

FINAL PROJECT REPORT

Project Title: Developing and validating models for tree fruit

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Cooperators: Louie Nottingham, WSU-TFREC

Percentage time per crop: Apple: 40% Pear: 50% Cherry: 10% Stone Fruit: 0%

Other funding sources

Agency Name: WSU Extension

Amt. awarded: \$ 198,268

Notes: This is the funding WSU Extension has committed to support maintenance of WSU DAS and implementation of new models.

WTFRC Collaborative expenses:

Item	2017	2018	2019	2020 (No-cost extension)
Salaries	6,000	4,000	4,000	0
Benefits	2,000	1,200	1,200	0
Wages/Benefits ¹	14,000	18,000	20,000	0
Supplies	0	0	0	0
Travel ²	2,500	2,600	2,700	0
Miscellaneous	0	0	0	0
Total	24,500	25,800	27,900	0

Footnotes:

¹ Wages/benefits adjusted in years 2 and 3 to reflect new WA minimum wage schedule.

² In-state travel to research plots.

Budget 1**Organization:** WSU-TFREC**Contract Administrator:** Susan Cao/Shelli Thompkins**Telephone:** 509-335-4564/509-293-8803 **Email:** bentjen@wsu.edu /shelli.tompkins@wsu.edu

Item	2017	2018	2019	2020 (No-Cost Extension)
Salaries ¹	34,020	35,380	36,796	0
Benefits ²	13,442	13,979	14,539	0
Wages ³	8,000	8,320	8,653	0
Benefits ⁴	216	225	234	0
Equipment	0	0	0	0
Supplies ⁵	2,500	2,600	2,704	0
Travel ⁶	4,000	4,160	4,326	0
Miscellaneous	0	0	0	0
Plot Fees	4,200	4,368	4,543	0
Total	66,378	69,032	71,795	0

Footnotes:¹ Matt Jones (0.25FTE, T. Melton 0.45 FTE).² 34.1% (Matt Jones); 48.3% (Melton).³ Student 40 hr/wk for 16 wks.⁴ 2.7%.⁵ Includes lab and field supplies.⁶ In state travel.**Total Project Funding:****Budget History:**

Item	Year 1: 2017	Year 2: 2018	Year 3: 2019	Year 4: no cost extension
Salaries	40,020	39,380	40,796	0
Benefits	15,442	15,179	15,739	0
Wages	22,000	26,320	28,653	0
Benefits	216	225	234	0
Equipment	0	0	0	0
Supplies	2,500	2,600	2,704	0
Travel	6,500	6,760	7,026	0
Plot Fees	0	0	0	0
Miscellaneous	4,200	4,368	4,543	0
Total	90,878	94,832	99,695	0

Objectives:

1. Develop and validate a demographic model for pear psylla to assess pesticide effects on population management.
2. Continue to collect validation data for demographic models for mites and aphids.
3. Development new fruit growth models for Honeycrisp, Fuji, and Golden Delicious.

Significant Findings:

- Psylla phenology is well defined at this point in time and the pesticide model has been developed and is available for testing and parameterization (pesticide efficacy and residual longevity) for our collaborator.
- A preliminary model for the pear psylla parasitoid, *Trechnites psyllae* was developed, but it needs to incorporate other data and be finalized next year.
- The phenology of pear bloom has been estimated for swollen bud, bud burst, green cluster, white bud, and bloom for the cultivars Bartlett, Bosc and D'Anjou.
- More extensive studies of the bloom period of the three pear cultivars showed that "rat-tailed" bloom is <3.5% of the total bloom.
- Analysis of rosy apple aphid and apple grain aphid phenology was completed, and we have implemented the models on DAS as well as pesticide-effects models also on DAS.
- Our two-spotted spider mite data shows that diapause coloration is not a good indicator of when reproduction starts in the spring; egg deposition occurs almost immediately in the spring.
- Predatory mites are found in large number in the ground cover during the spring and fall, but most appear to migrate up into the canopy in June and remain there until the start of August. Management of the ground cover during the spring or fall could thus disrupt integrated mite management in the current or following year.
- Work on the fruit growth models for Cosmic Crisp, Fuji, Jonagold, and Honeycrisp was completed and implemented on DAS.

