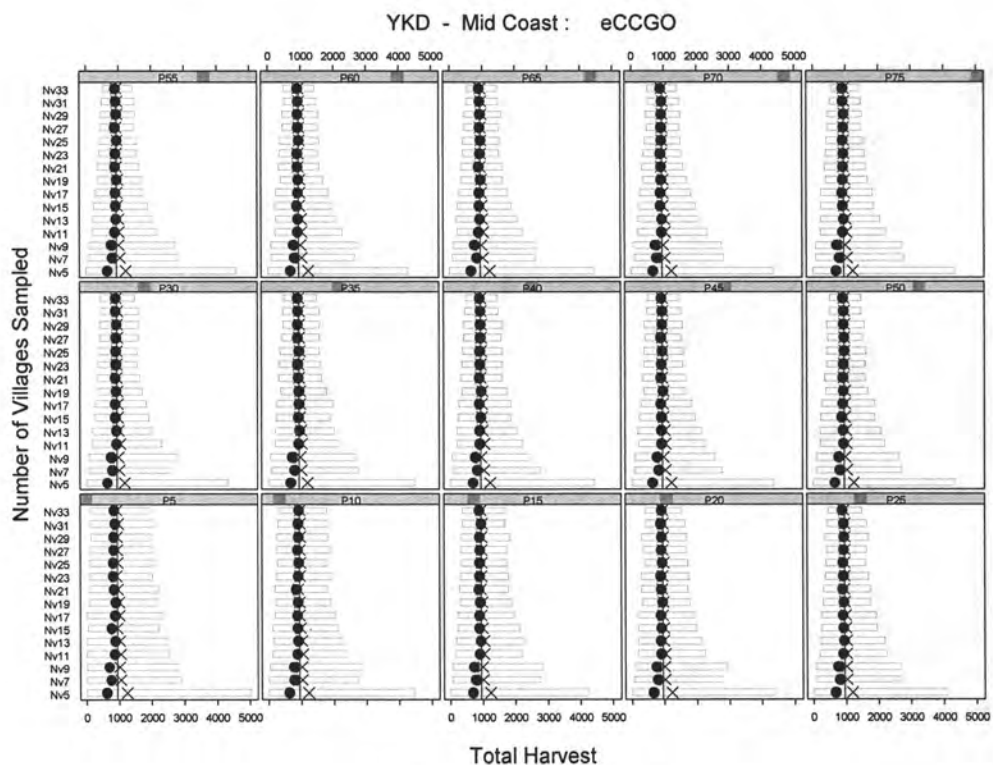
YKD - Mid Coast : eEMGO



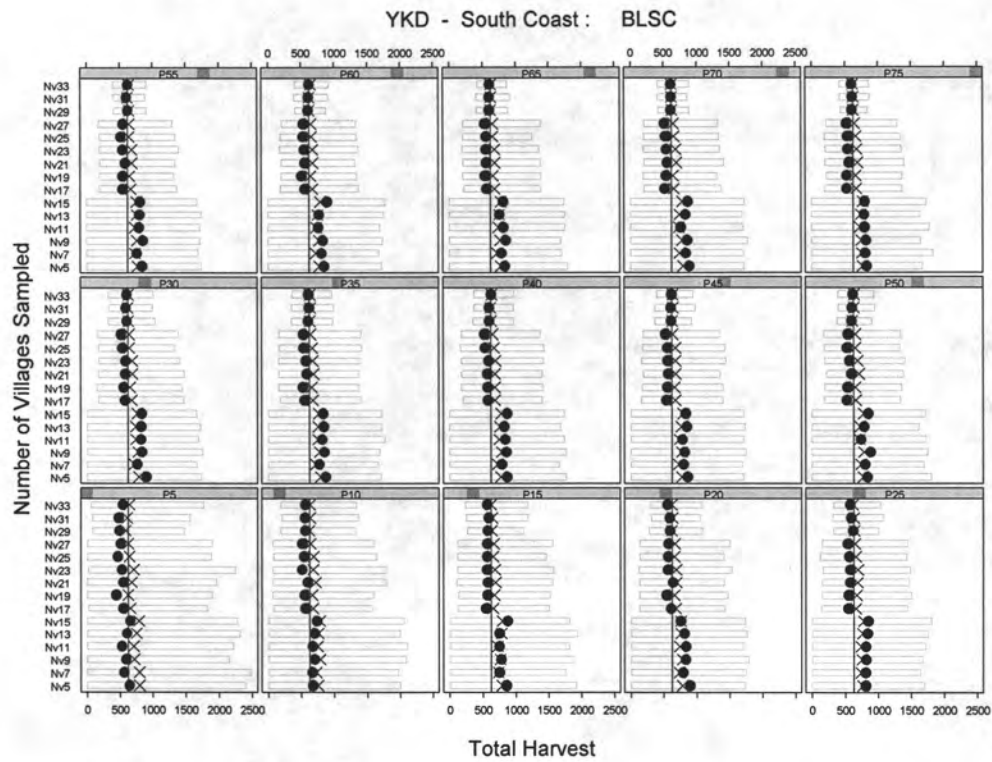
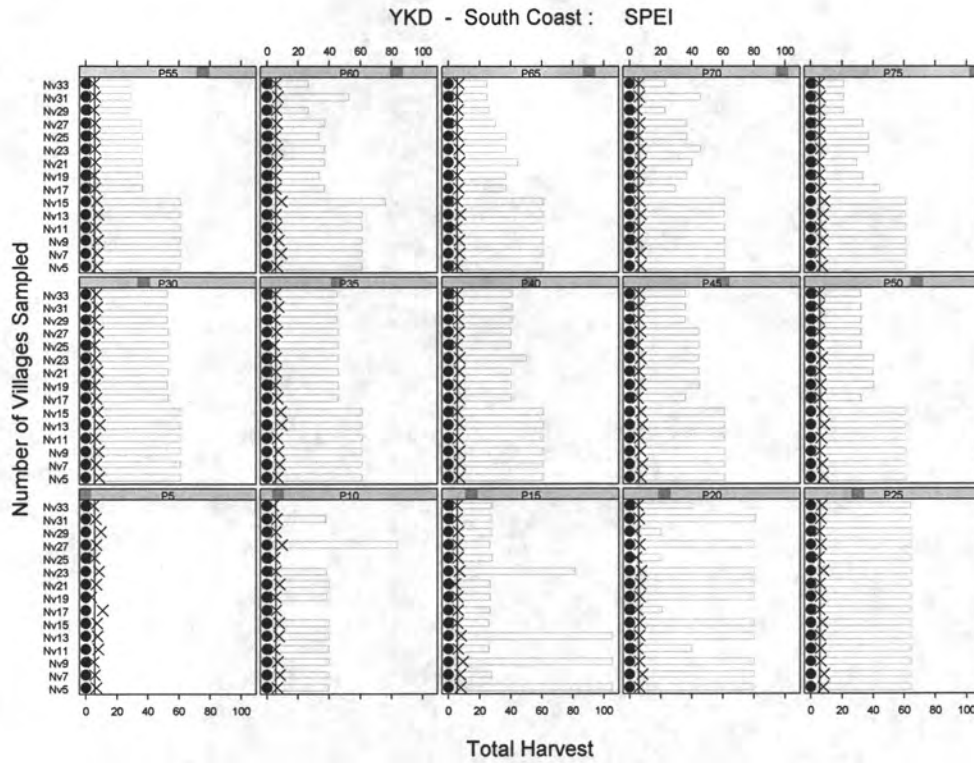
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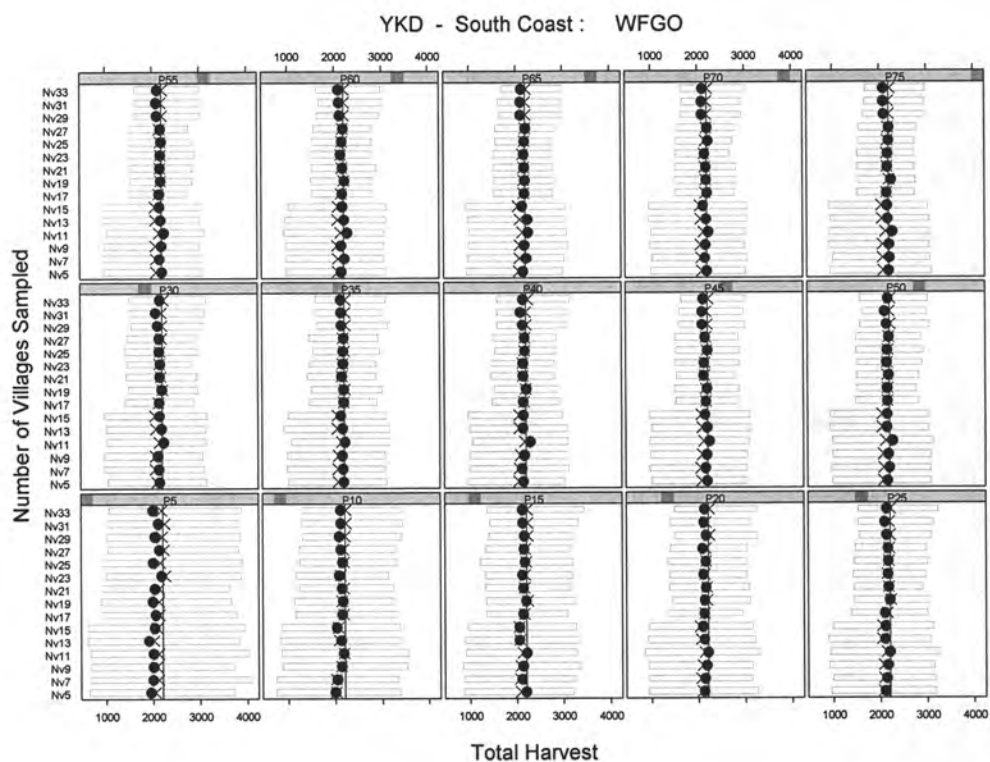
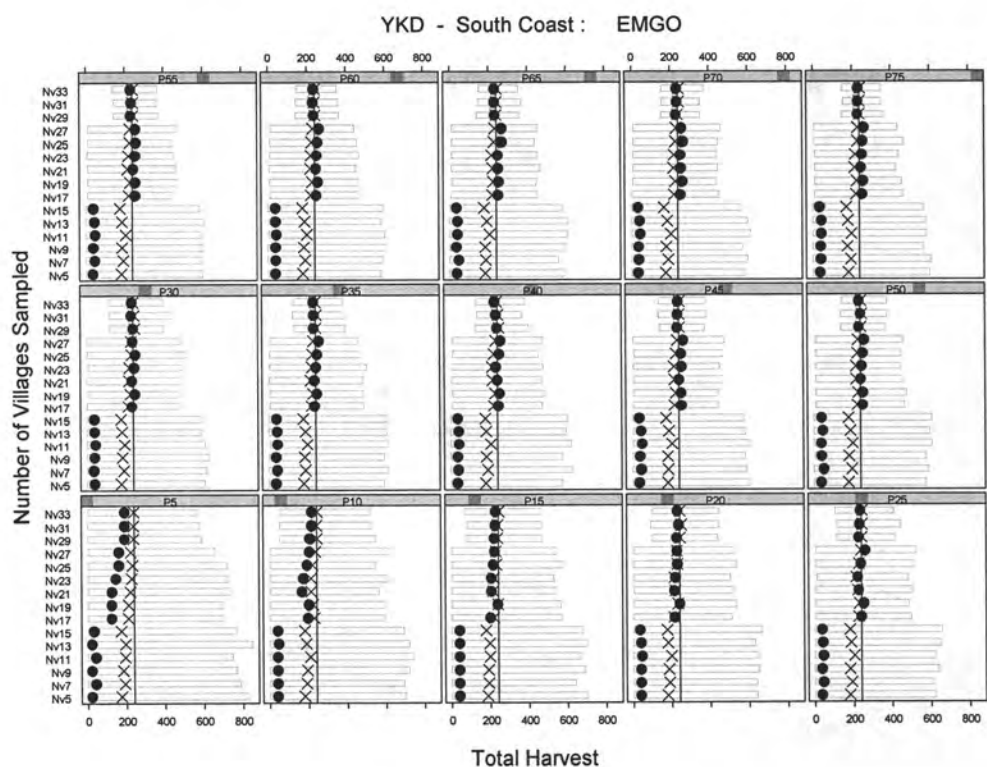
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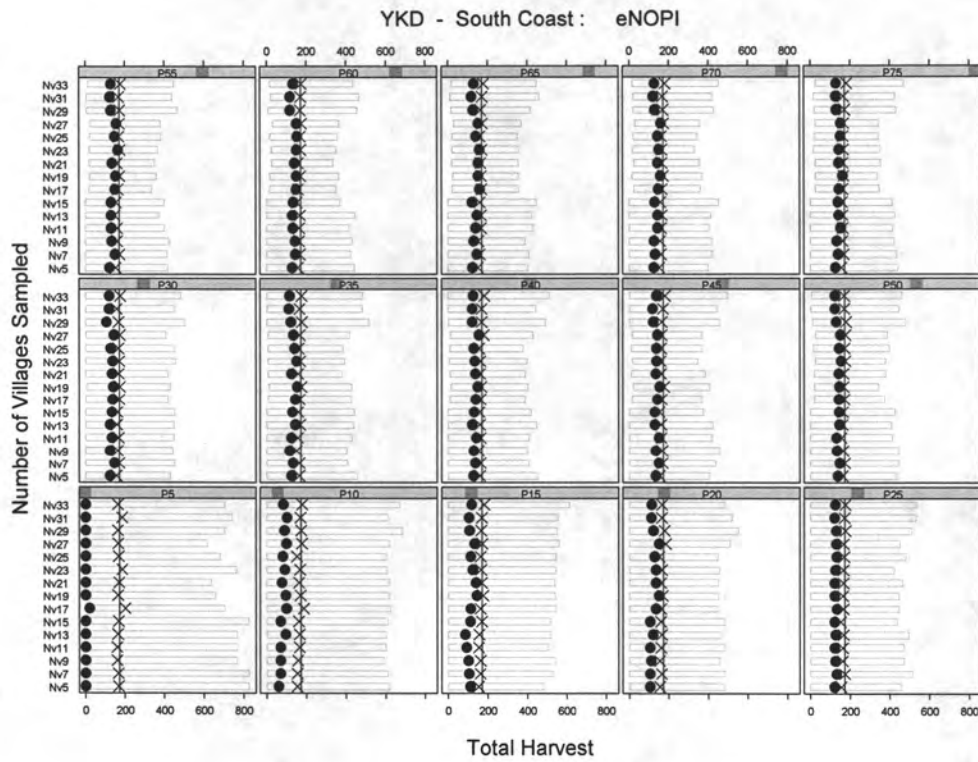
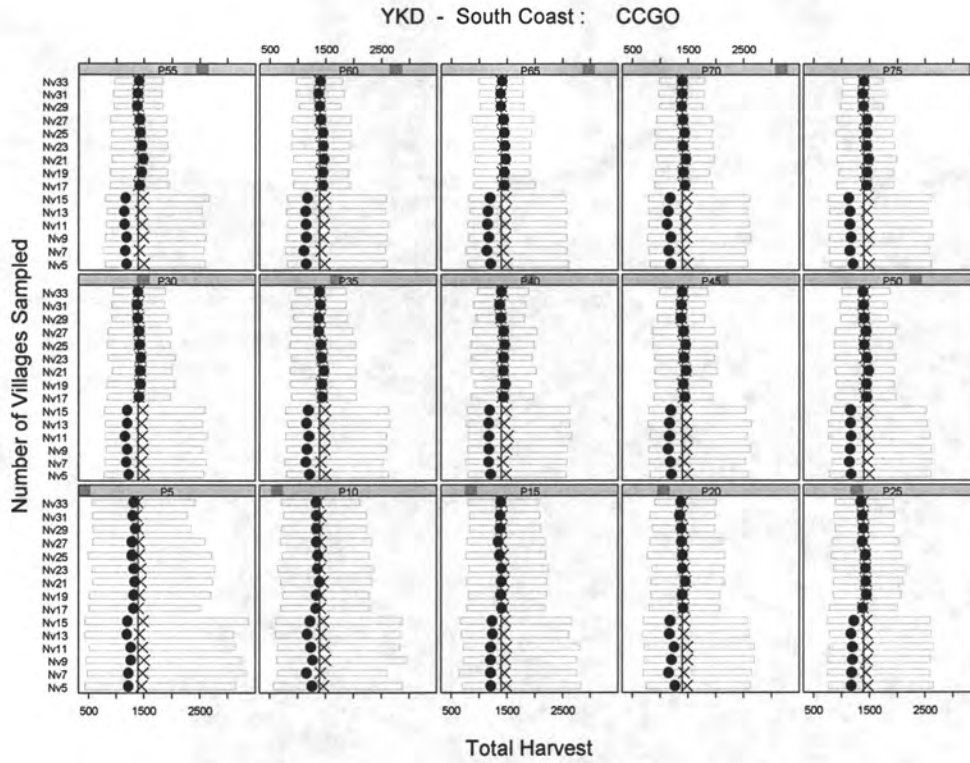
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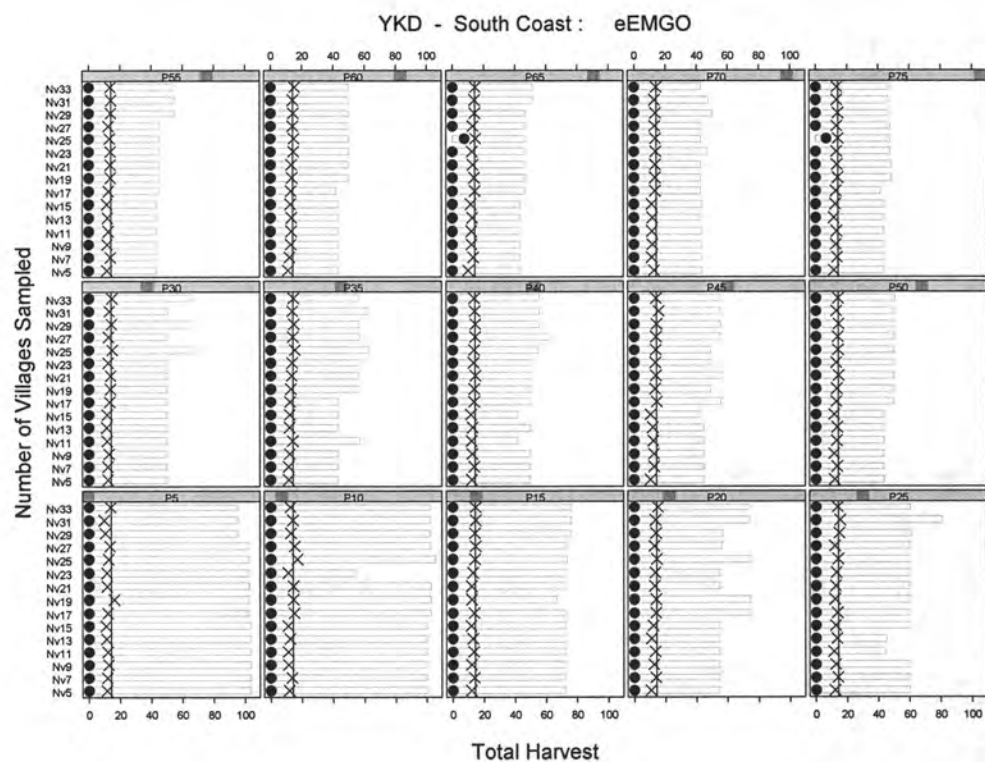
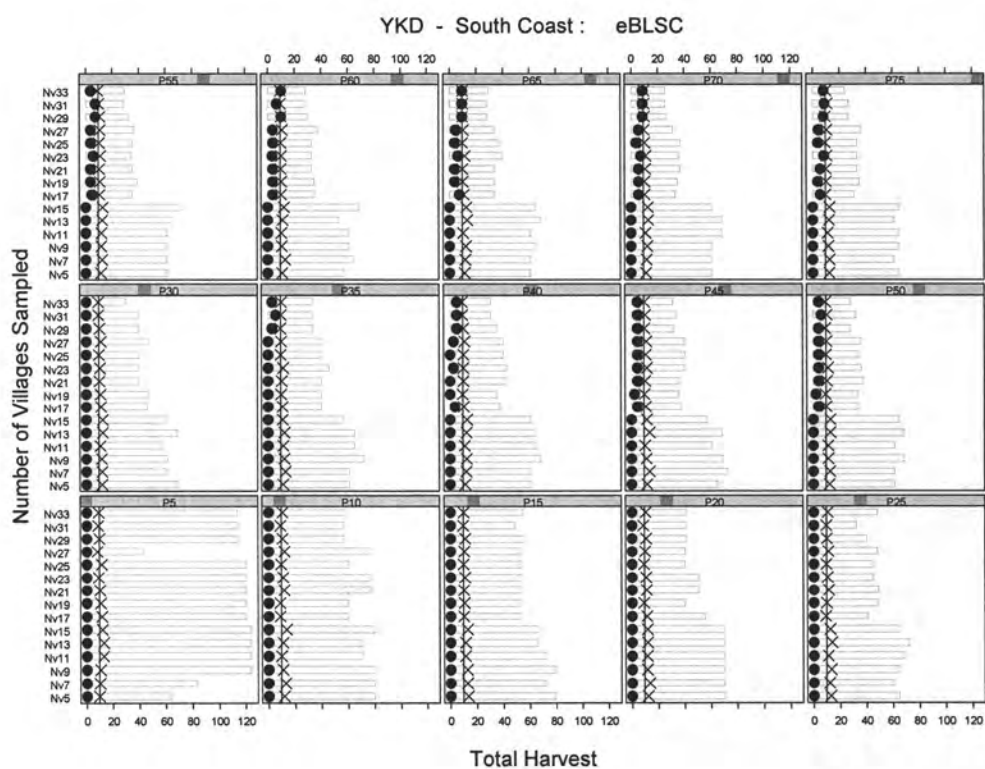
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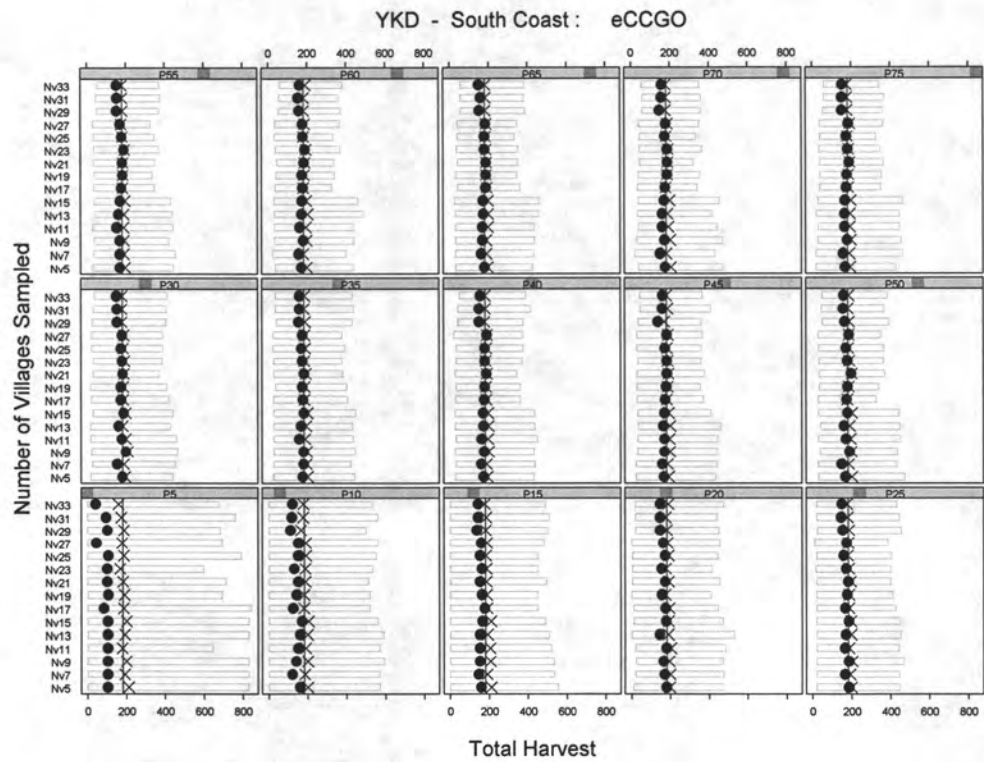
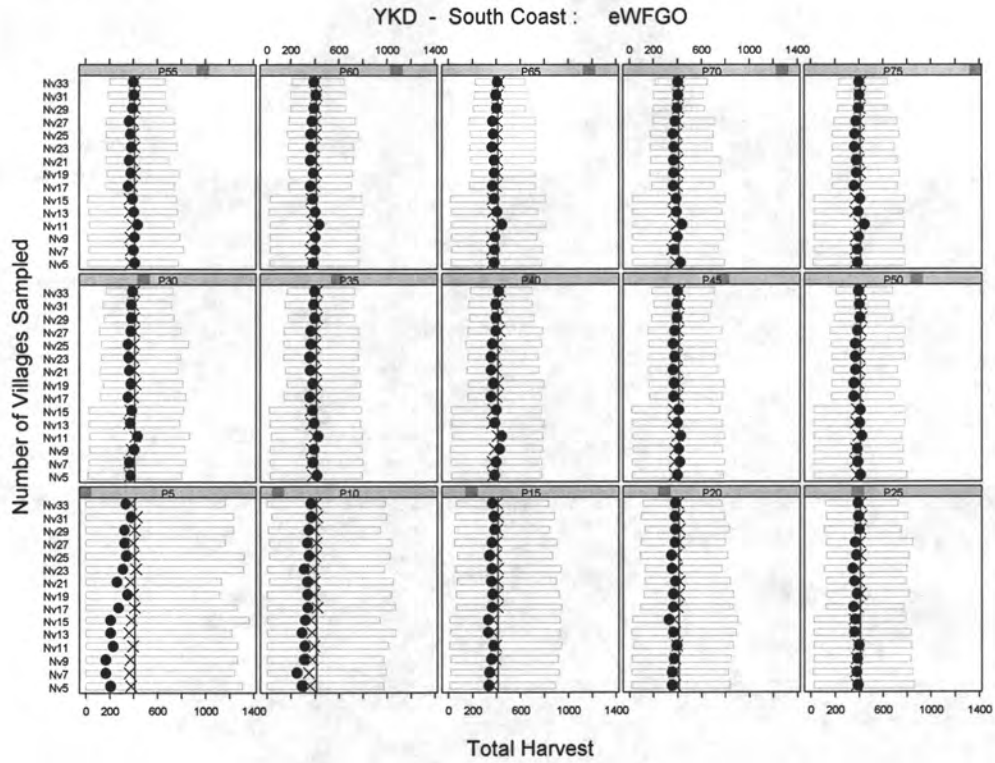
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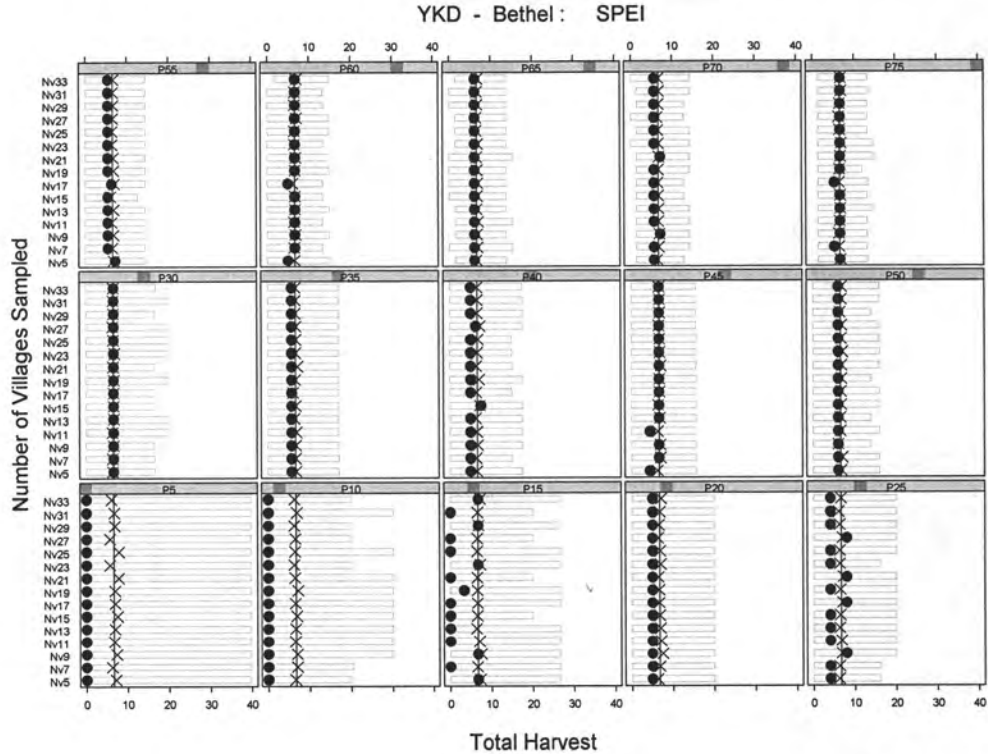
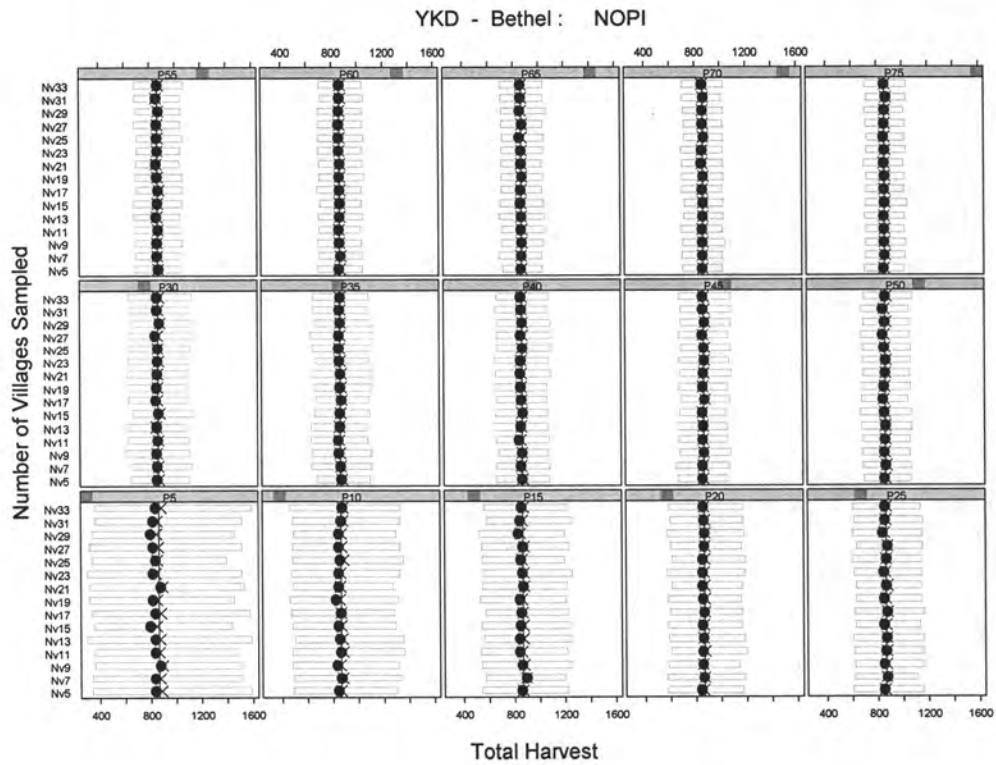