Obj. 1. Develop and validate a demographic model for pear psylla to assess pesticide effects on population management.

Methods Pear Psylla. Phenology data for pear psylla were collected at five locations with low-intensity management; samples were taken twice a week from February until the end of October from 2016-2019. The number of adults (winterform and summerform), eggs, and immature stages (instars 1-3 and instars 4-5) was determined from beat samples and shoot samples. Shoot samples were visually inspected before leaves were developed, and subsequently processed through the mite brushing machine as the leaves became close to full size. In addition, unbaited sticky yellow cards were placed in each orchard (8/site) to catch more adults as well as the pear psylla parasitoid, *Trechnites psyllae*.

Weather data came from the high-resolution historical data provided by daymet which provides data at 0.6 x 0.6-mile resolution as well as from data loggers placed in the orchard from the period 2016-2019. Data was fit by maximum likelihood to five different statistical distributions and examined for the best overall fit across the range.

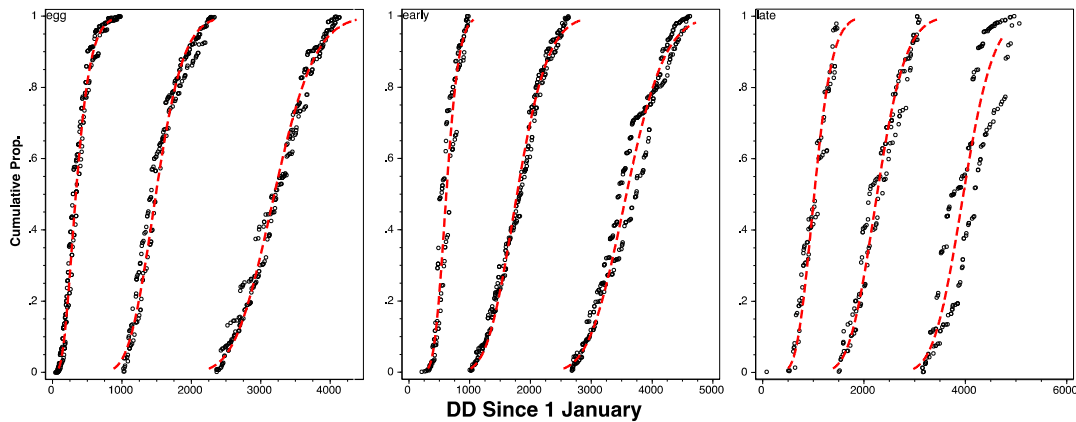
Methods Pear Bud Stage Development. Pear bloom phenology was evaluated at four locations with the cultivars Bartlett (3 locations), Bosc (1 location), and D'Anjou (2 locations). At each location we evaluated 60 fruiting buds (4 buds per tree from 15 randomly chosen trees – one bud per quadrant of each tree) and classified them as dormant, swollen bud, bud burst, green cluster, white bud, bloom, and petal fall. We visited each location twice per week to evaluate the clusters. Data analysis was done for each cultivar by using a maximum likelihood fit to one of five statistical distributions: (normal, lognormal, gumbel, gamma, Weibull).

Methods Bloom Progression

The second trial was run in 2020 which is called the bloom progression series. This one only considered the bloom period but used many more buds per tree. We used 10 trees per cultivar for each location and looked at as many buds as could be found on a branch. The numbers were counted initially on each tree and varied from about 30 to 100. We then came back 3x a week to evaluate how many blooms were open on each sampling date. This gave us up to 1000 buds per cultivar per location and the total numbers were from about 5500 to 9751 buds examined compared to around 1300-1600 for the bud stage studies. The result with the larger sample size is to catch more of the “rat tailed” bloom than the bud stages studies showed us.

Results and Discussion.

Fig. 1. Phenology of pear psylla egg, early instars (1-3) and late instars (4-5). Dashed line is model predictions, circles are observed.

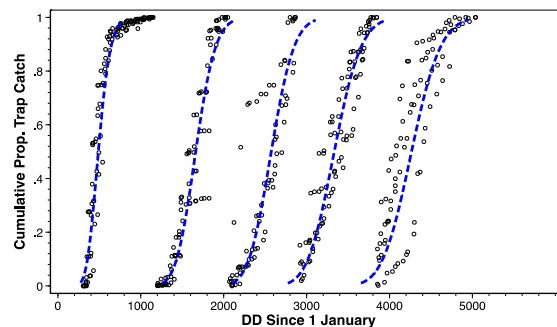


Pear Psylla Phenology. We completed evaluation of the pear psylla model for the winterform and summerform adults, eggs, early instars (1-3), and late instars (4-5) (Fig. 1). Our model shows that psylla begin laying eggs almost immediately – the adult and egg stages overlap almost completely when plotted on the same graph. We saw some variation in the late instars near the end of the season compared to the other stages, which was actually caused by a slight difference in DD between the sites at the end of the season. One of the changes compared to last year is that we found that the phenology was better estimated using a horizontal upper threshold for development.

We have also already finished the pesticide effects model for pear psylla. We have made this model available to Dr. Louie Nottingham and will work with him to evaluate the optimal control strategies for pear psylla.

We have also made a preliminary model for the pear psylla parasitoid, *Trechnites psyllae* (Fig. 2). The yellow panel data showed very large numbers of *Trechnites* present and we merged this with data collected by Drs. Dave Horton and Peter Shearer during the SCRI Enhancing biological control in Western Orchards grant. This data were combined with the same parameters for the lower threshold and type of cutoff as pear psylla and it allowed us to make the preliminary model just using the field data. However, when we did a literature search for information on *T. psyllae*, but there were no

Fig. 2. Phenology of trap catch of adult *Trechnites psyllae*. Dashed lines are preliminary model predictions, open circles are observed data.



laboratory data on developmental times which could be used to finalize the model. The status of this model is therefore unchanged as a preliminary model until validation of the thresholds.

Pear Bud Stage Development. This was the third year of collecting data on pear bloom for the three cultivars. The bud stage data was evaluated using not only the maximum likelihood estimates, but also simple summary statistics. We had reasonable numbers of all stages collected that allowed us to define the different stages and the variation associated with them at the different locations. We did not fit the distribution to the dormant stage, because we may have started a bit late in some cases and early in others so that you would get different distributions (since everything is in that stage until development starts). For the case of petal fall, we also did not run that fit because it would be easy to define as being “past bloom”. For the maximum likelihood estimates for the different stages, the normal distribution was sufficient in most cases and for simplicity sake, we just used it for all the stages and cultivars (Figs. 3 & 4 shown for examples). These models are being incorporated into DAS and will be available next year.