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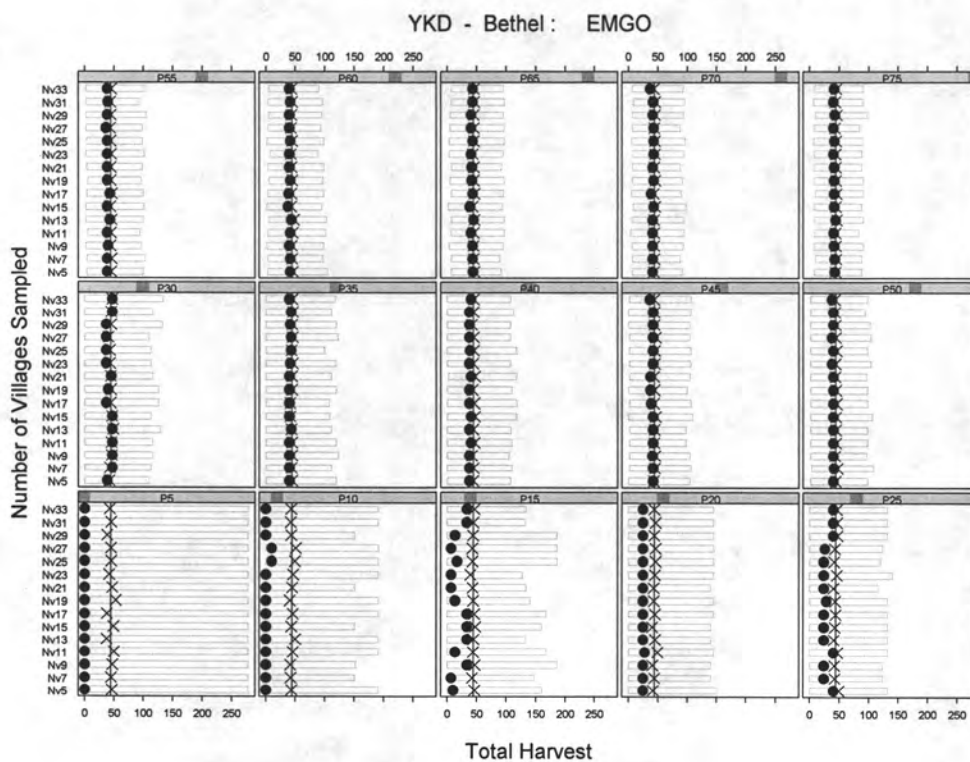
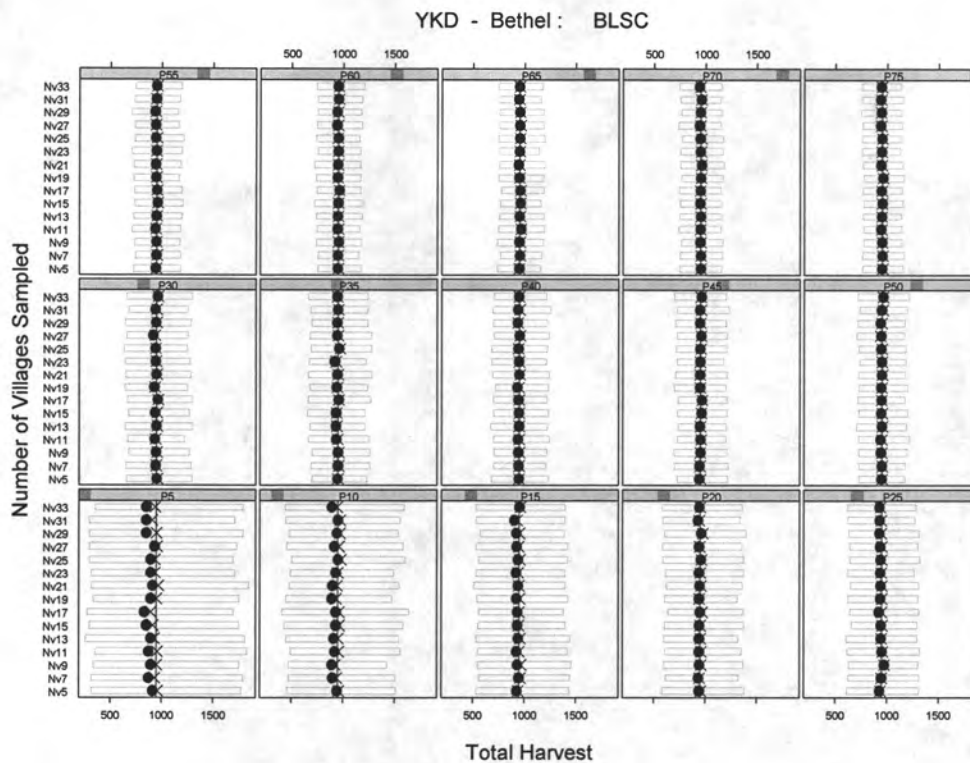
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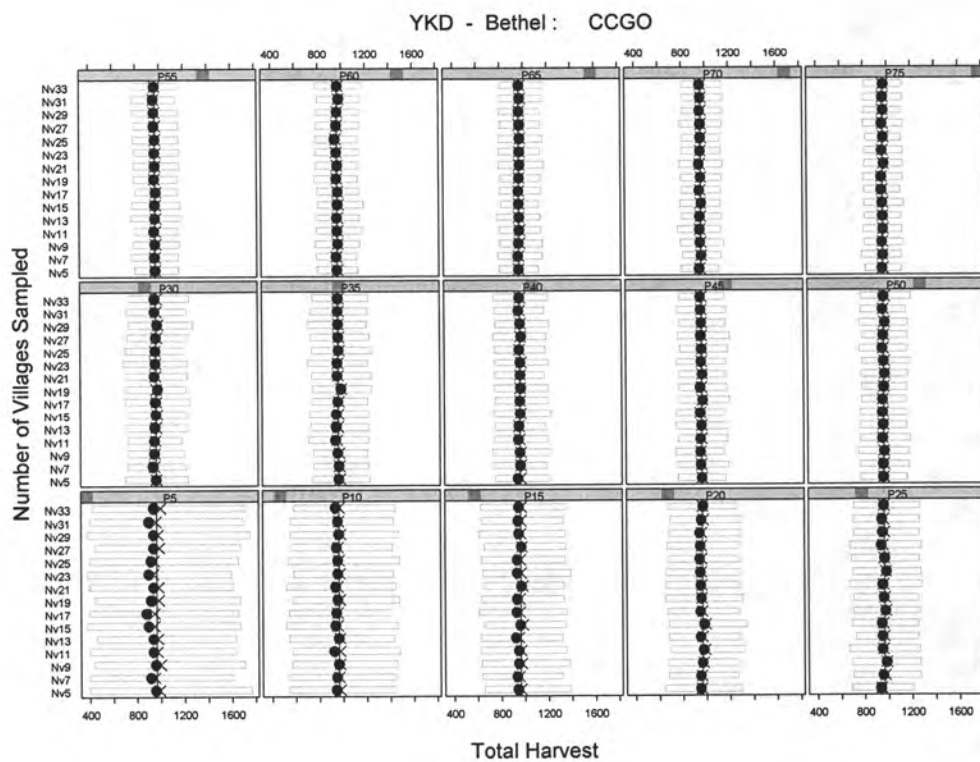
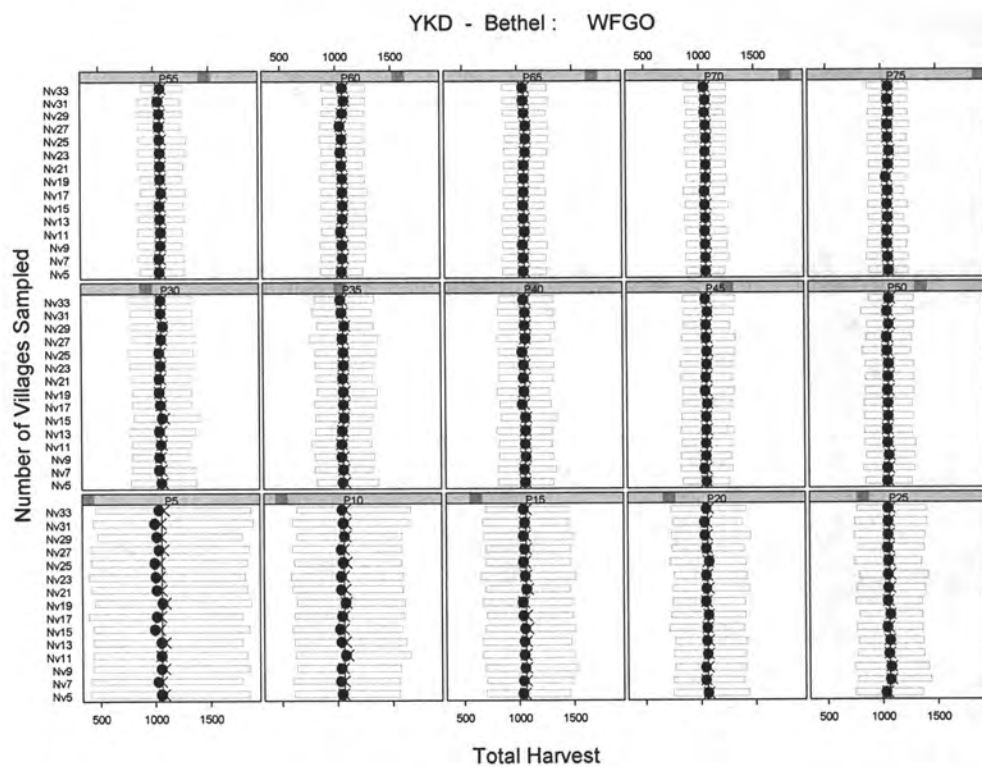
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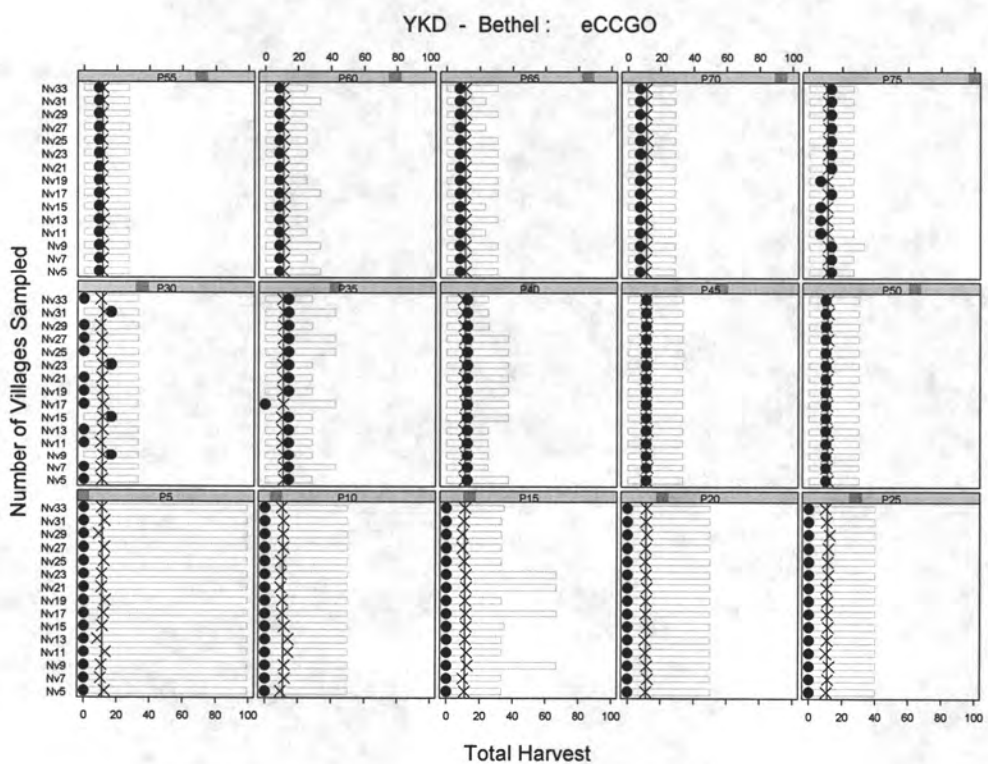
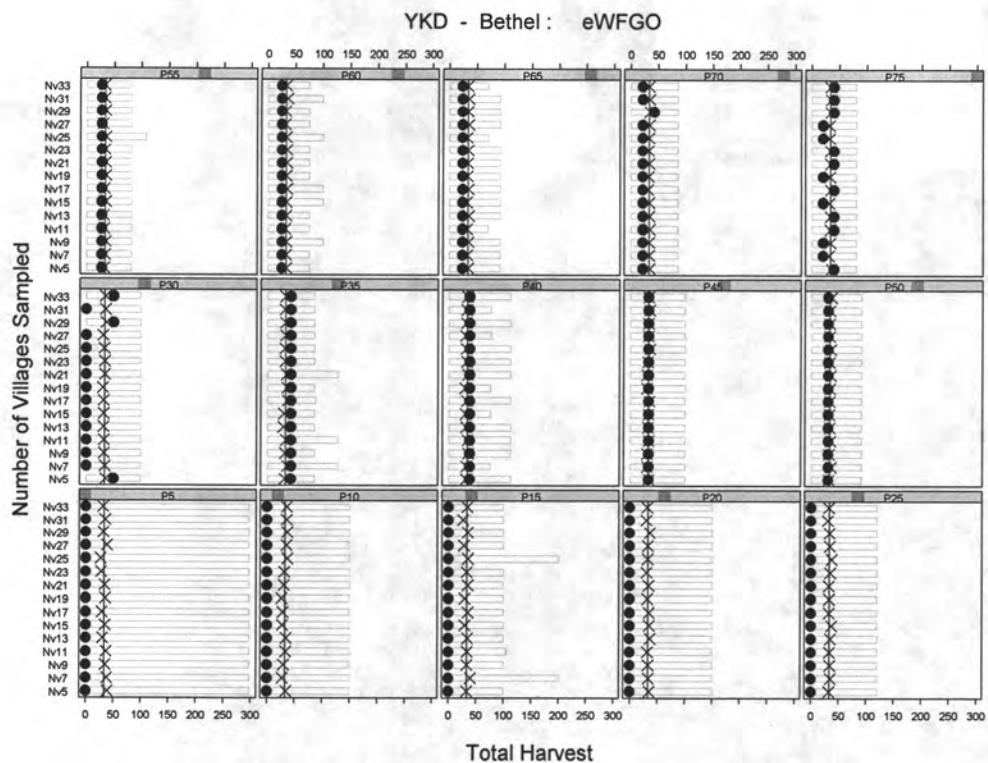
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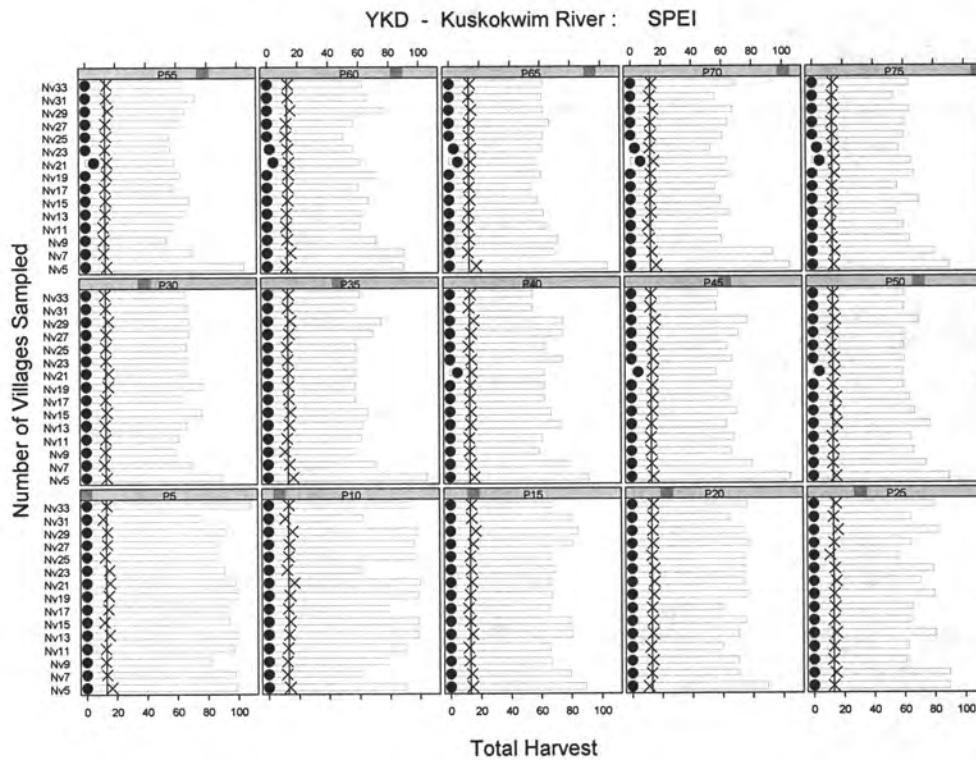
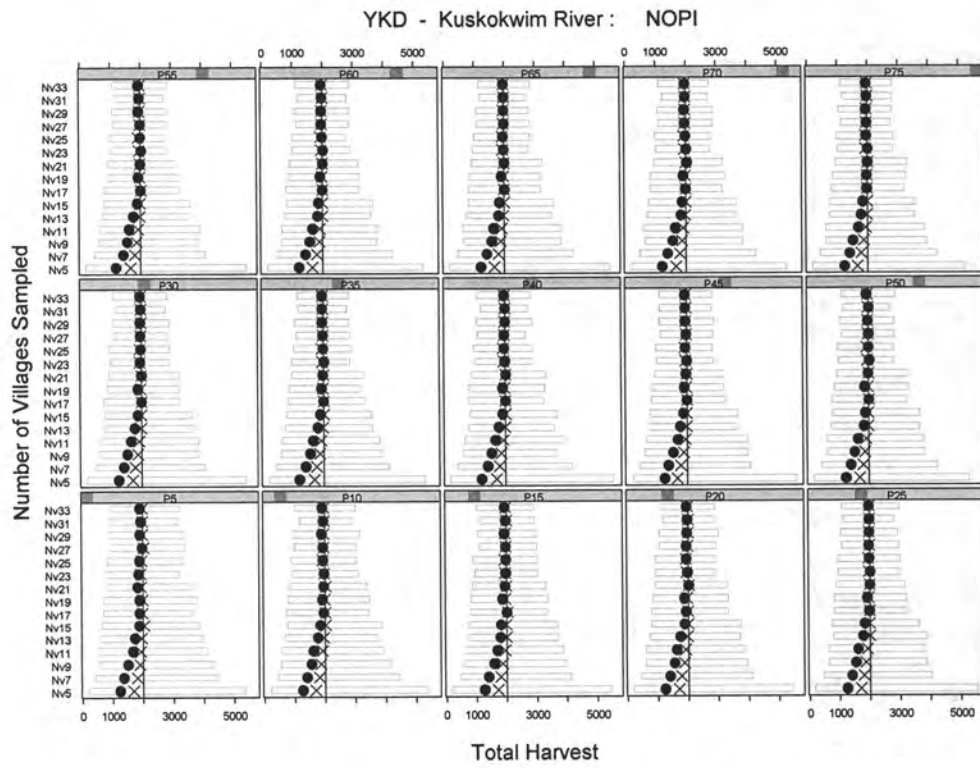
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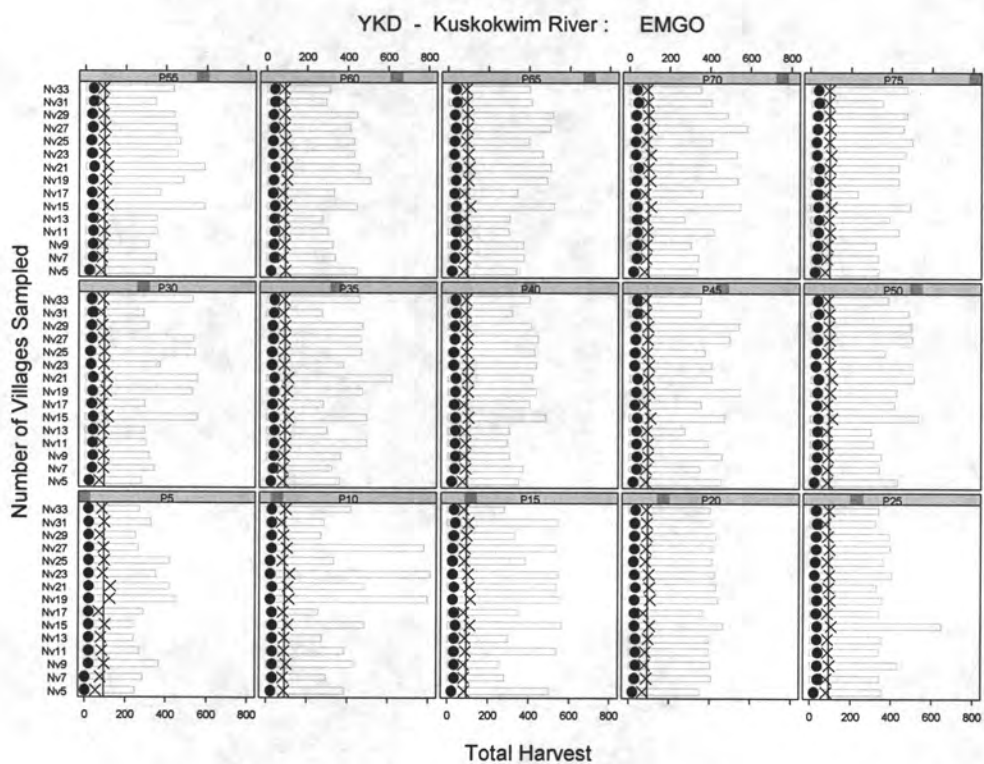
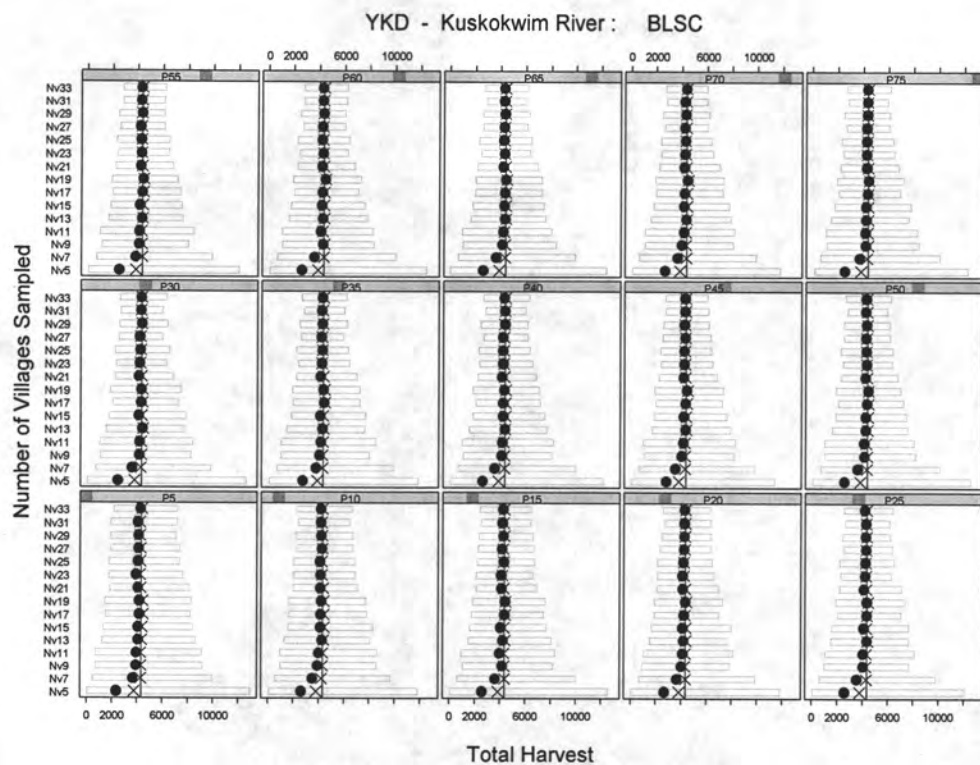
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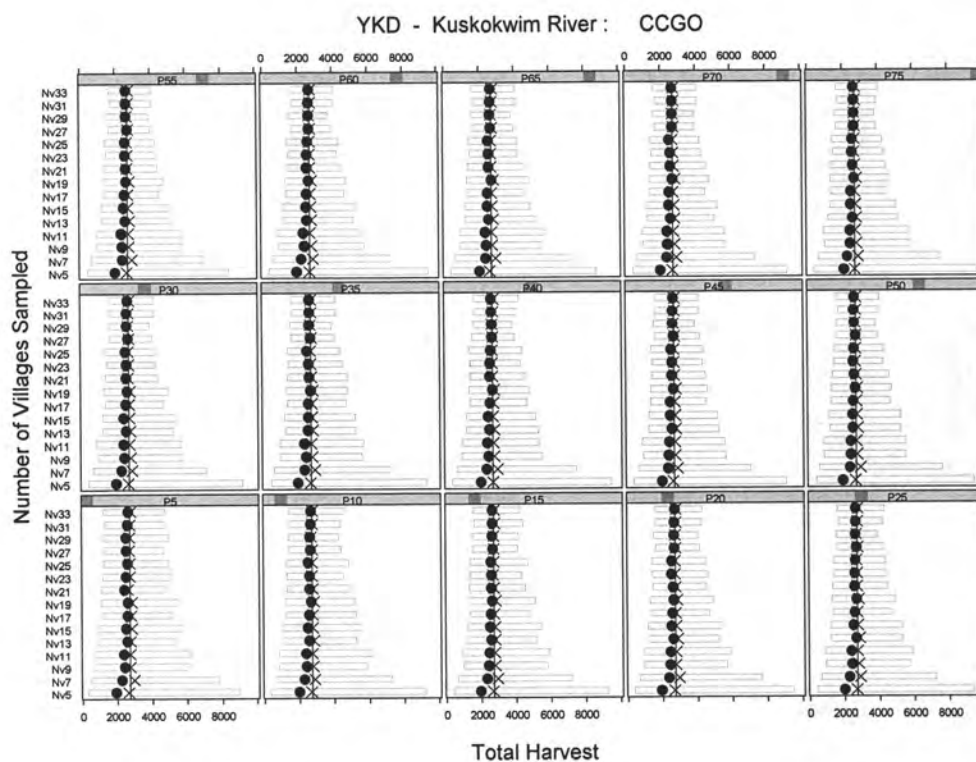
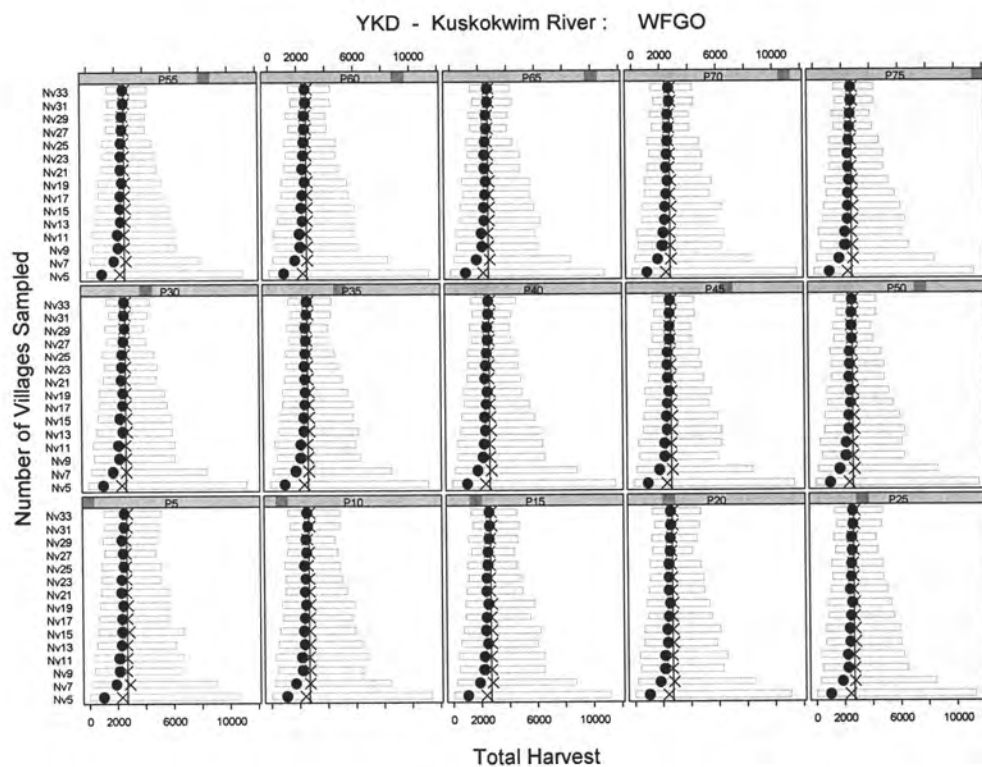
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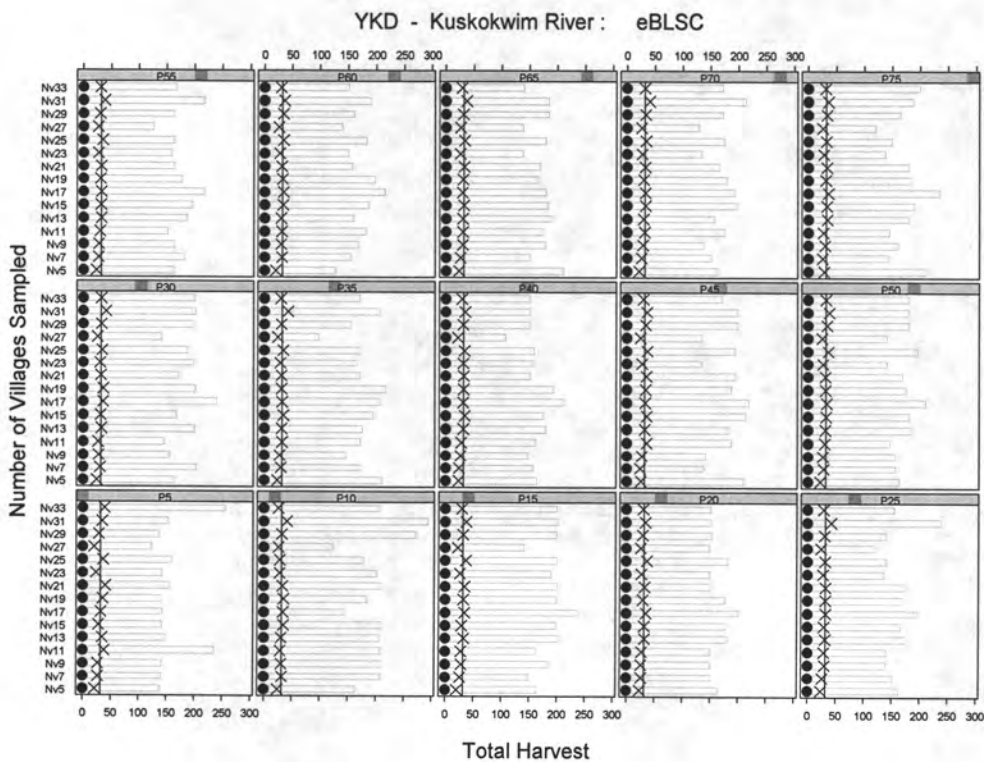