Fig. 3. Bud stage distribution for D’Anjou fruit using the normal distribution

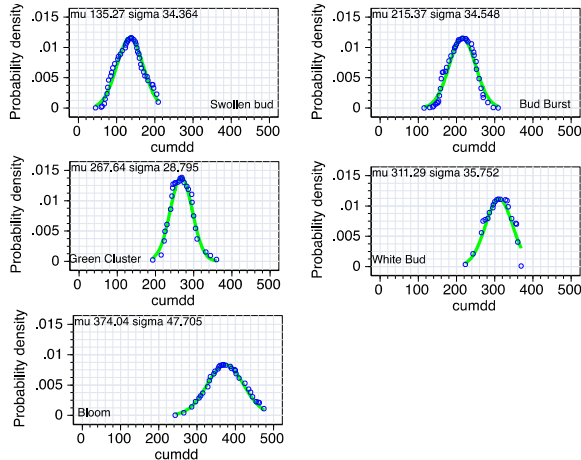
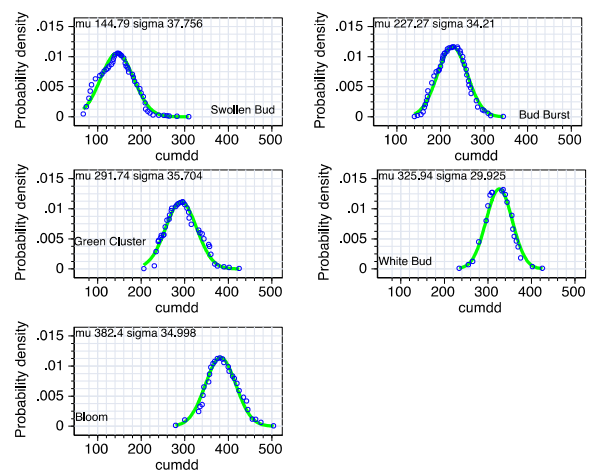


Fig. 4. Bud stage distribution for Bartlett fruit using the normal distribution



Pear Bloom Progression: The data for the bloom stage progression showed a much-extended period of what would normally be called “rat-tail bloom”. The mean for the bloom period is not much different than the Bud Stages experiment values (max 10 DD difference), but the maximum time of any bloom occurring was about 335 DD longer than observed in the pear bud stage development experiment for the Bartlett and Anjou and only about 100 DD longer for Bosc. For Bartlett, only 3.5% of the 5598 bloom observations occurred after 550 DD, and 1.7% of the 9751 observations for D’Anjou. For Bosc, only 5 of 5645 observations occurred after 550 DD. In comparison to the Bud Stage data for bloom where the normal distribution provided a good fit, the data had a longer right tail which was better fit by the gumbel distribution. In reality, it probably doesn’t make much difference except for the situation where fireblight is considered. In this case, the rat-tail bloom means that there is still a possibility for fireblight infection through a considerably expanded bloom period. However, it is still a very rare occurrence.

Obj. 2. Continue to collect validation data for demographic models for mites and aphids.

Methods. Phenology data were collected for woolly apple aphid (WAA), green apple aphid (GAA), two-spotted spider mite (TSSM), European red mite (ERM), and brown mite (BM). For GAA and WAA, four apple orchards were sampled twice a week from the end of March to mid-October. We sampled 100 shoots early in the year and 100 leaves later in the year (10 randomly chosen per 10 randomly chosen trees). The number of nymphs, nymphs w/ wing buds, wingless adults, and winged

adults was recorded for each aphid species.

Phenology data for ERM and BM were collected from six apple orchards, twice a week from start of April until late-October. Initially, when eggs started to hatch, double-sided sticky tape was placed tightly around 50 branches per site (1 per tree) to detect mobile immature stages. After leaves expanded, a total of 100 leaves from 20 trees per site were collected and run through the mite brushing machine. Mite numbers were recorded by species and stage. In addition to the canopy samples, we also collected mites from the ground cover. Our results from last year showed that common mallow (button weed) consistently had high numbers of TSSM, so all the ground samples focused on that plant.

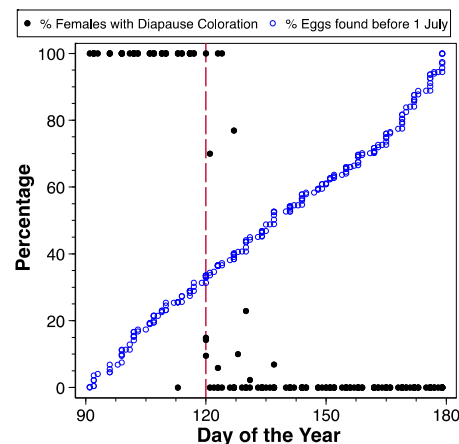
Results and Discussion

Rosy apple aphid & apple grain aphid. The phenology of rosy apple aphid and apple grain aphid from 2015-2019 were quantified and models were developed that allow to predict phenology and develop pesticide effects models (found at pesticides.decisionaid.systems). These models have been incorporated into WSU-DAS and were available for beta users this year. They will be available for all users next year.