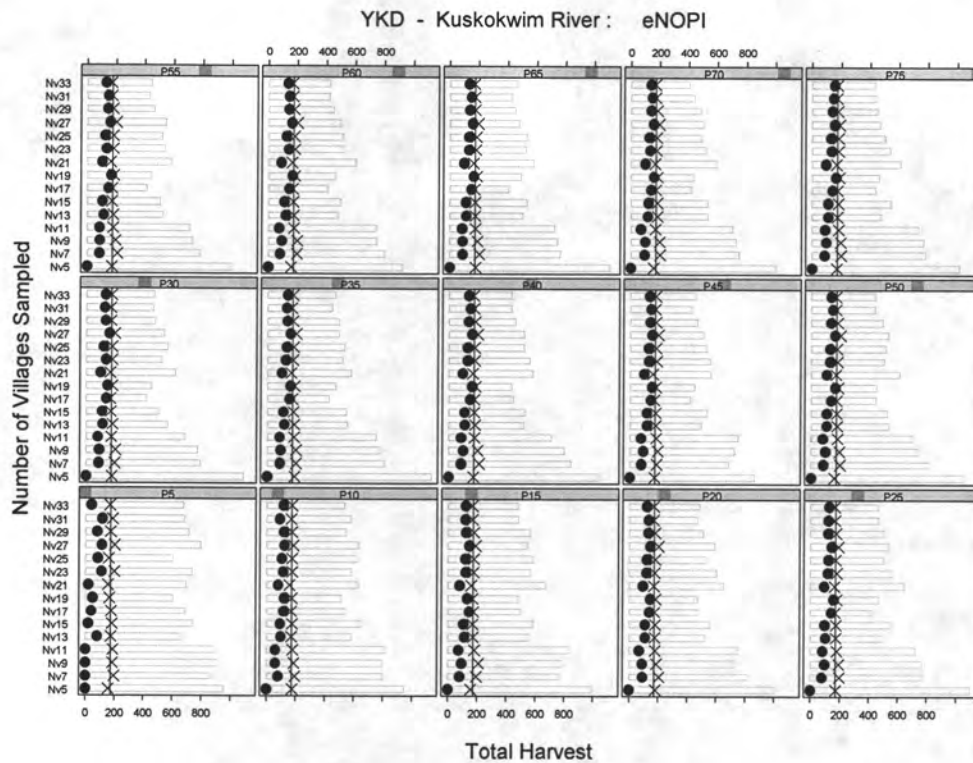
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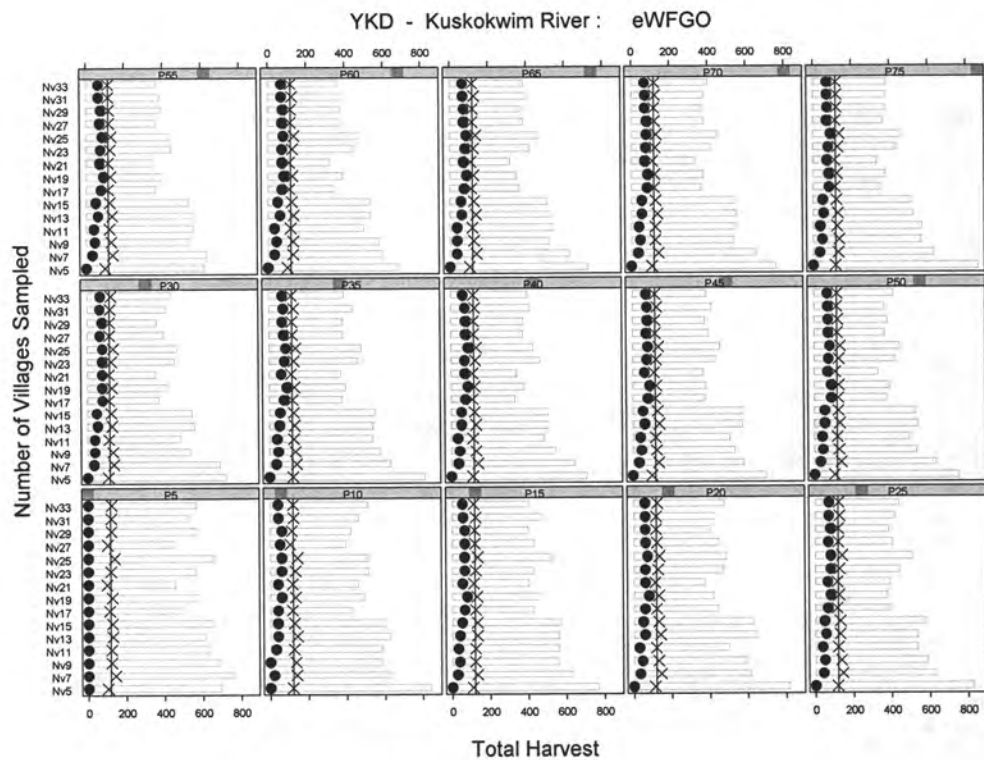
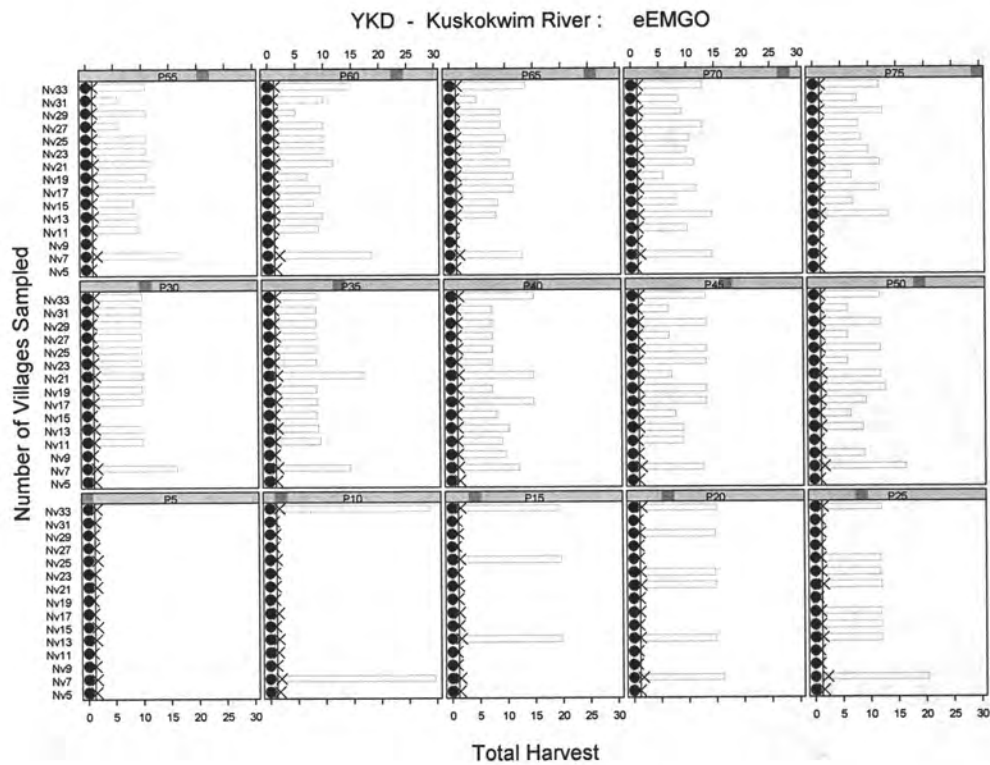
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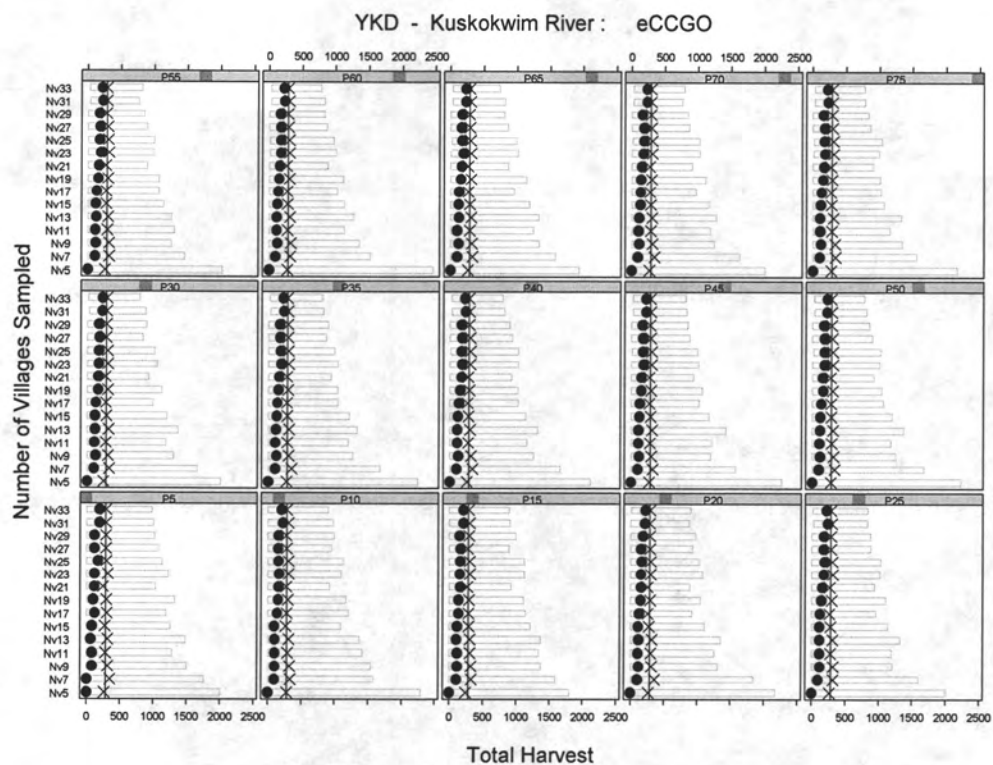
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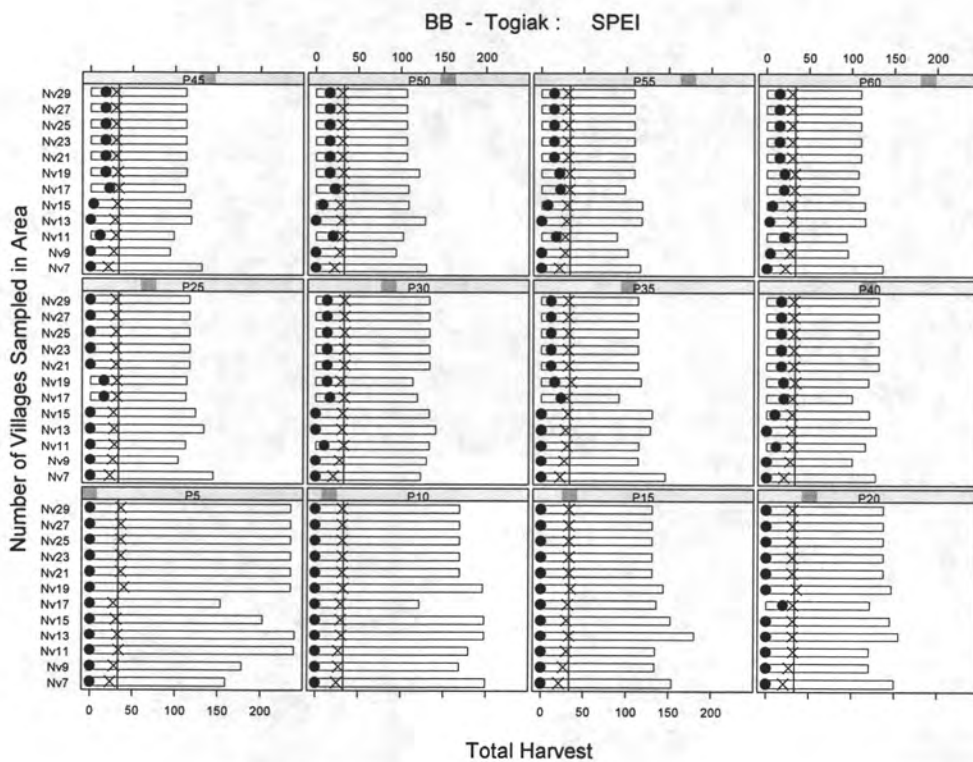
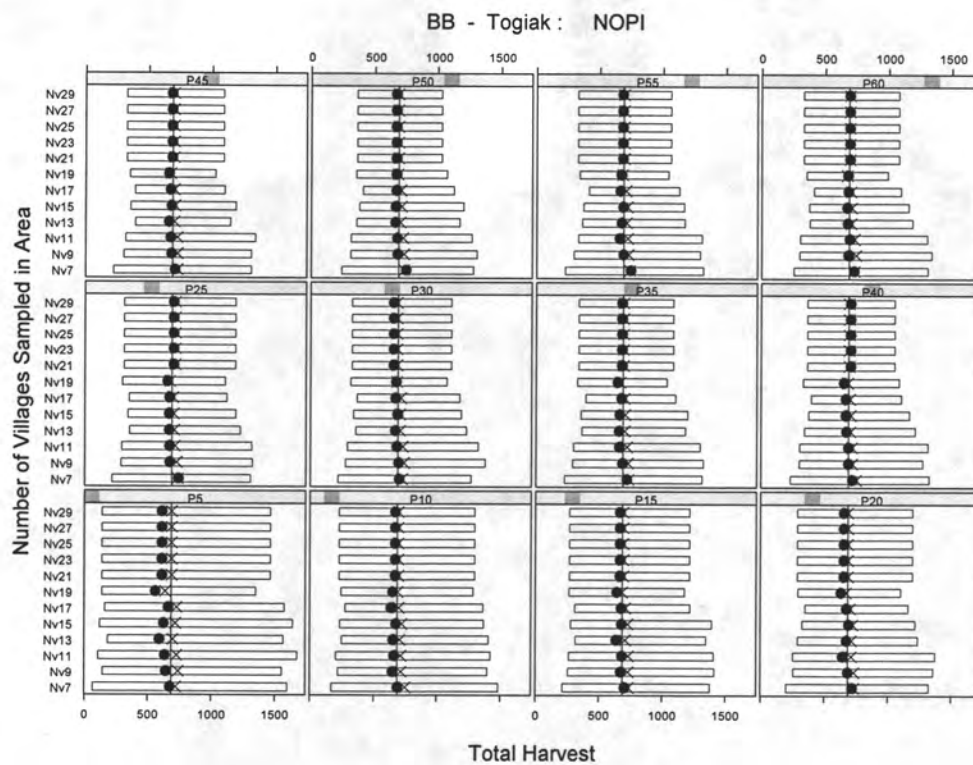
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APPENDIX 4. BRISTOL BAY AREA REGION RESULTS

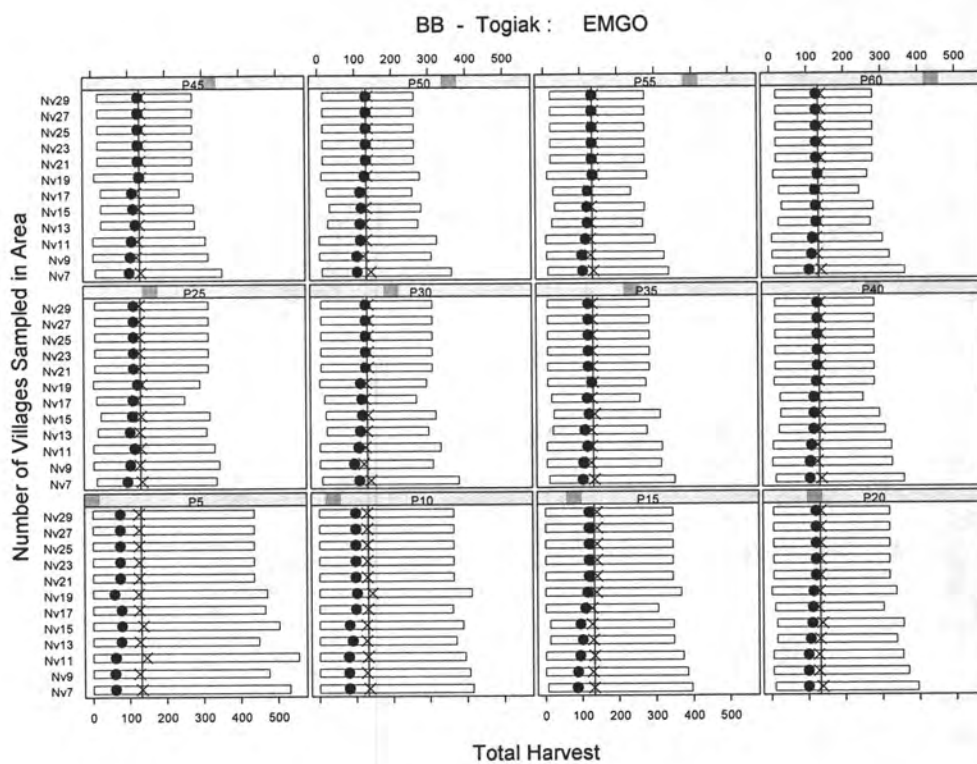
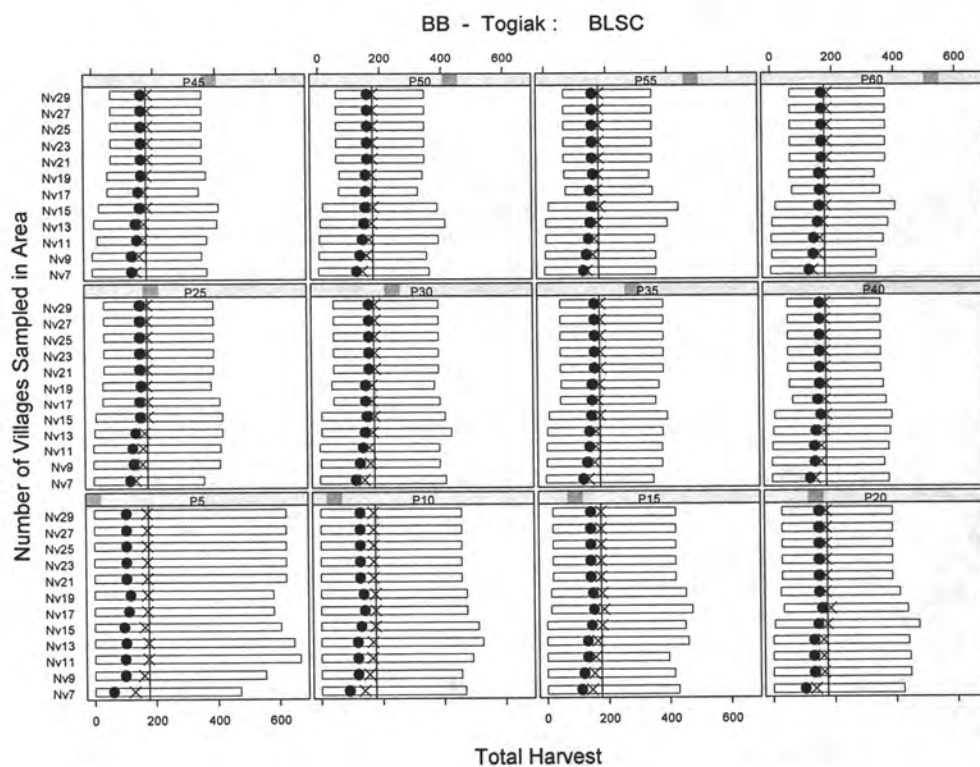
The species- and response-specific simulation results are given for each region in the BB area, in the following order: Togiak, Dillingham, Nushagak, Iliamna, King Salmon, North Peninsula, South Peninsula. Figure details are described in the legend to Figure 5.