Green apple aphid. Analysis of the green apple aphid showed no big drop off related to temperature as occurs with WAA. There is a significant reduction in immature survival during peak heat, but adults do not seem to drop off as much, so that recovery is quick once temperatures drop. Part of the problem with GAA is that populations in the orchards build up significantly before any heat-induced mortality and thus the populations stay high throughout the season. We were not able to quantify phenology to any significant degree as we have with the other aphid species because the generations overlap very quickly and they are present all season long (an average of >8 generations per year) – this makes it impossible to validate generation based models which are needed for the pesticide effects models. In comparison the RAA and AGA models have 3 and 2 generations/year, respectively.

Mites. Our work on mites has focused on both emergence times and whether we can develop a model that simulates what we observe in the field. We examined European red mite (ERM), Brown Mite (BM), and two-spotted spider mite (TSSM). TSSM analysis initially showed that the winter diapause-mediated color change (adult females turn orange when in winter diapause and return to greenish-tan when out of diapause) could be predicted by the daylength. The TSSM overwinters as adult females in reproductive diapause (if the temperatures are warm, they can feed or move about, but they are not reproducing until the temperatures & photoperiod rise above a certain level). Above 15.5 hours of light (roughly 1 May depending on site), we found the proportion of the adult female population switched relatively quickly to non-diapausing females (Fig. 4). However, we had also been taking leaf samples in the orchard and we found that eggs were produced at roughly the same rate per female when the female population was solely showing diapause coloration versus just after the female population showed no diapause coloration. Obviously, diapause coloration is not a true indicator of female reproductive status and cannot be used to guide management tactics for TSSM.

Fig. 4. Percentage of females showing diapause coloration and the percentage of the total eggs found before July 1 during the early season using data from 2017-2019.



During the studies of TSSM, we have examined both ground cover weeds (primarily button weed which is an excellent host) and sampled the canopy for all stages as well as for the presence of predatory mites. Our data for the predatory mites shows that we have a fast early season build up in the weeds from early April through the end of May, a drop off during the period of June through the first week of August, then a large build up until the end of the season. At first, we thought the drop off in mid-season was related to high temperatures that start about that time, but examining the canopy samples, that period is the same as when a large increase in predatory mites were collected in the canopy. This suggests there is a net migration upwards from the ground cover and that ground cover effects are key to making sure that predatory mites are available when spider mite populations in the canopy are peaking. Timing of weed control is therefore as critical with predatory mites as it is with TSSM.

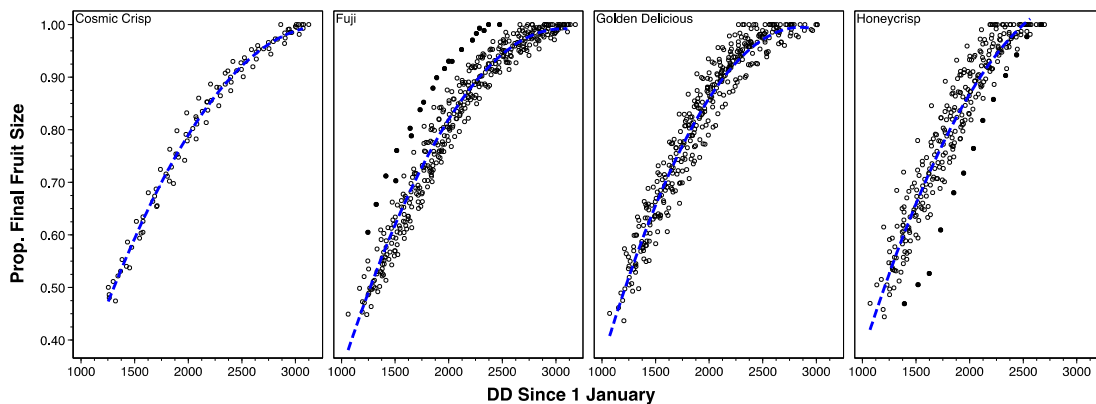
We had high hopes that we could develop a phenology model for the egg hatch of ERM and BM. However, collections done both before this grant started and during the grant period provided inconsistent data that could not be traced to time of collection in the field or to photoperiod that they were reared under. Both species exhibited very high variability with some years having and very low variability in others. Unfortunately, there was no consistent trend in emergence time related to the number of degree days and collection times in the field. The ERM data we collected reflects the sort of variation seen in the literature from a survey of six different studies. It is possible that some of the variation is just a natural adaptation to variable spring conditions, but the data we had is just not appropriate for developing a management model for ERM or BM.