If a species and take had only zero harvests records in the region, the graph is not given.

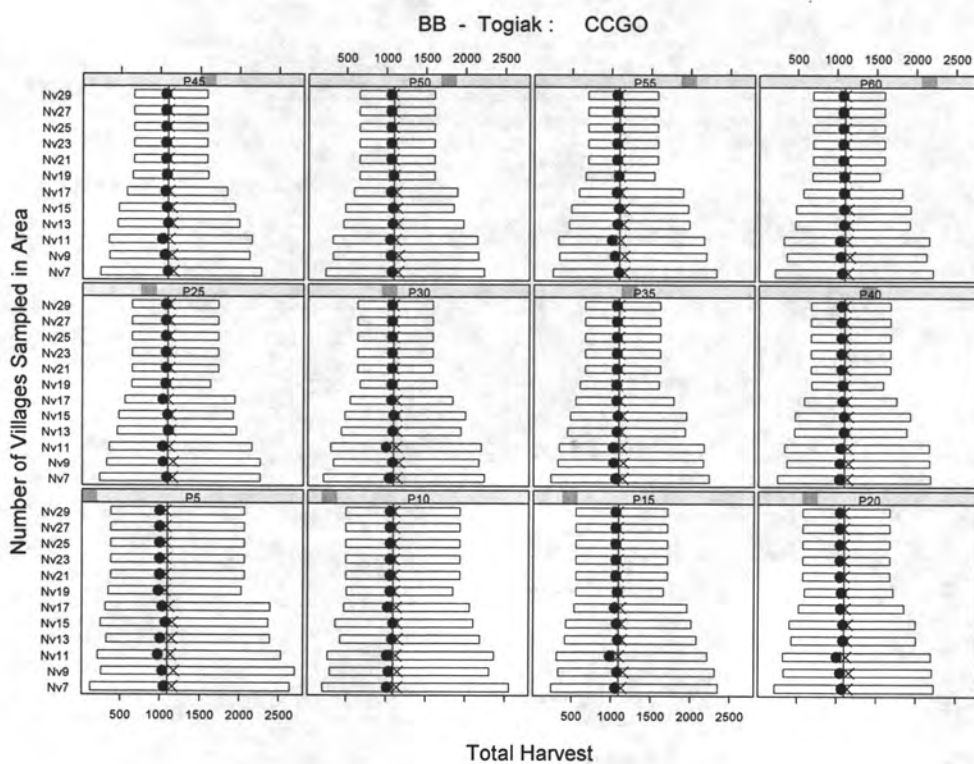
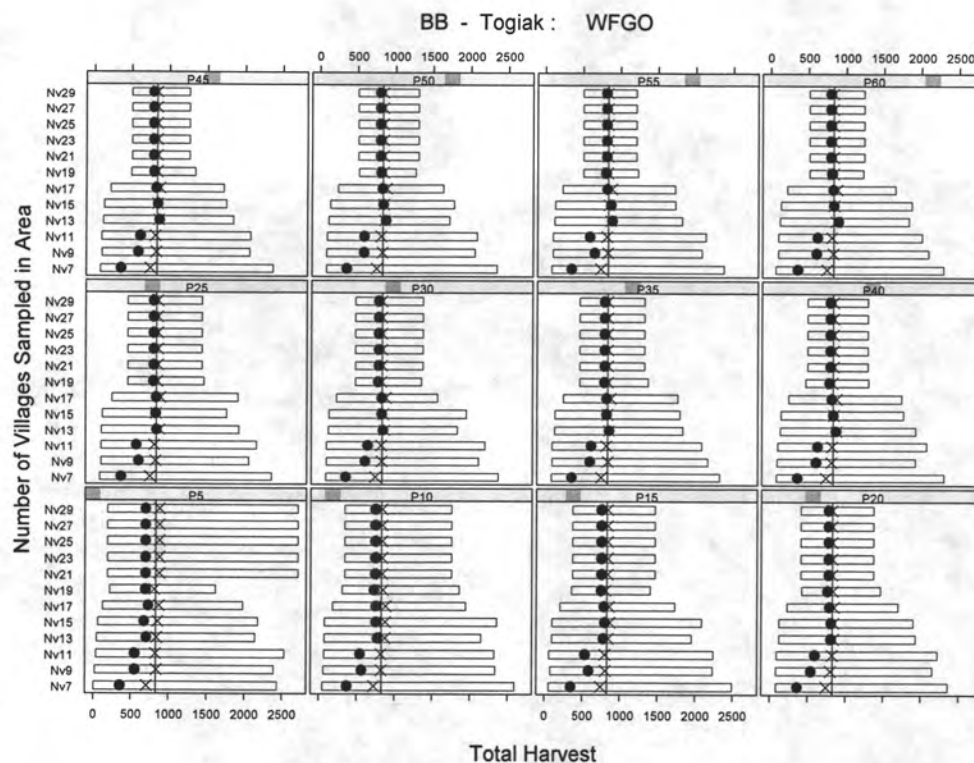
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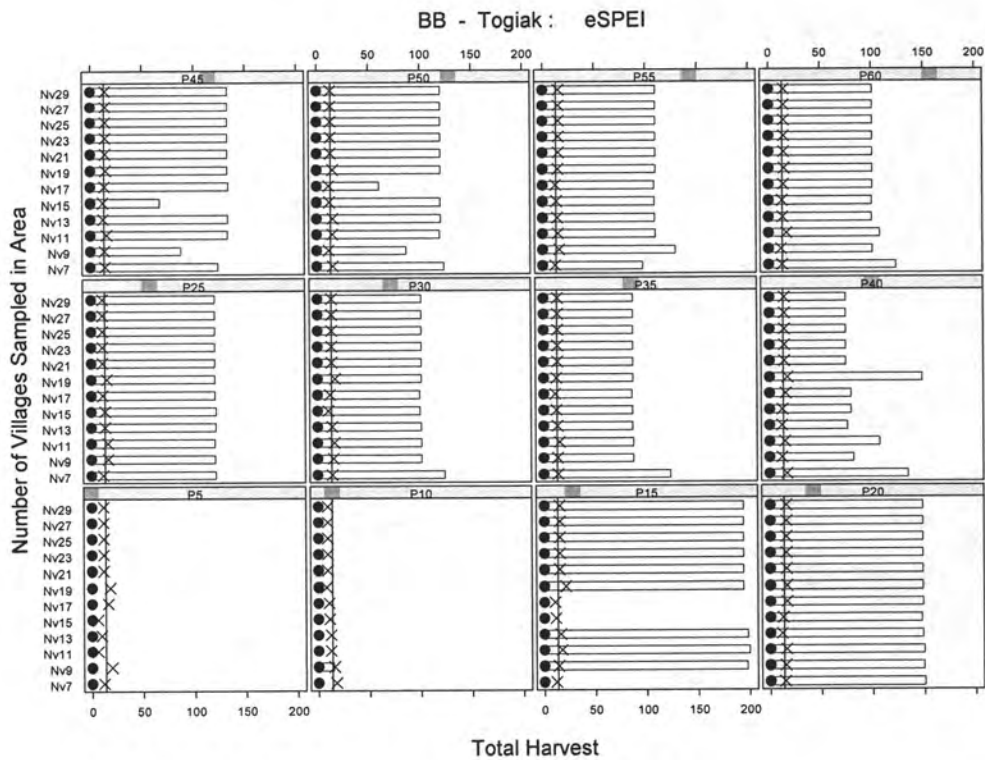
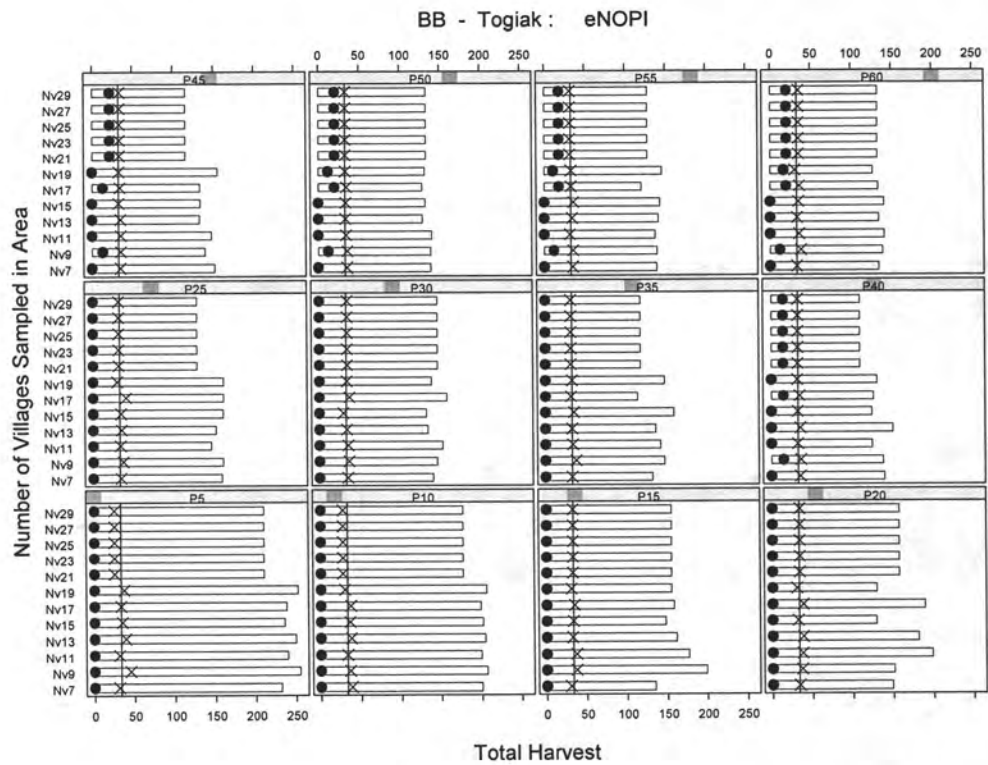
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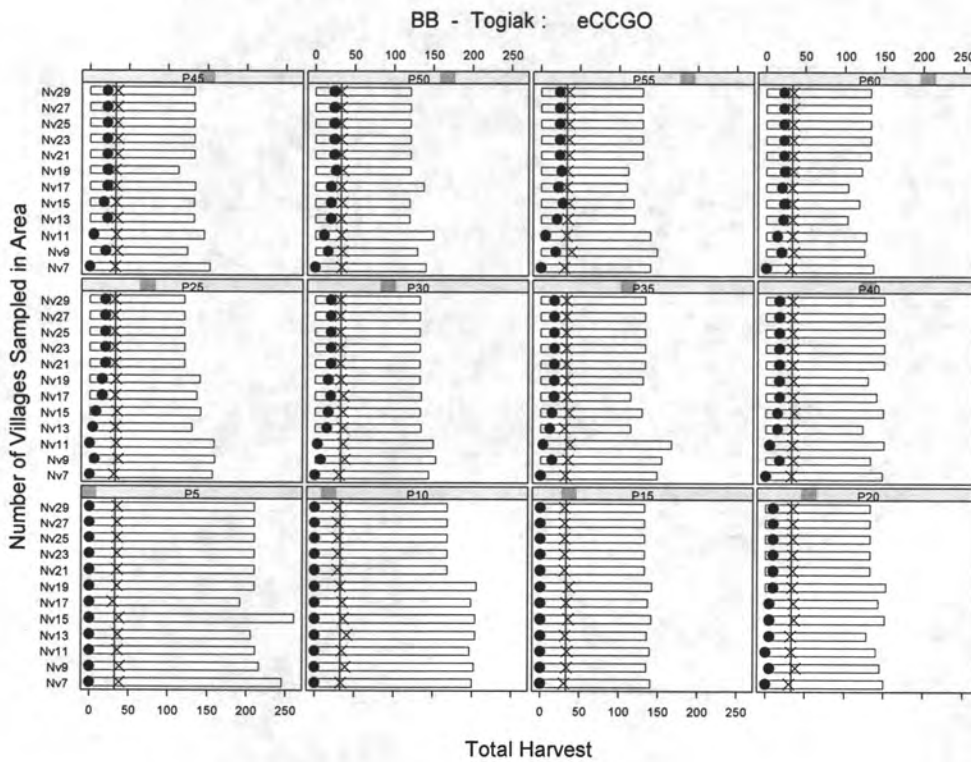
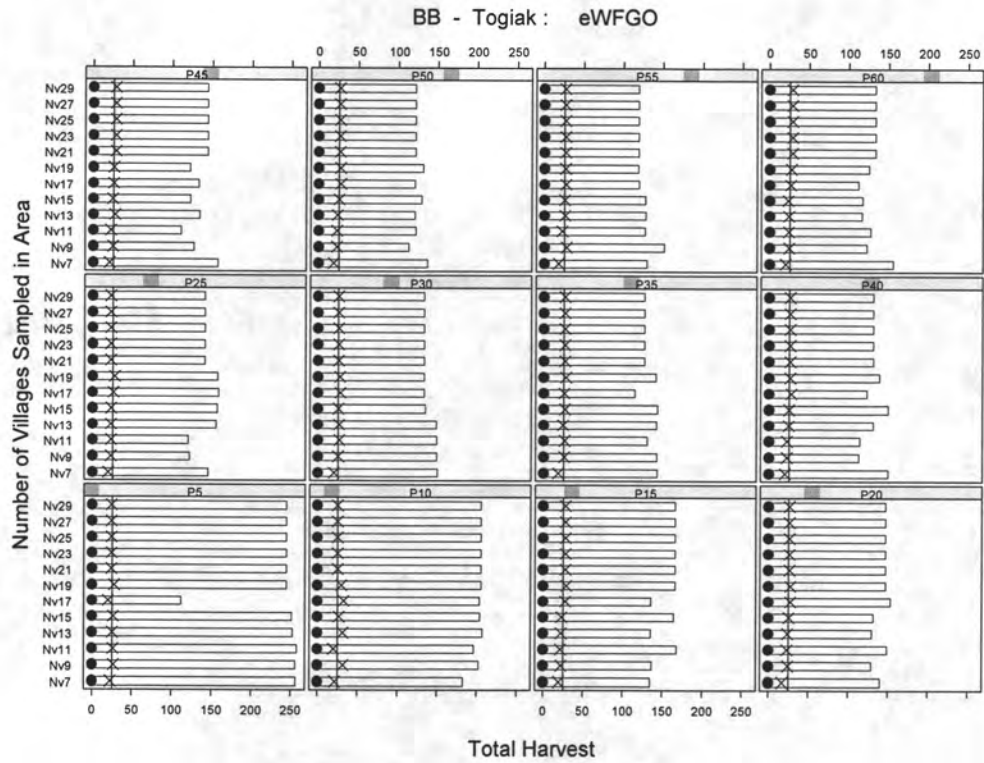
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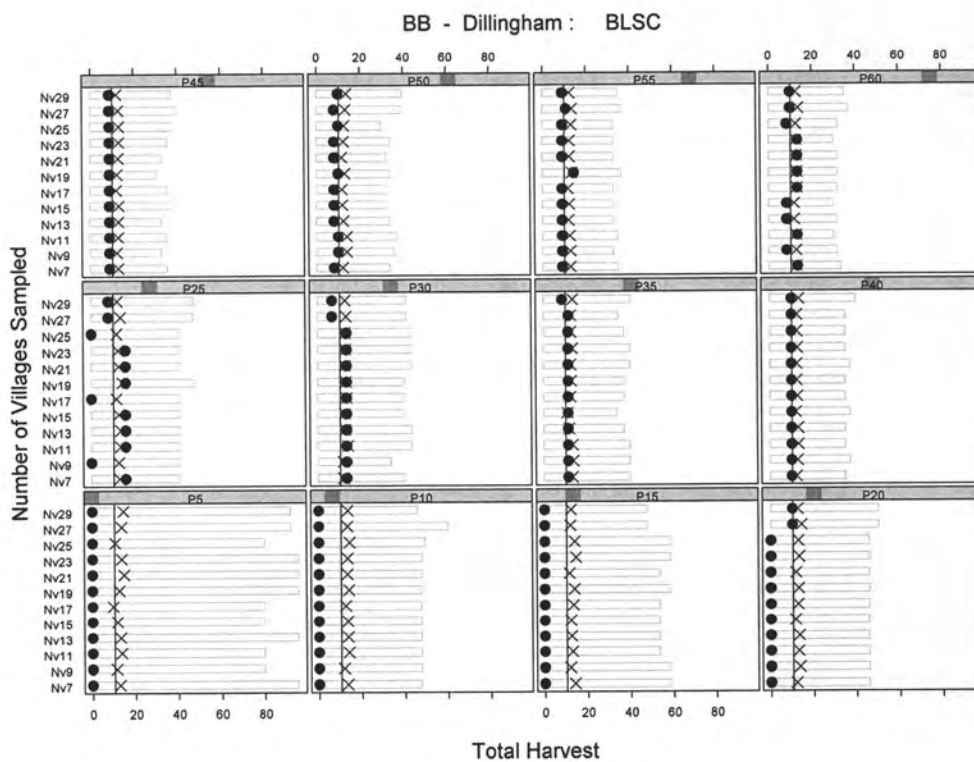
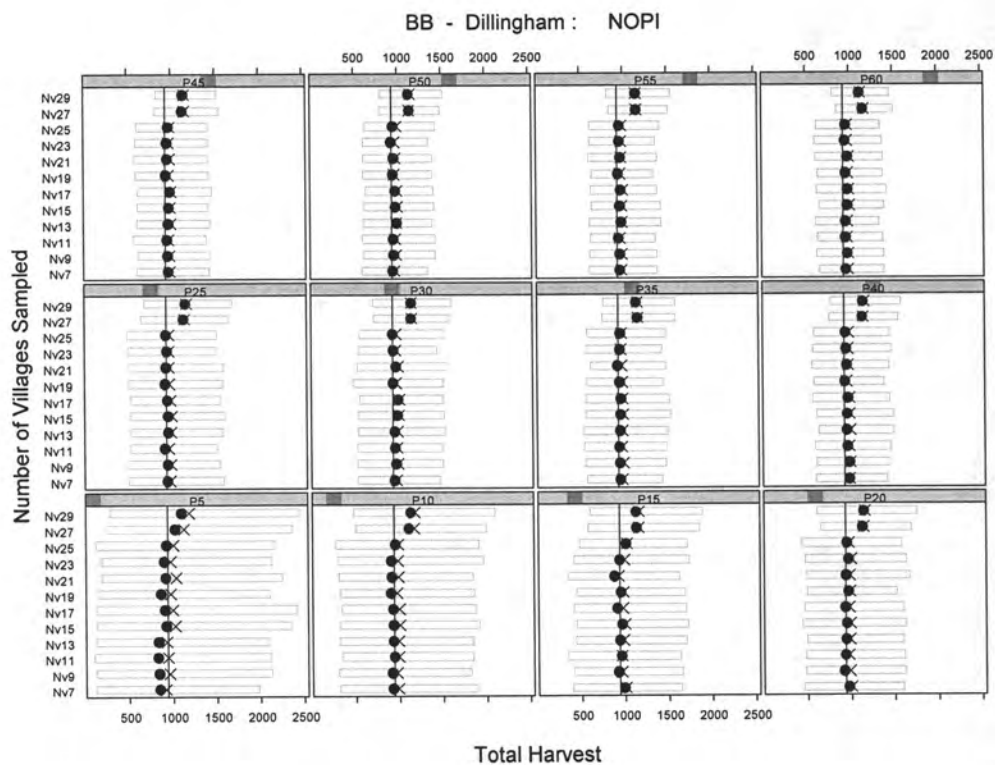
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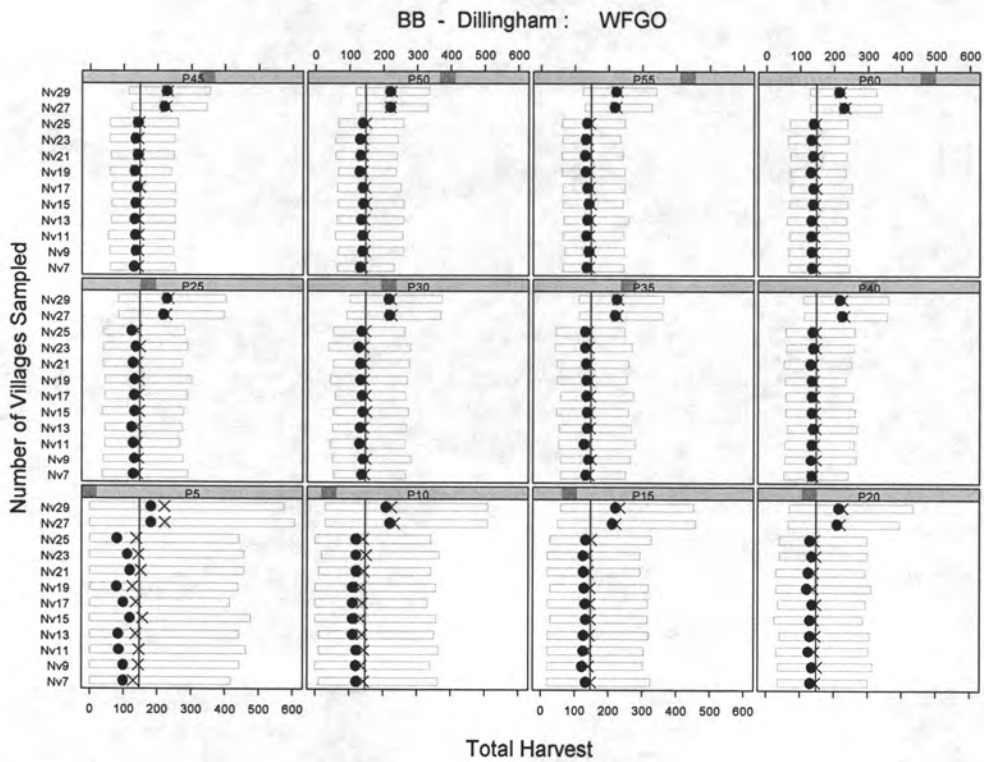
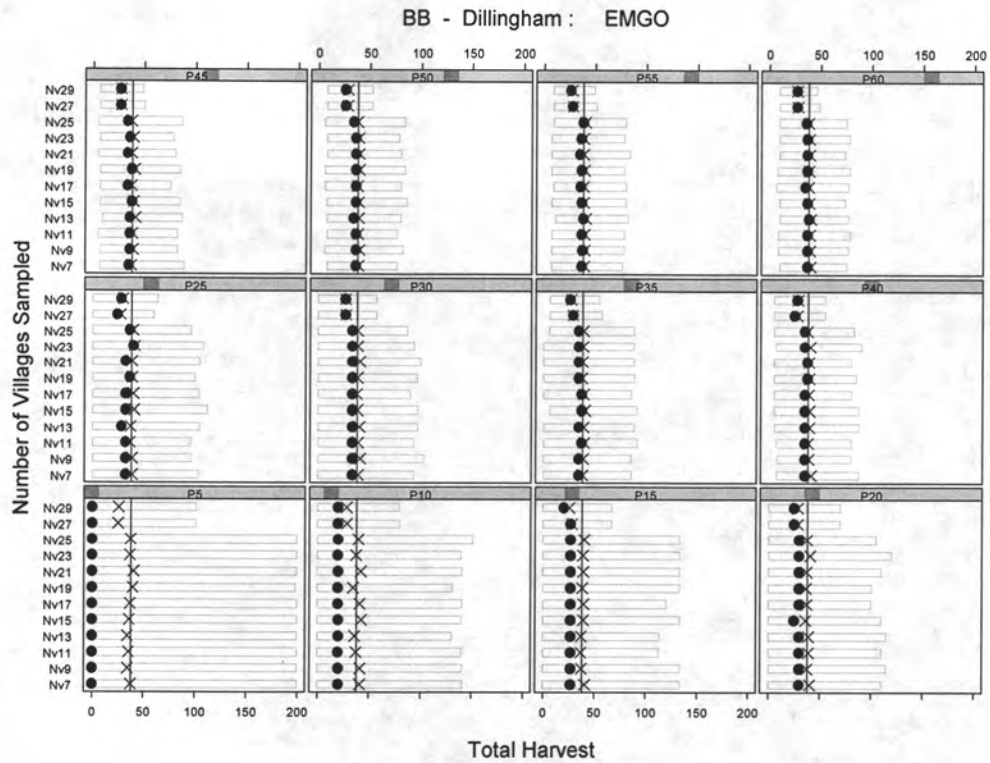
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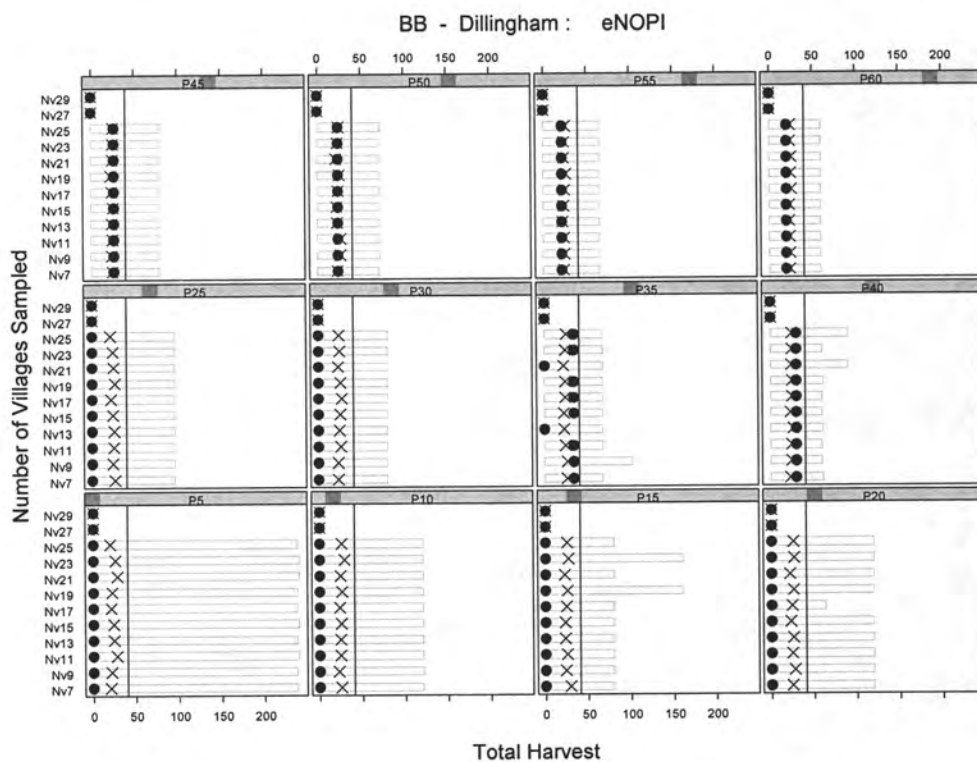
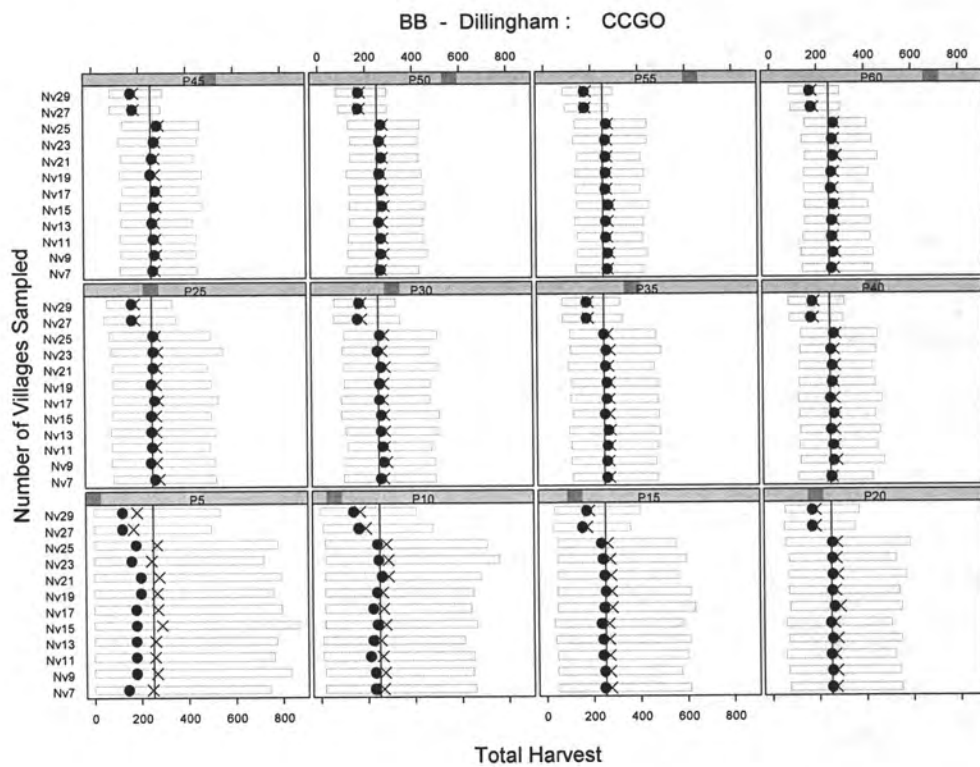
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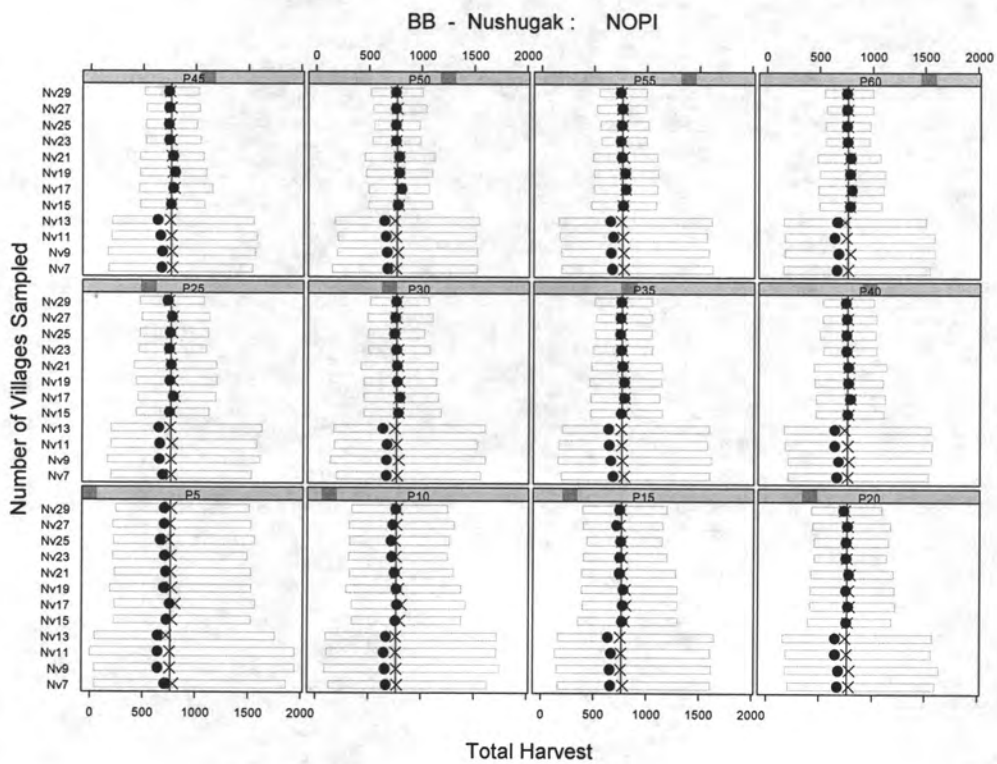
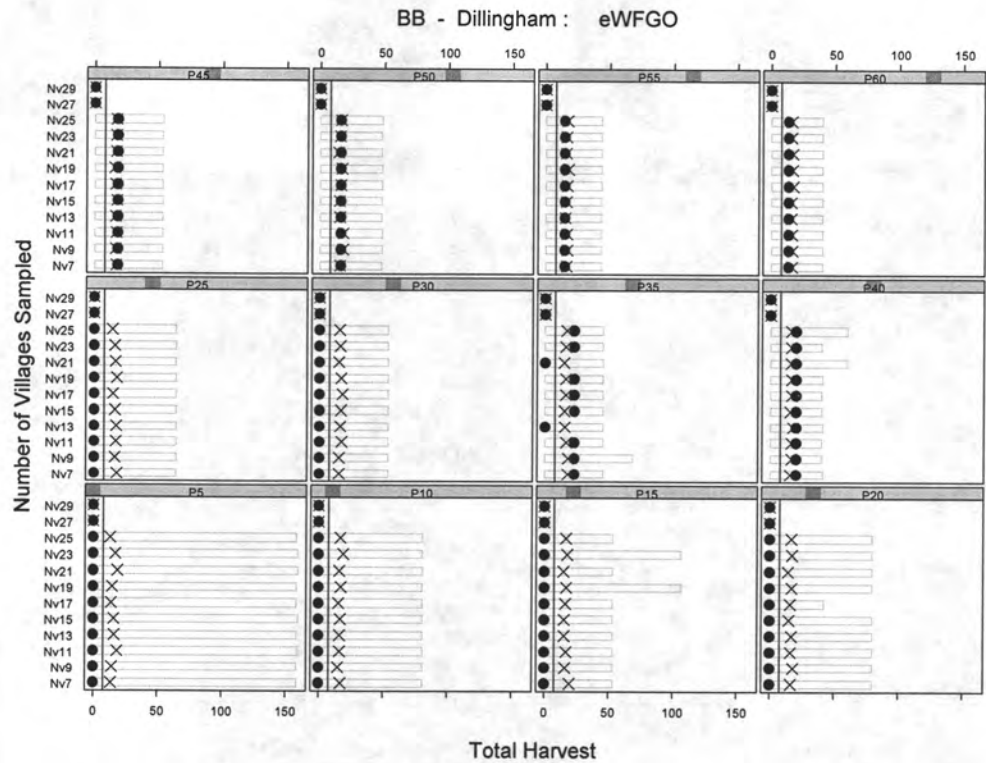
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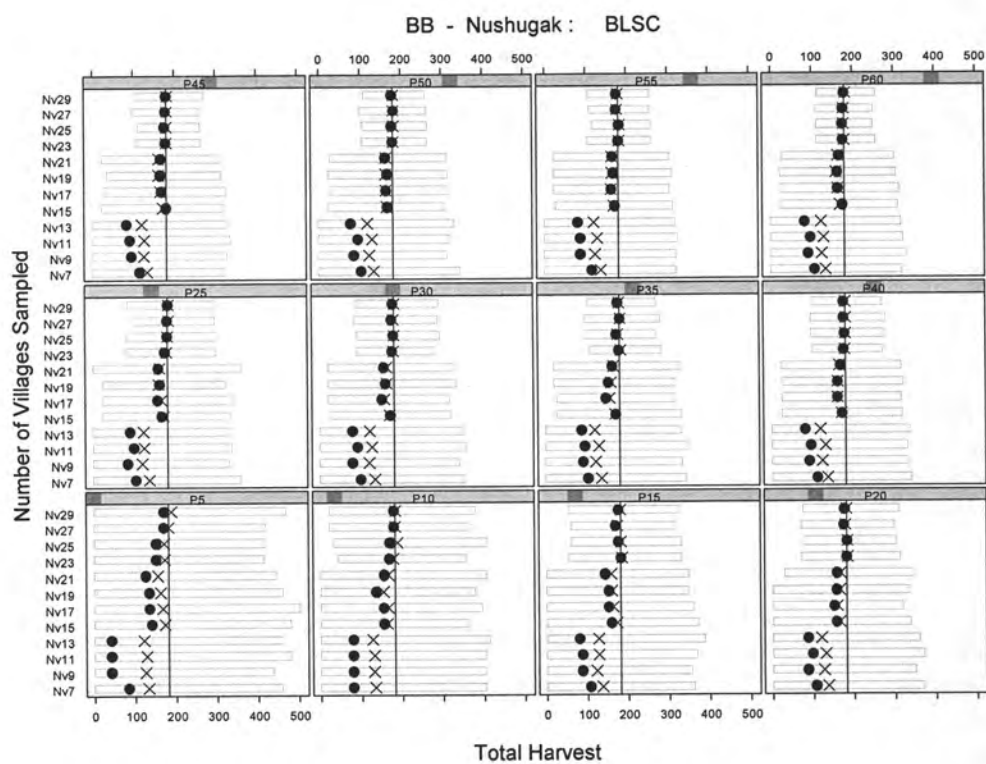
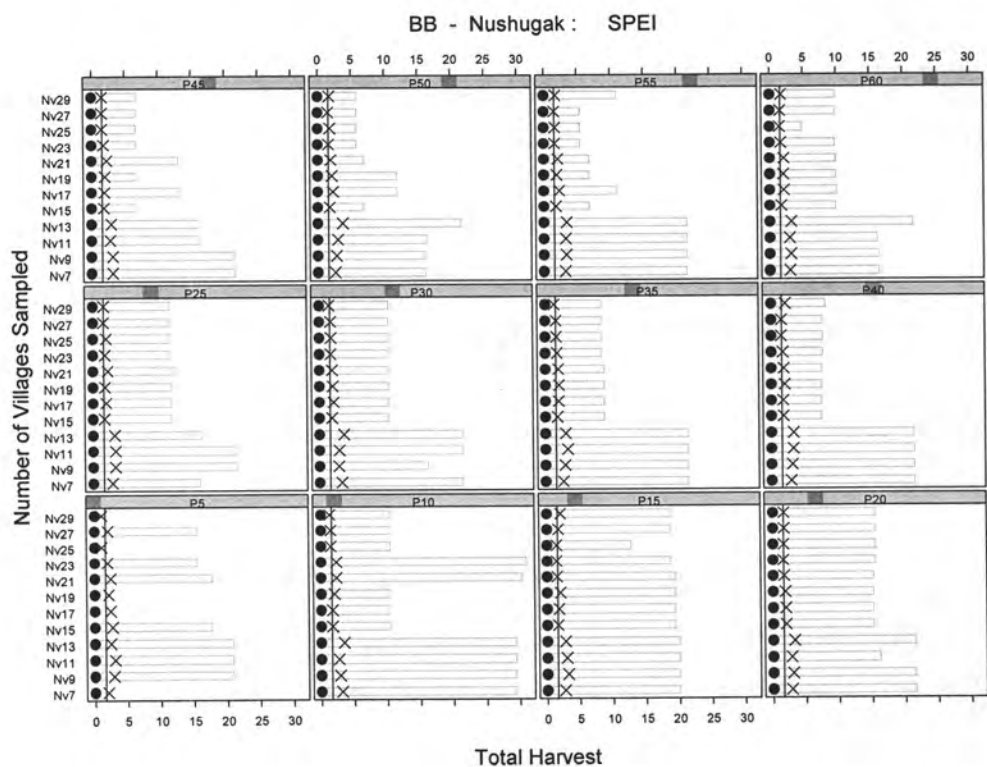
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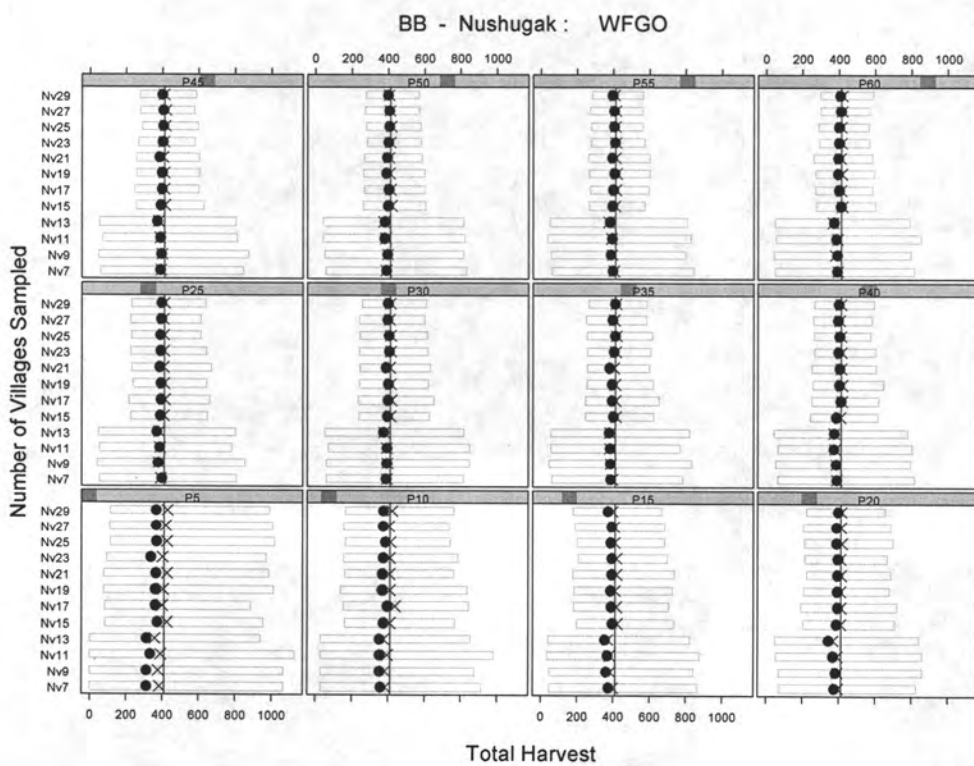
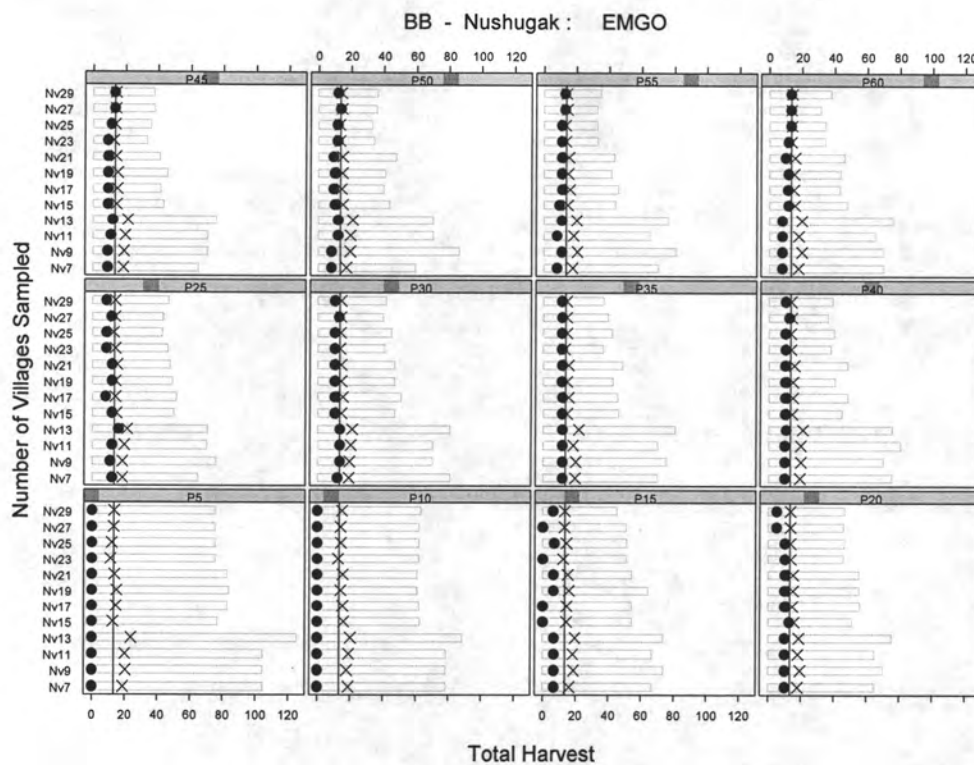
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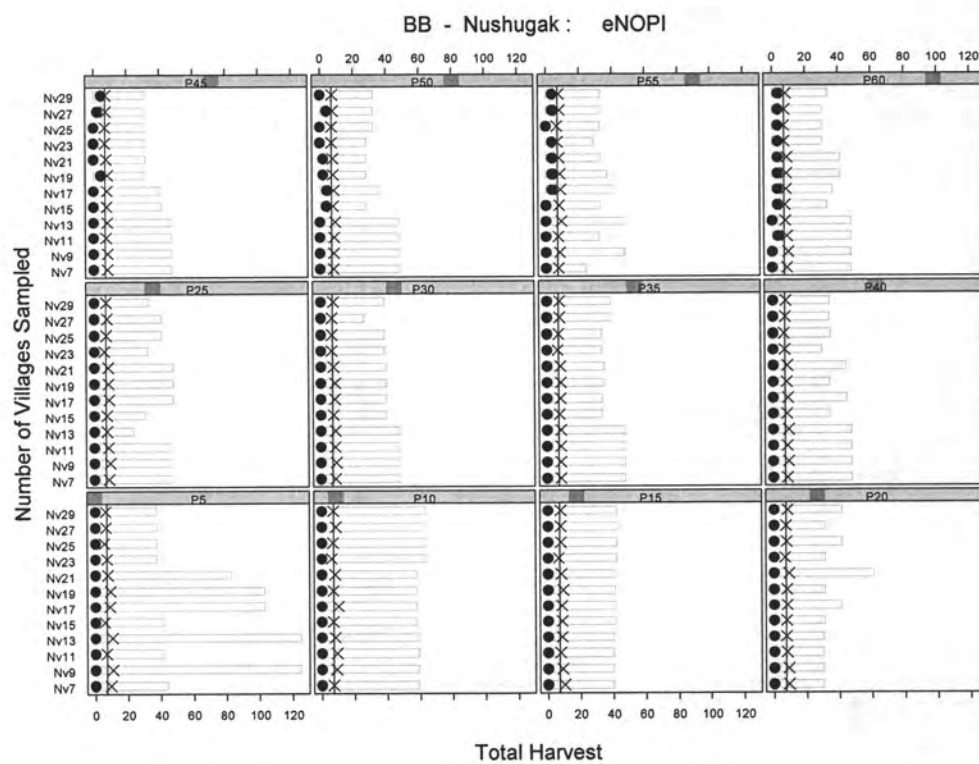
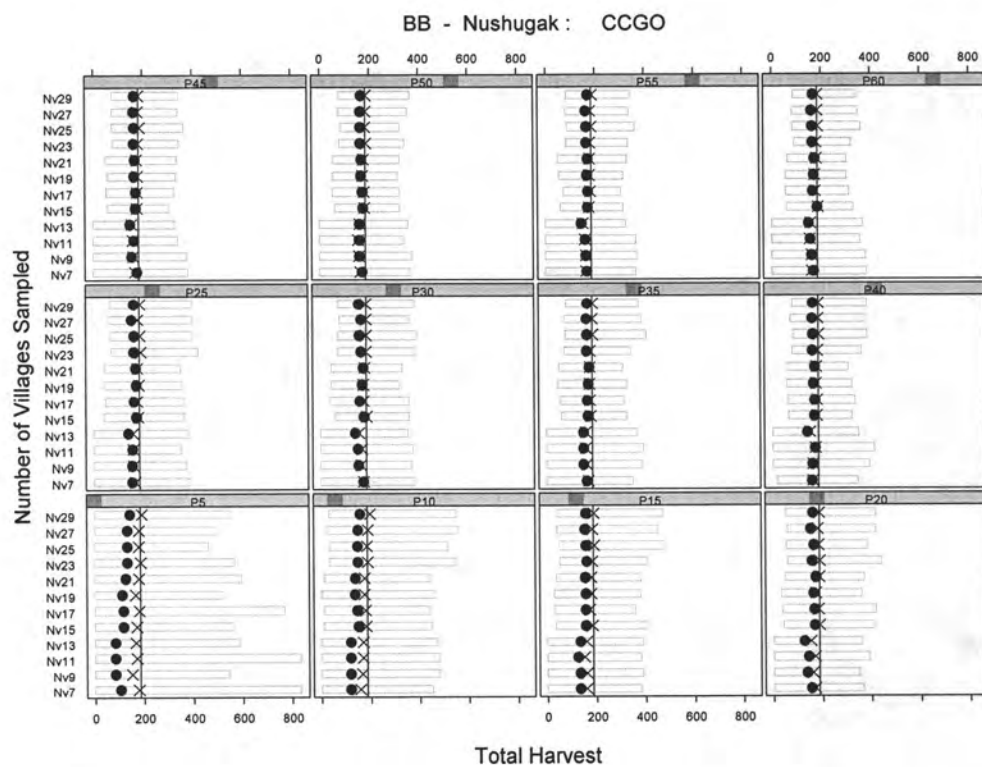