Obj. 3. Development of new fruit growth models for Honeycrisp, Fuji, and Golden Delicious

Methods. We collected data from 11 geographic areas representing the topographic and climatic diversity of Central Washington production areas from Brewster Heights to North Pasco. We concentrated on Golden Delicious, Fuji and Honeycrisp, but also collected data on Cosmic Crisp at the WSU Sunrise location. After early drop was completed, we tagged fruit and then measured the same fruit each week until harvest. Each fruit measurement was recorded separately, so that we could assess how the individual fruit size changed over the course of the season. We analyzed the data as the proportion of the final fruit size for each fruit, so that we don't have to worry about the effects of thinning, fruit load, or return bloom size. This method allows us to predict when the fruit reaches a given percentage of the final fruit size. The fruit size data was paired with temperature data, and degree days from 1 January (base temperature 42, upper threshold 77.6).

Results. Our average fruit growth data showed good agreement for most sites and cultivars for 2017-2019. The one variable site was in south Orondo (near Baker Flat) where the orchard was on a south

Fig. 5. Fruit growth throughout the season versus model predictions for each cultivar. Black solid circles indicate areas with anomalous data from South Orondo (Fuji) and Mattawa (Honeycrisp in



facing slope that probably affected the Fuji grow size estimates by being warmer – this showed the same problem in 2017 and 2018 (black dots) (Fig. 5). The Honeycrisp data from 2019 at the Mattawa location in 2019 where the fruit growth appeared delayed (black dots) compared to all the others (Fig. 5). Because these sites were so anomalous, we dropped them from the final predictive model. These models were available on DAS this past year.

Executive Summary

Project Title: Developing and validating models for tree fruit

Keywords: Modeling, pear, apple, pear psylla, rosy apple aphid, apple grain aphid

Abstract. We developed models to predict pear psylla phenology and pesticide effects models to help determine optimal timings for management activities. The models are complete and have been provided to our collaborator (Dr. Louie Nottingham, WSU-TFREC) to help provide the information needed to make the models available to growers; this includes the longevity of different types of pesticides as well as stage specific activity needed. At the same time that we were collecting the data for pear psylla in the early spring, we collected data for models predicting the different bud stages of pear and an extensive collection of bloom timing. Those models will be available on DAS this coming year.

Evaluation of data for mites and aphids allowed us to create two aphid models, one for Rosy apple aphid, and the other for apple grain aphid. These models have been implemented on DAS and were available for our beta users this past year. Both models have also been developed as pesticide-effects models so that users can estimate the efficacy of control programs aimed at those two insects. Models for European red mite, twospotted spider mite, and brown mite were not feasible because of variation in the data, even though we had collected data from multiple locations and years before the current grant period.

Fruit growth models were also completed for the cultivars Cosmic Crisp, Fuji, Golden Delicious, and Honeycrisp, bringing our total number of models for fruit growth to seven different cultivars. These models are currently available on DAS.