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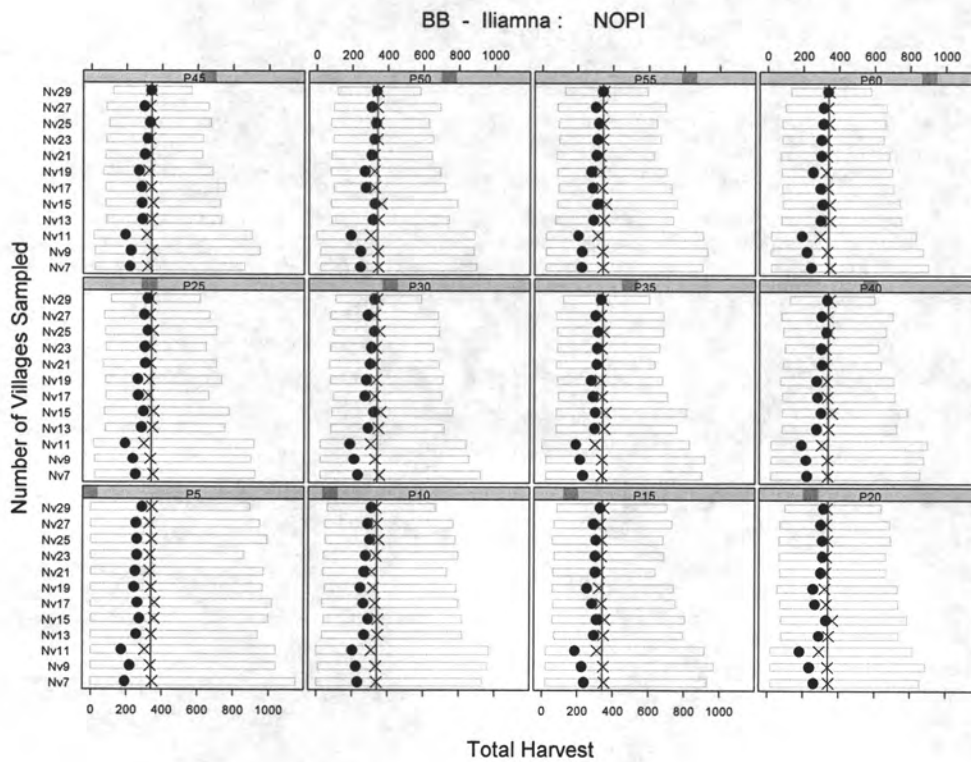
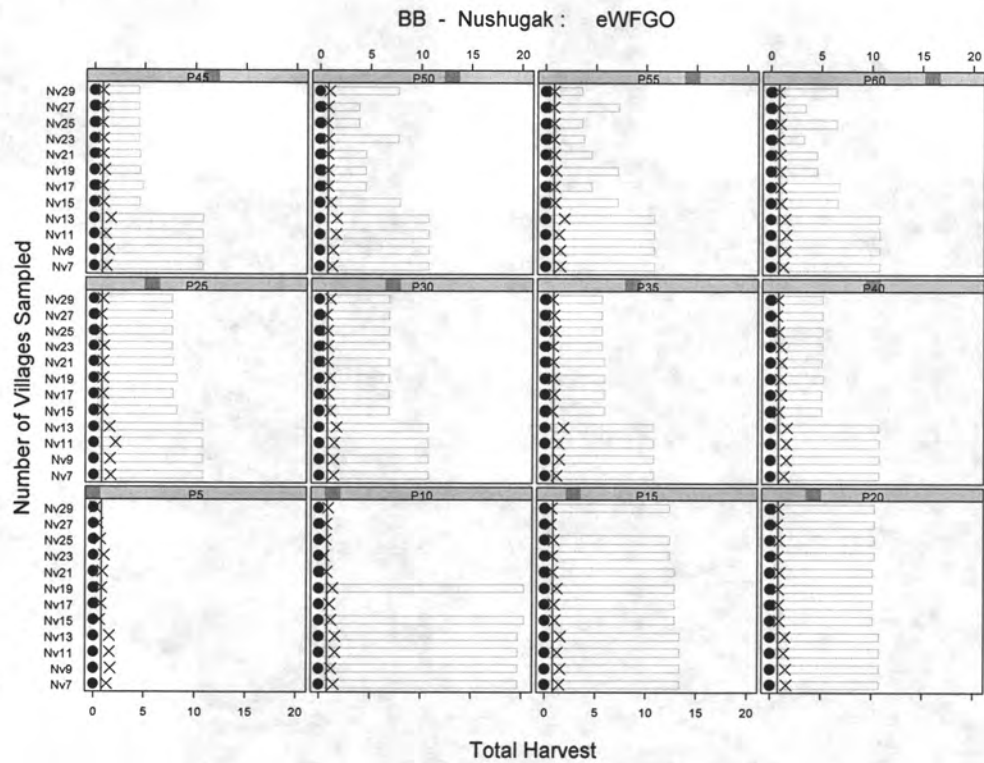
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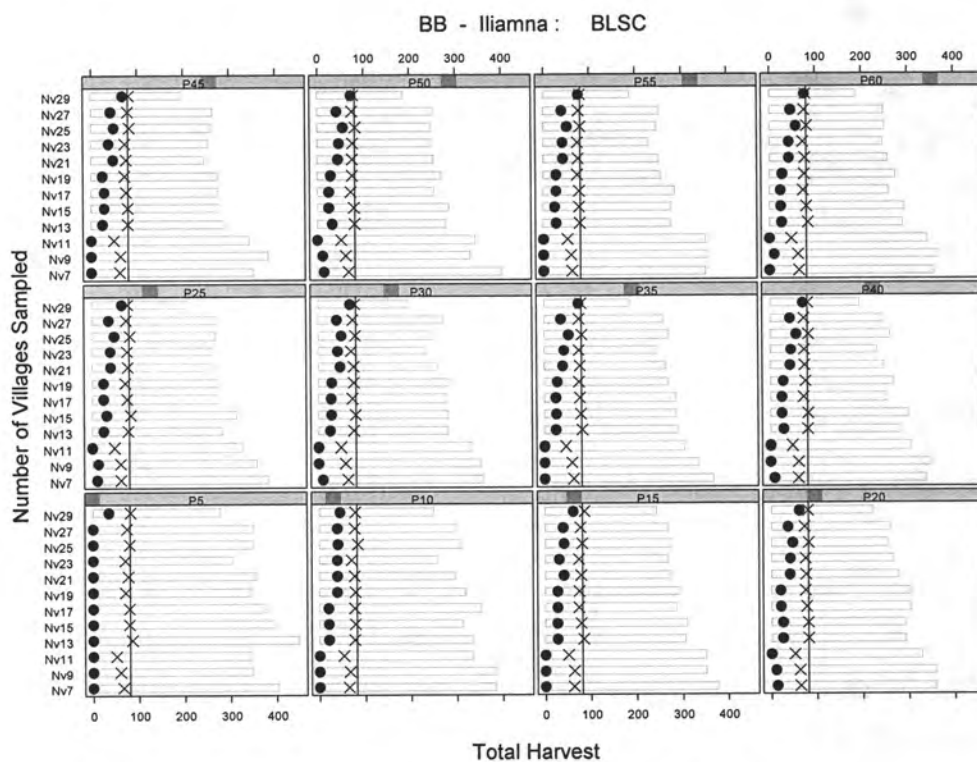
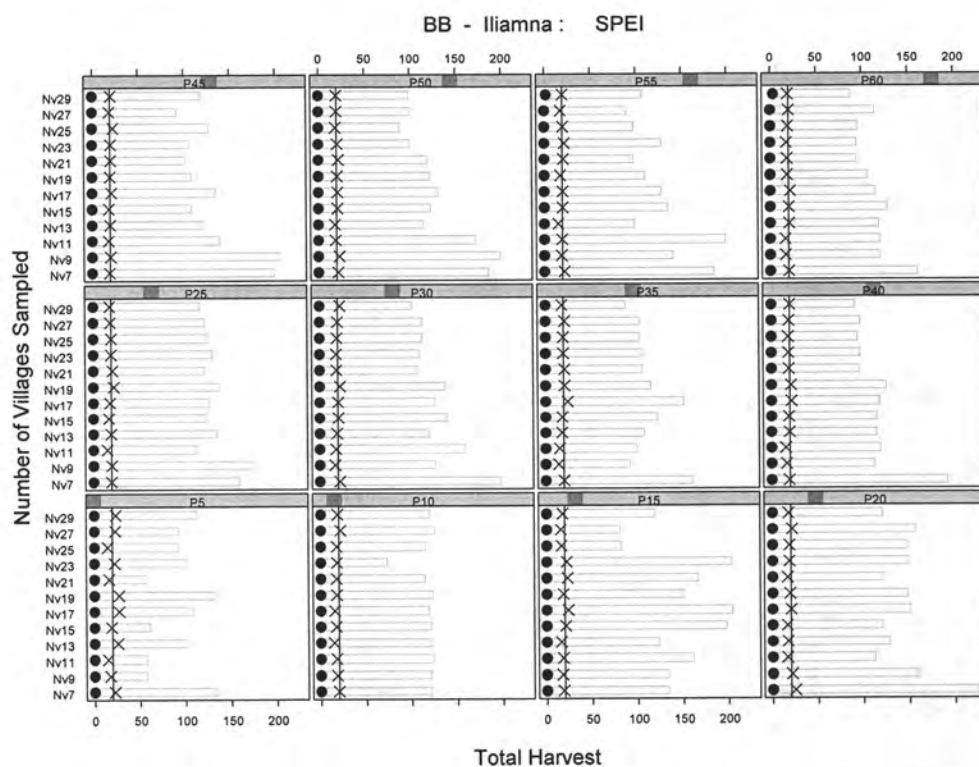
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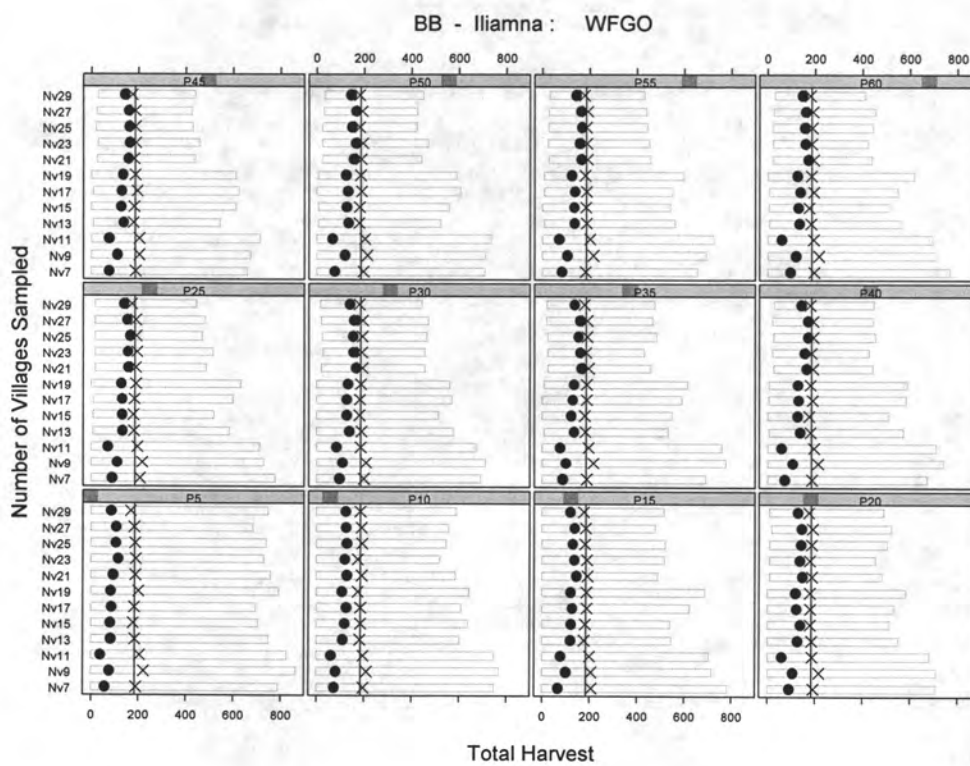
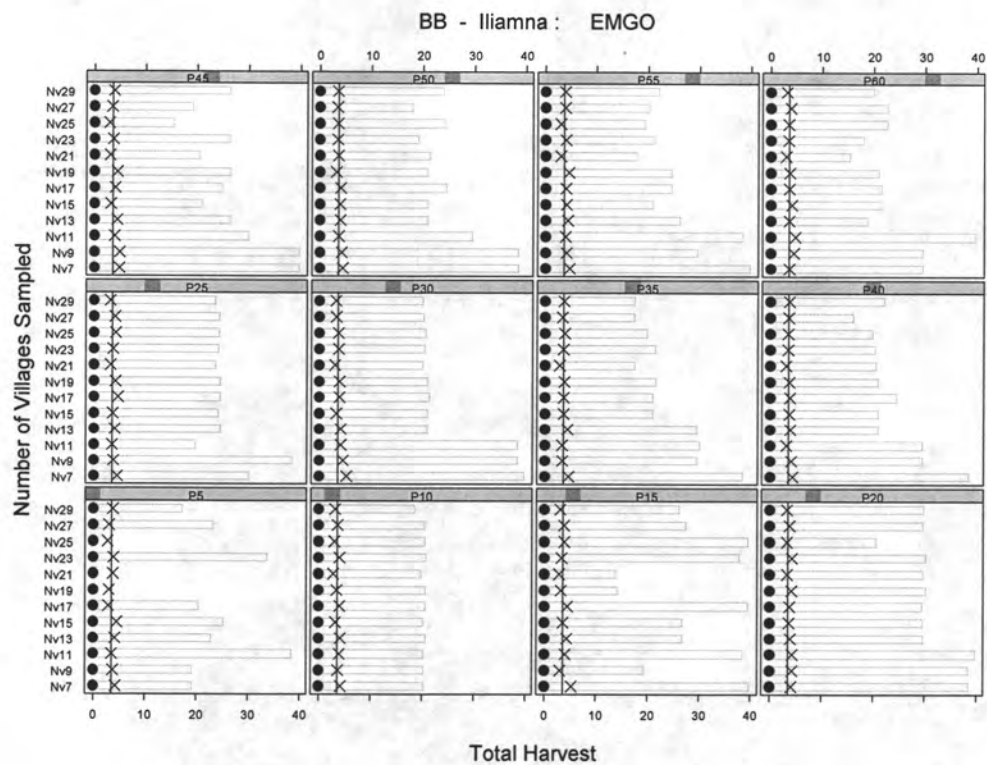
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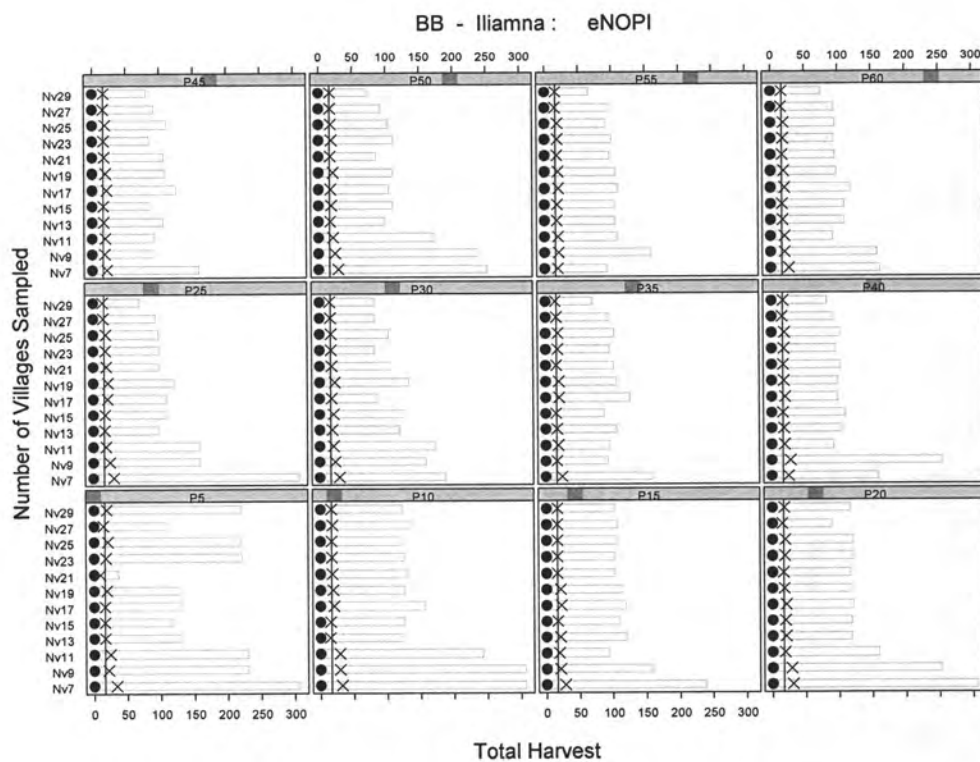
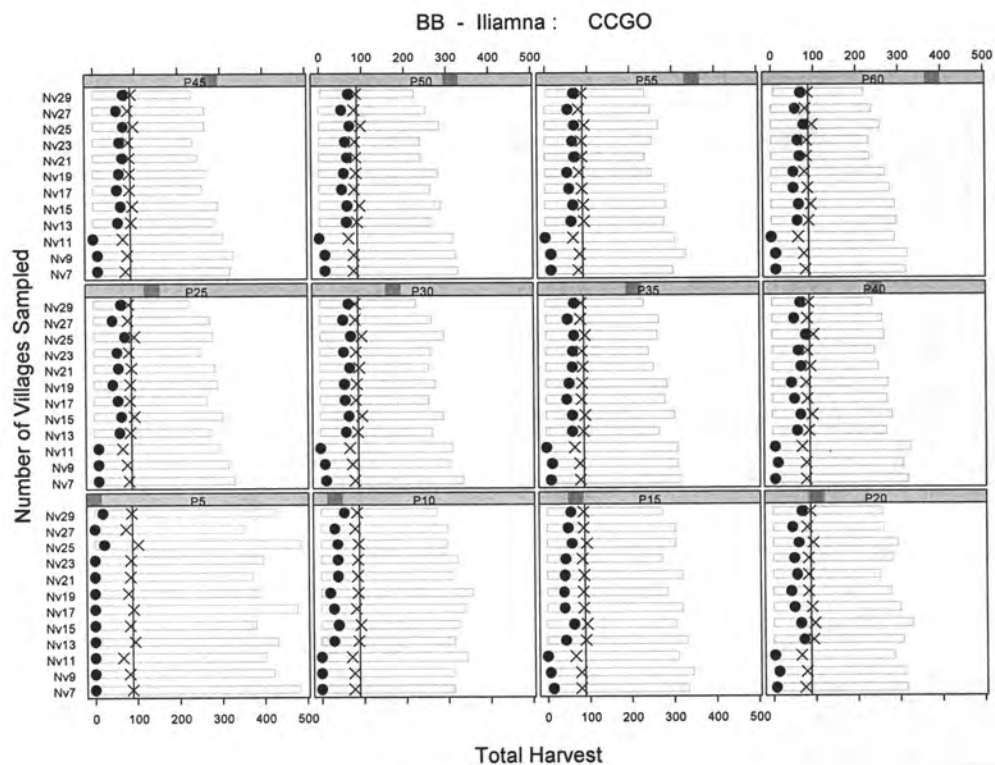
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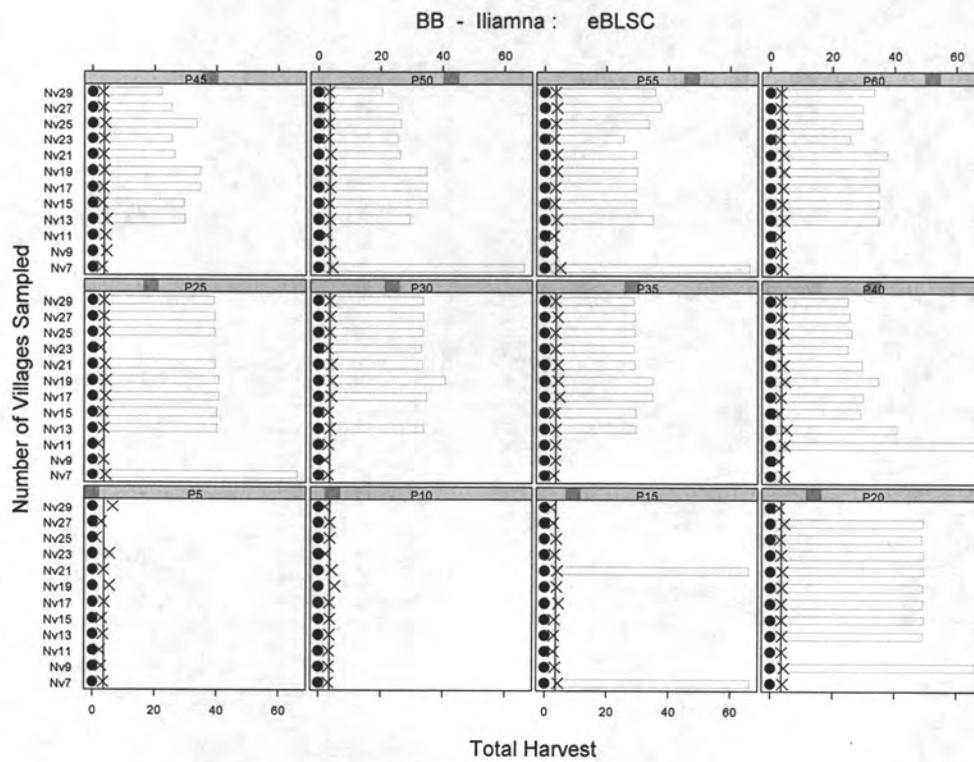
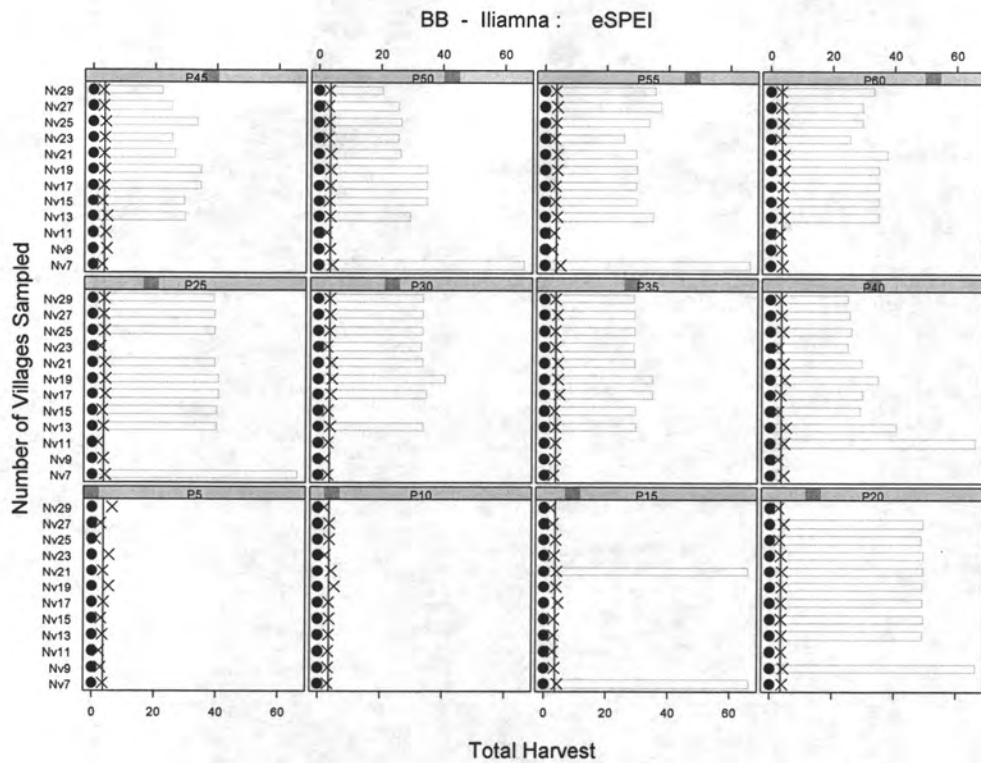
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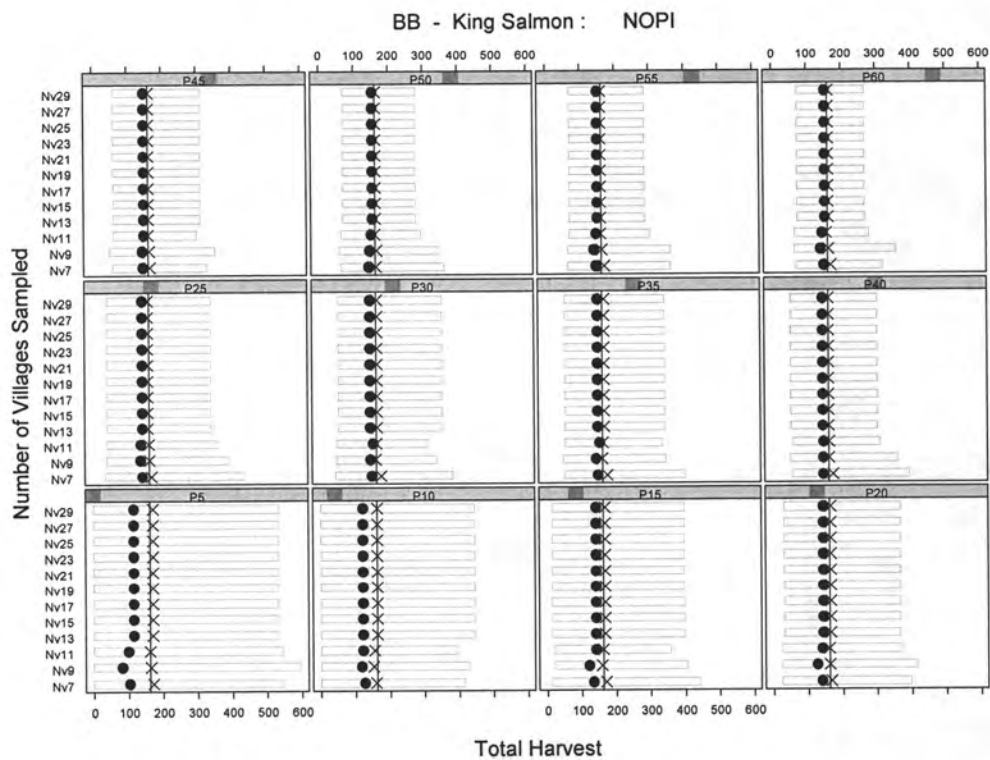
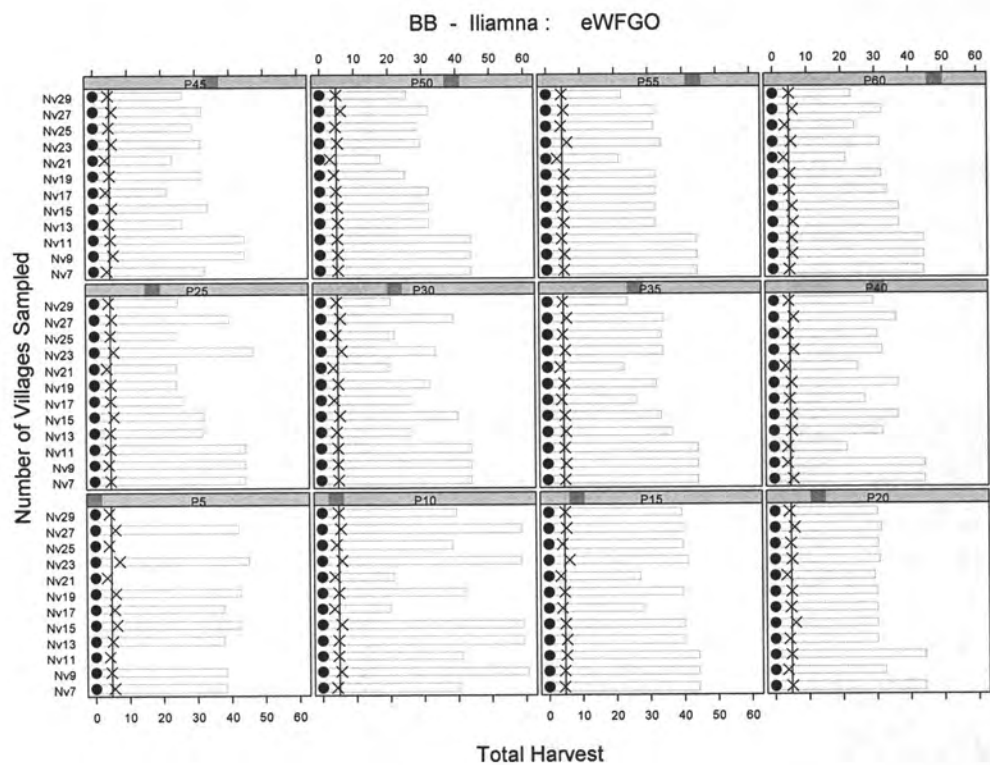
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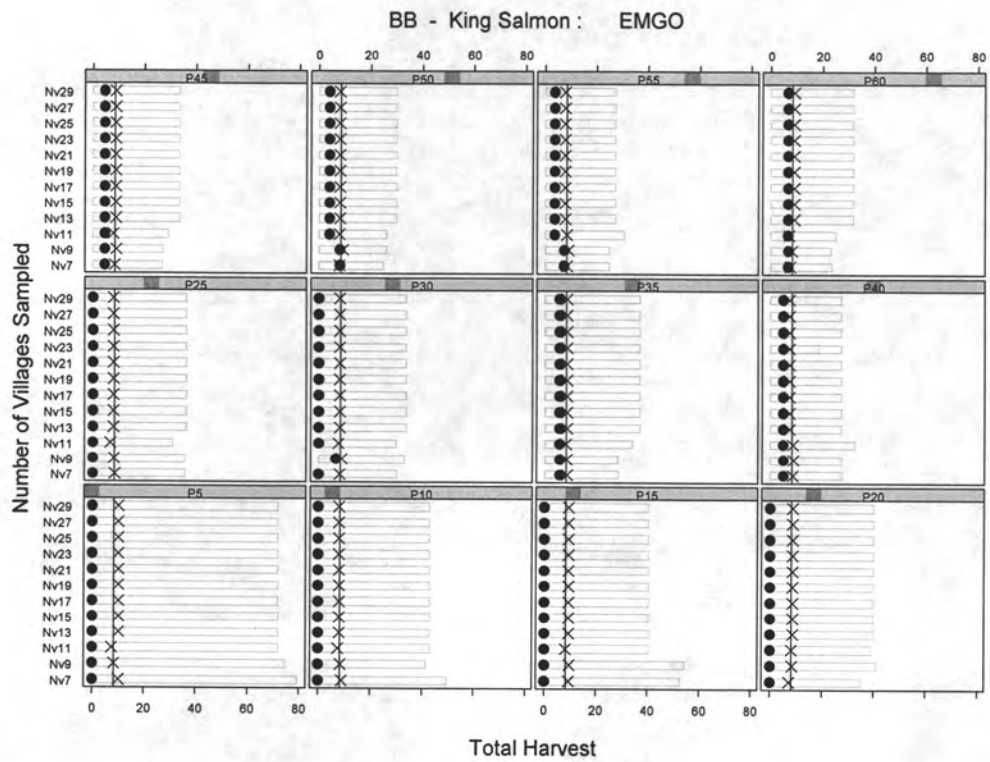
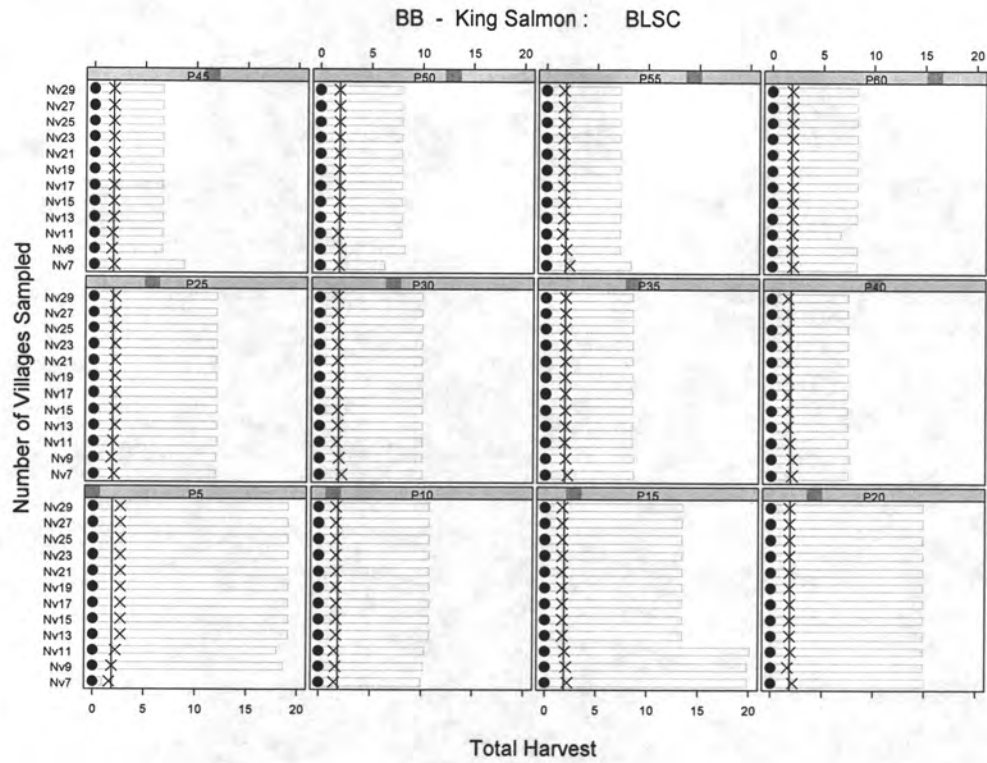
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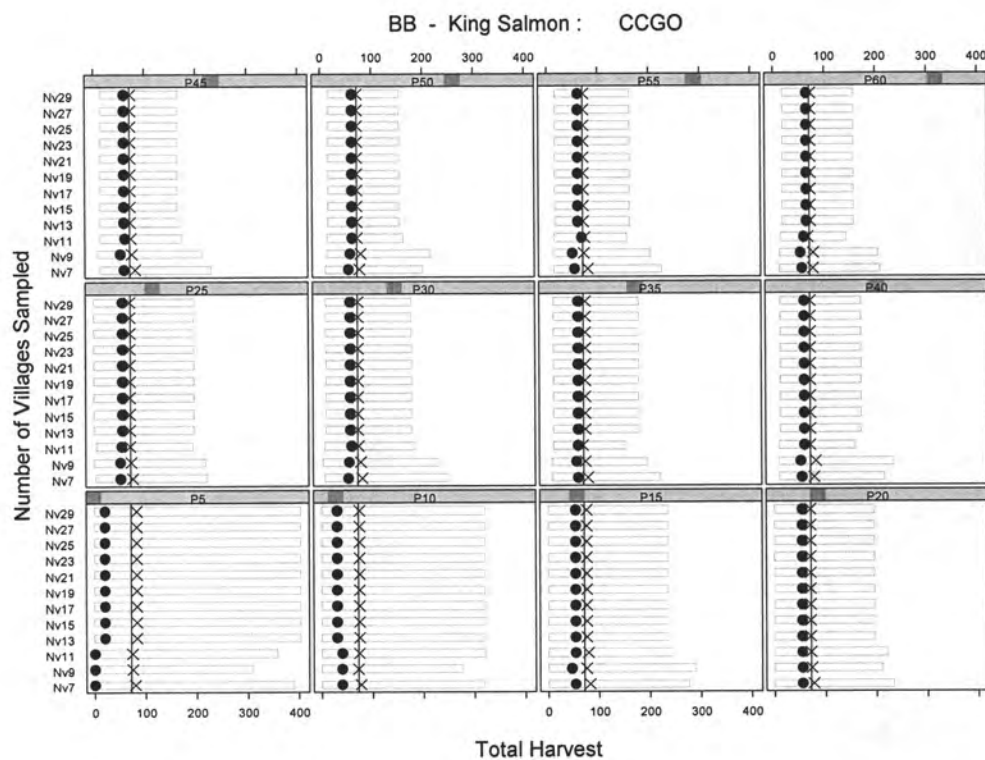
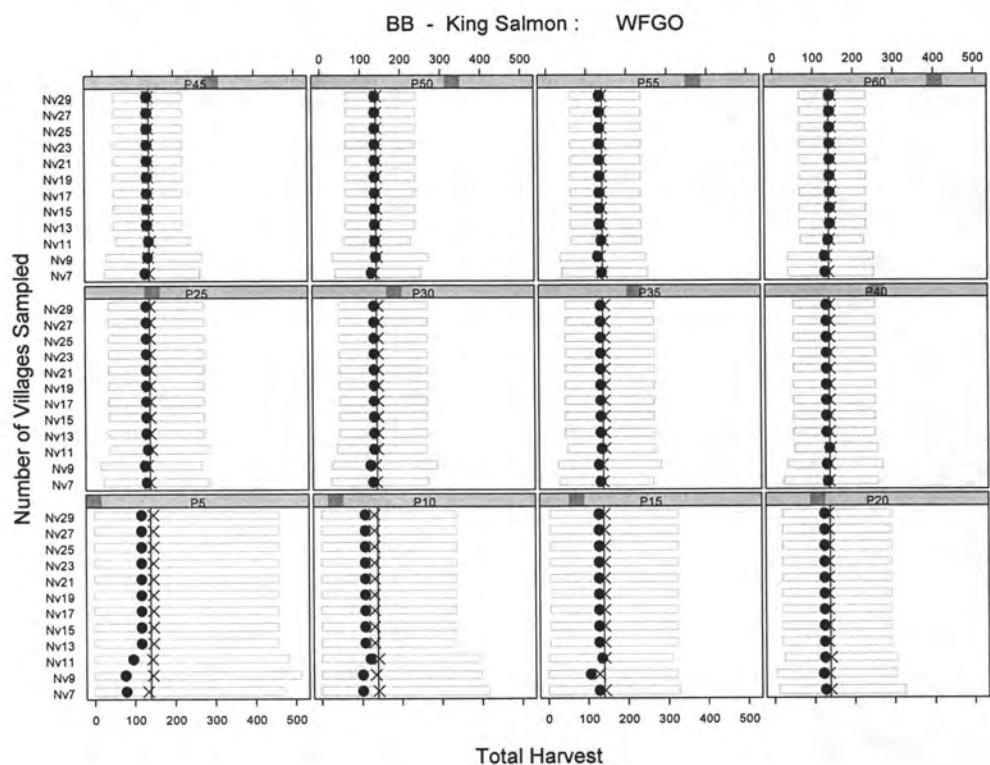
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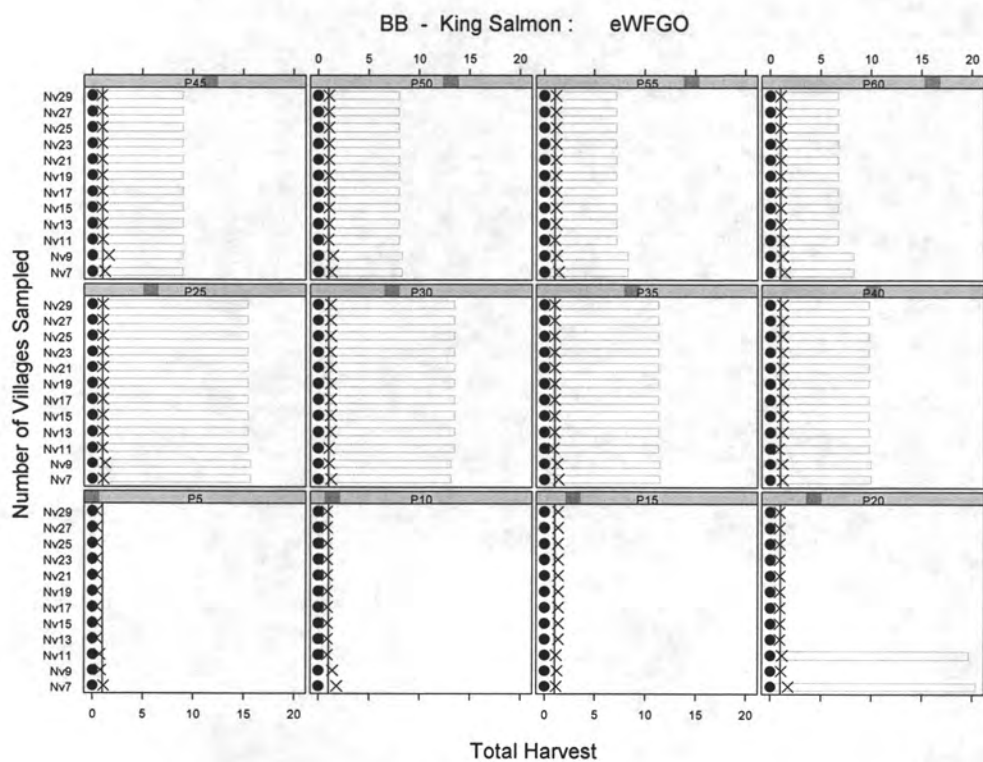
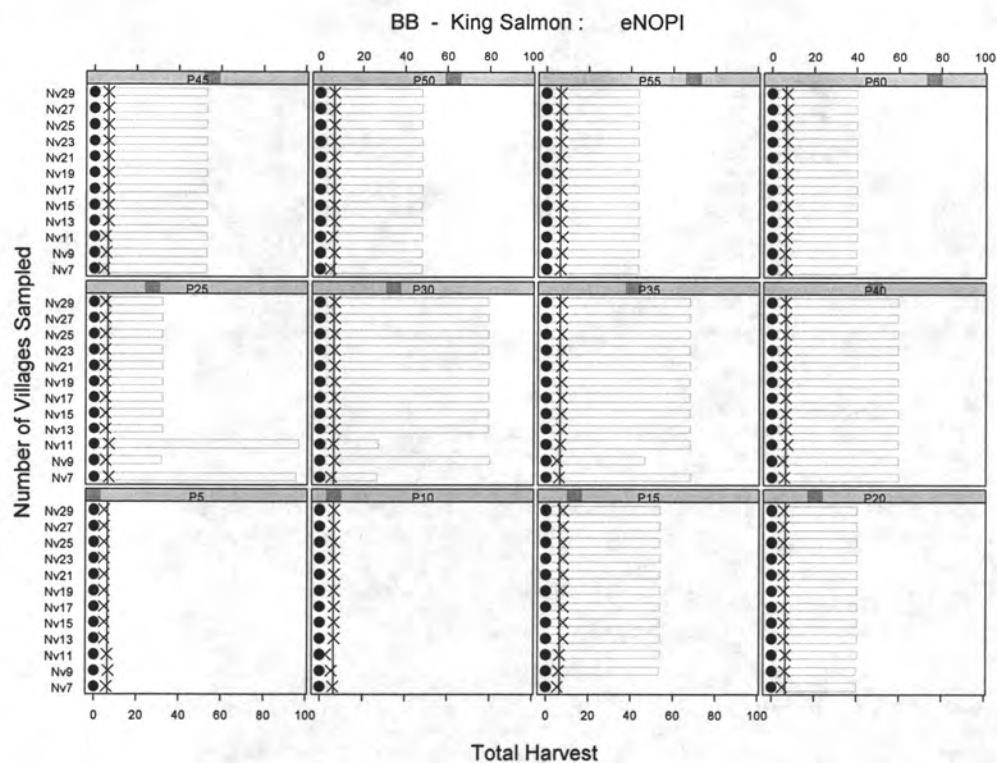
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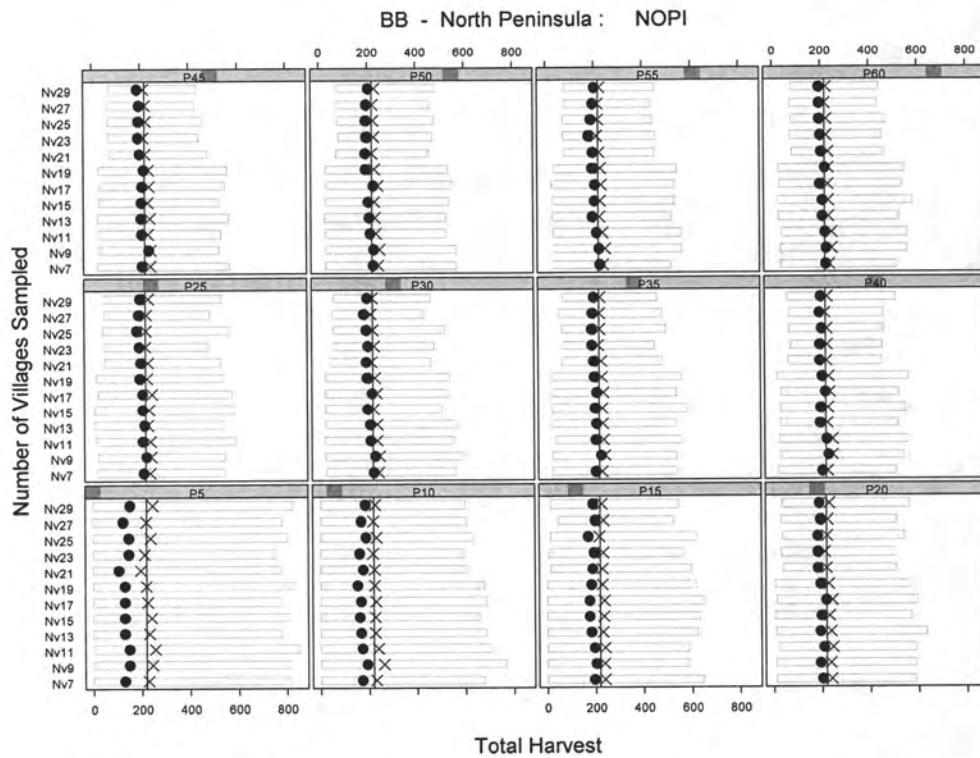
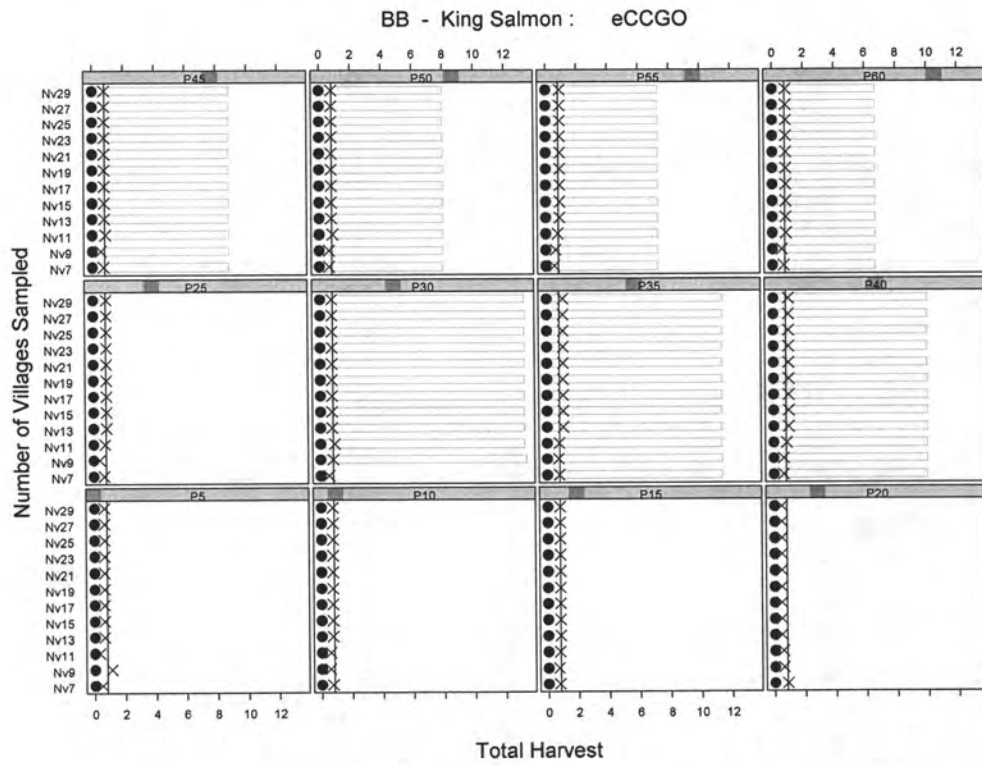
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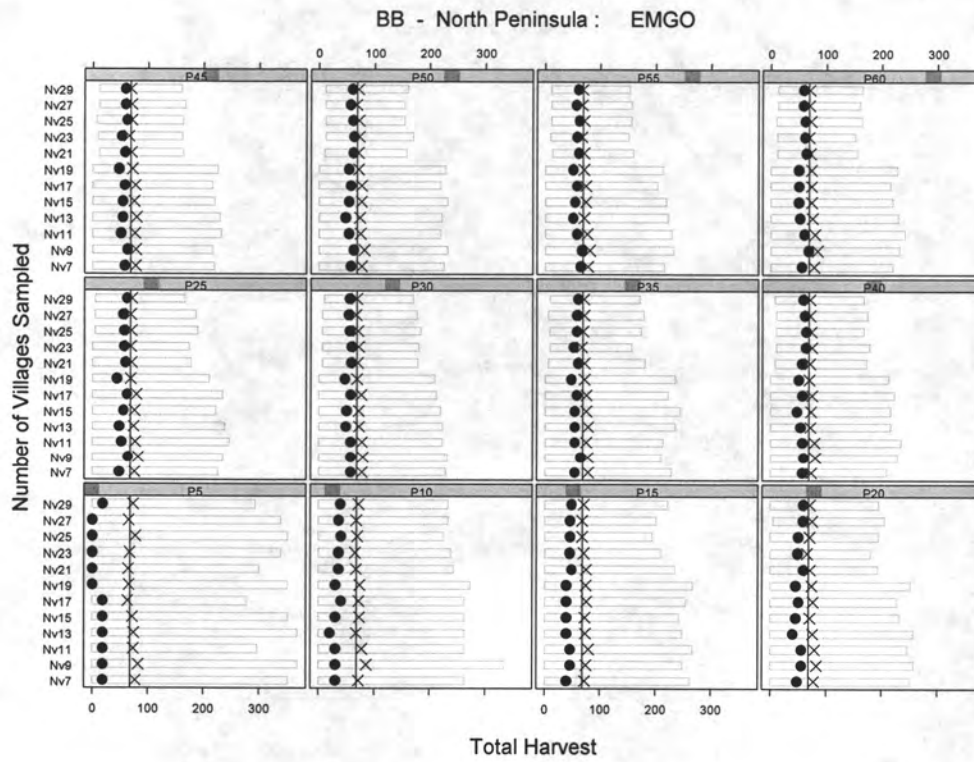
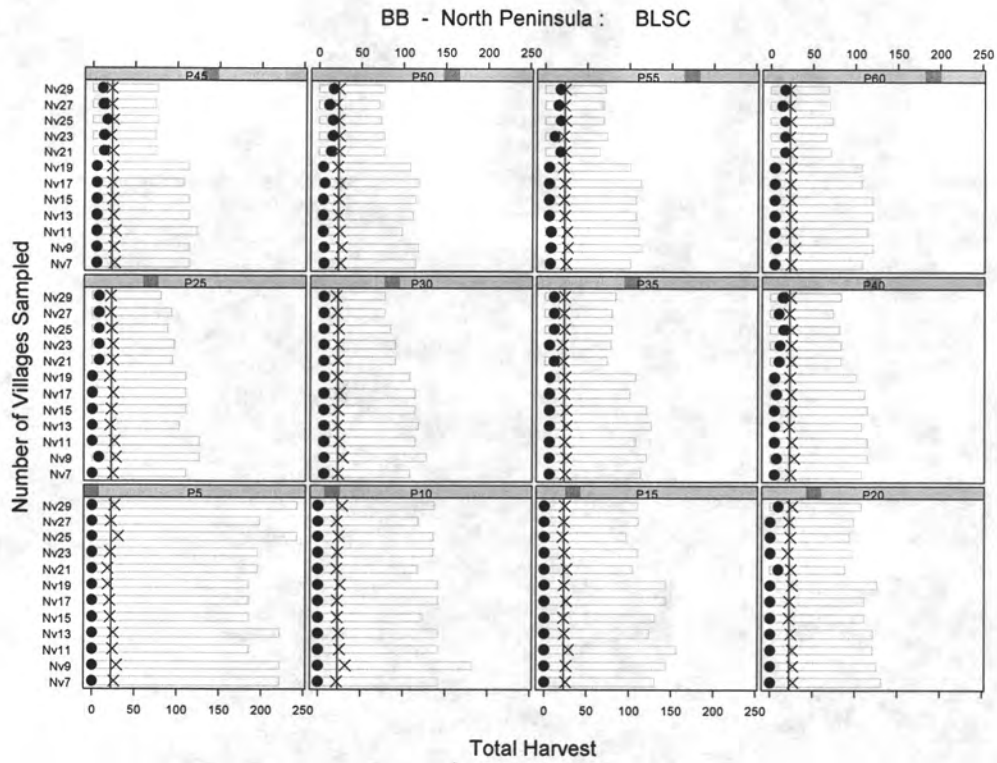
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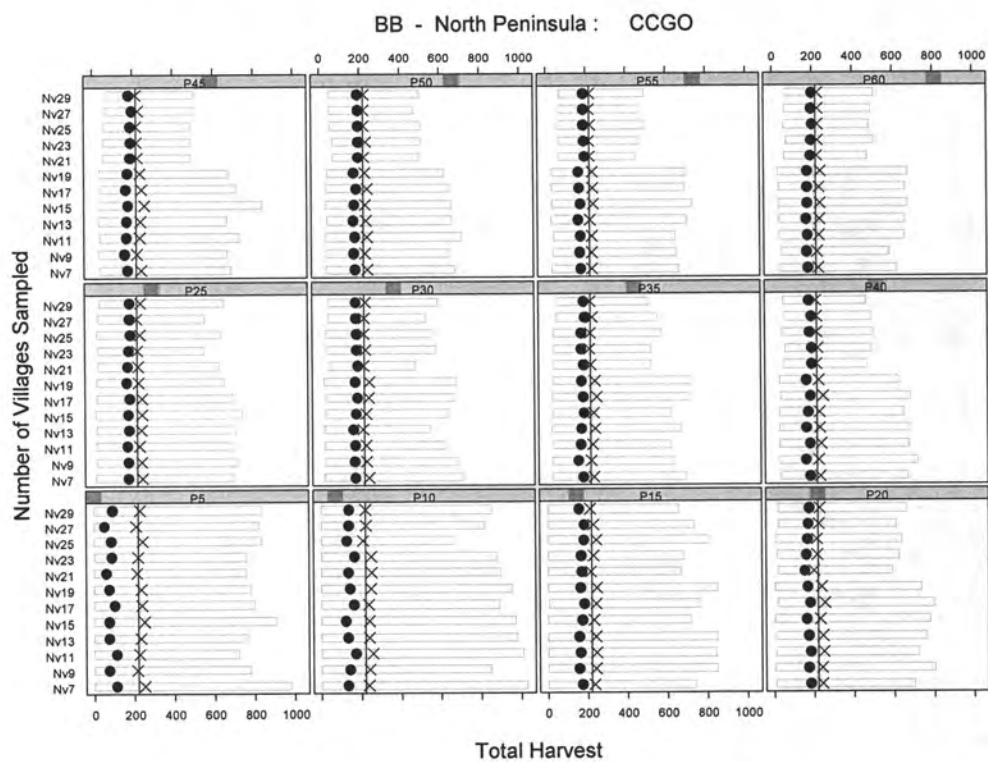
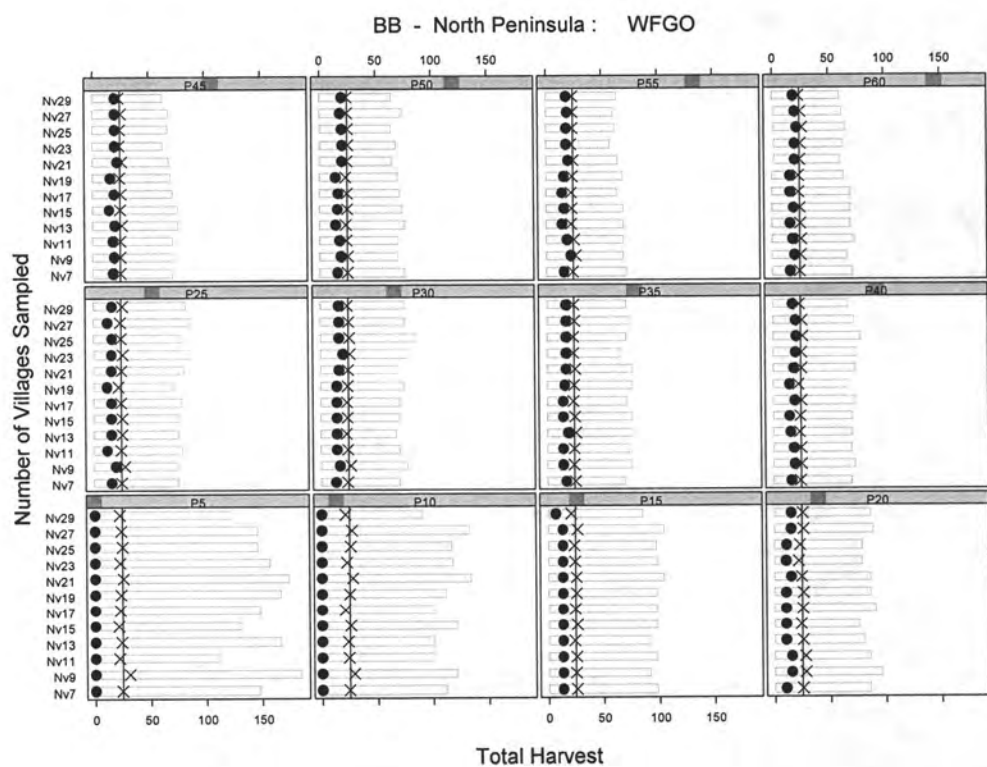
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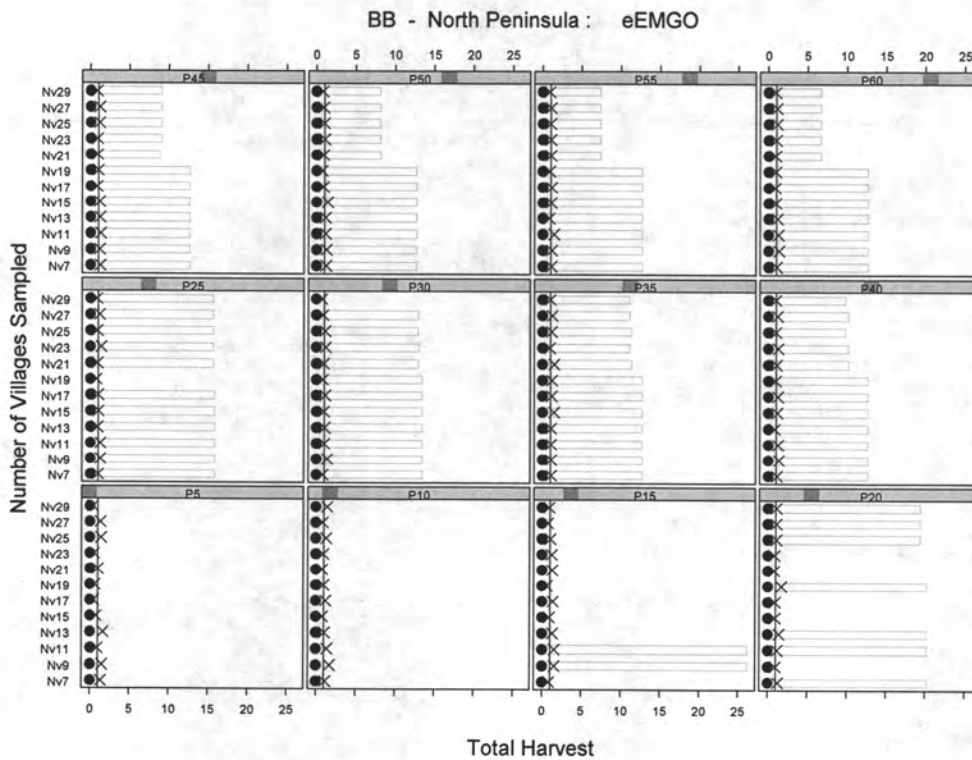
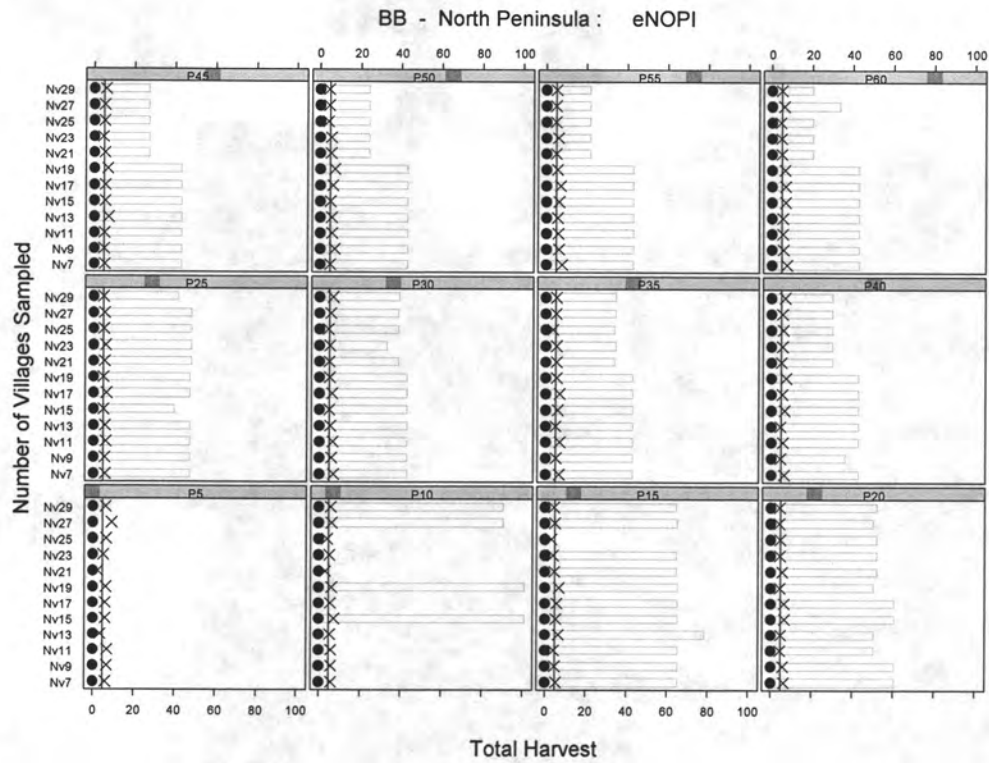
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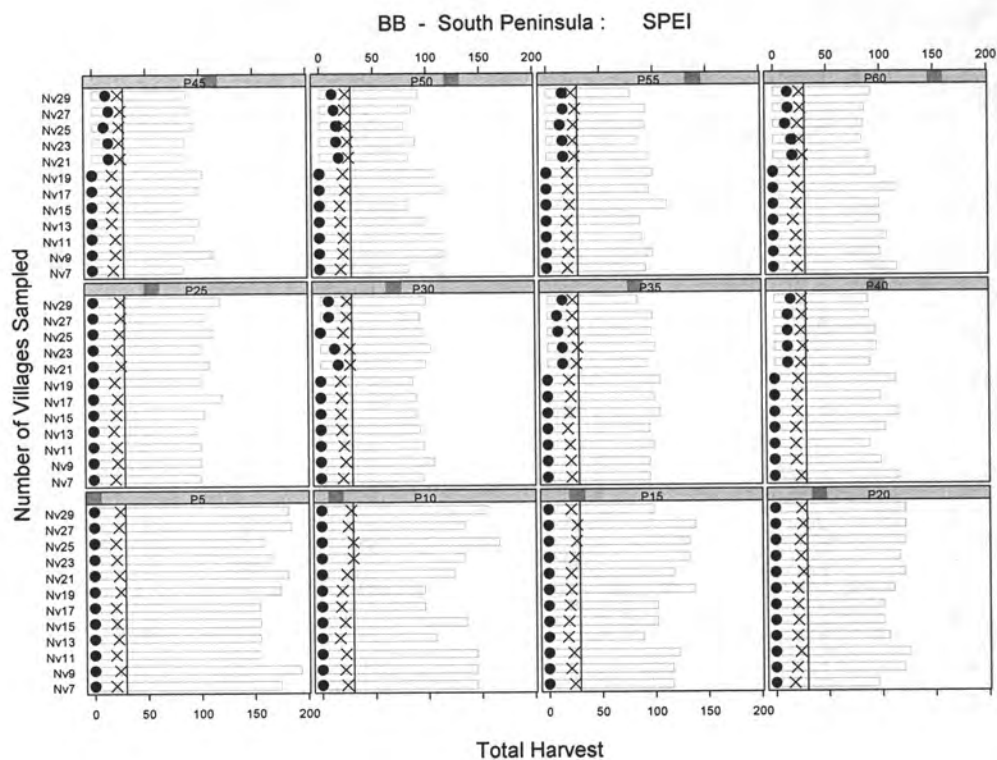
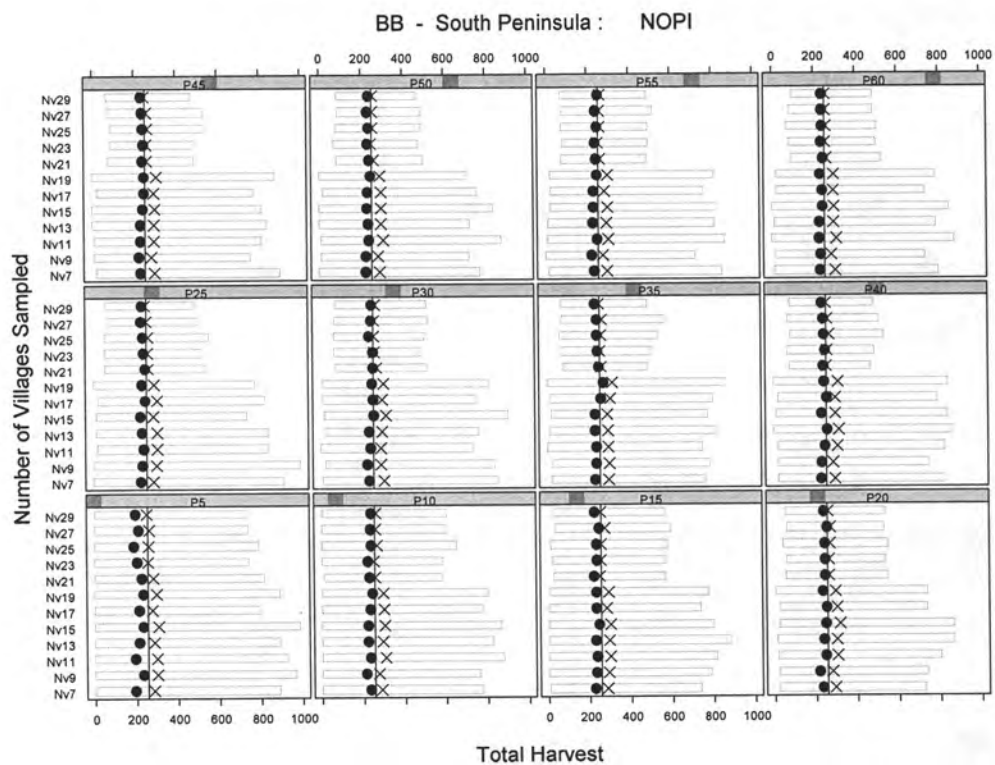
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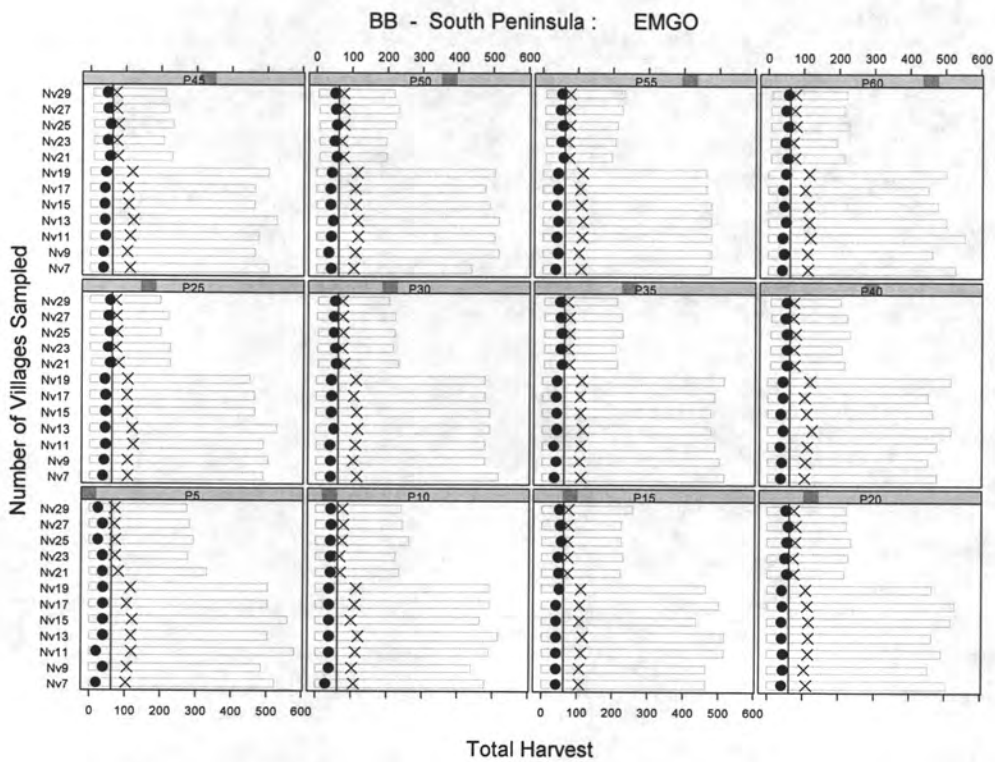
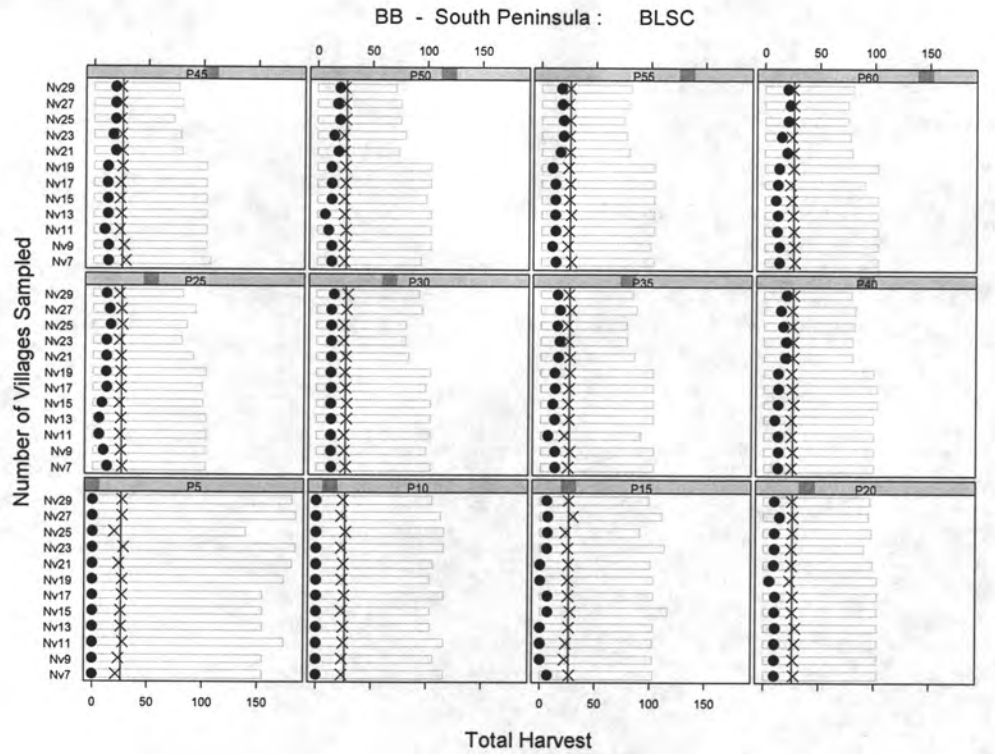
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