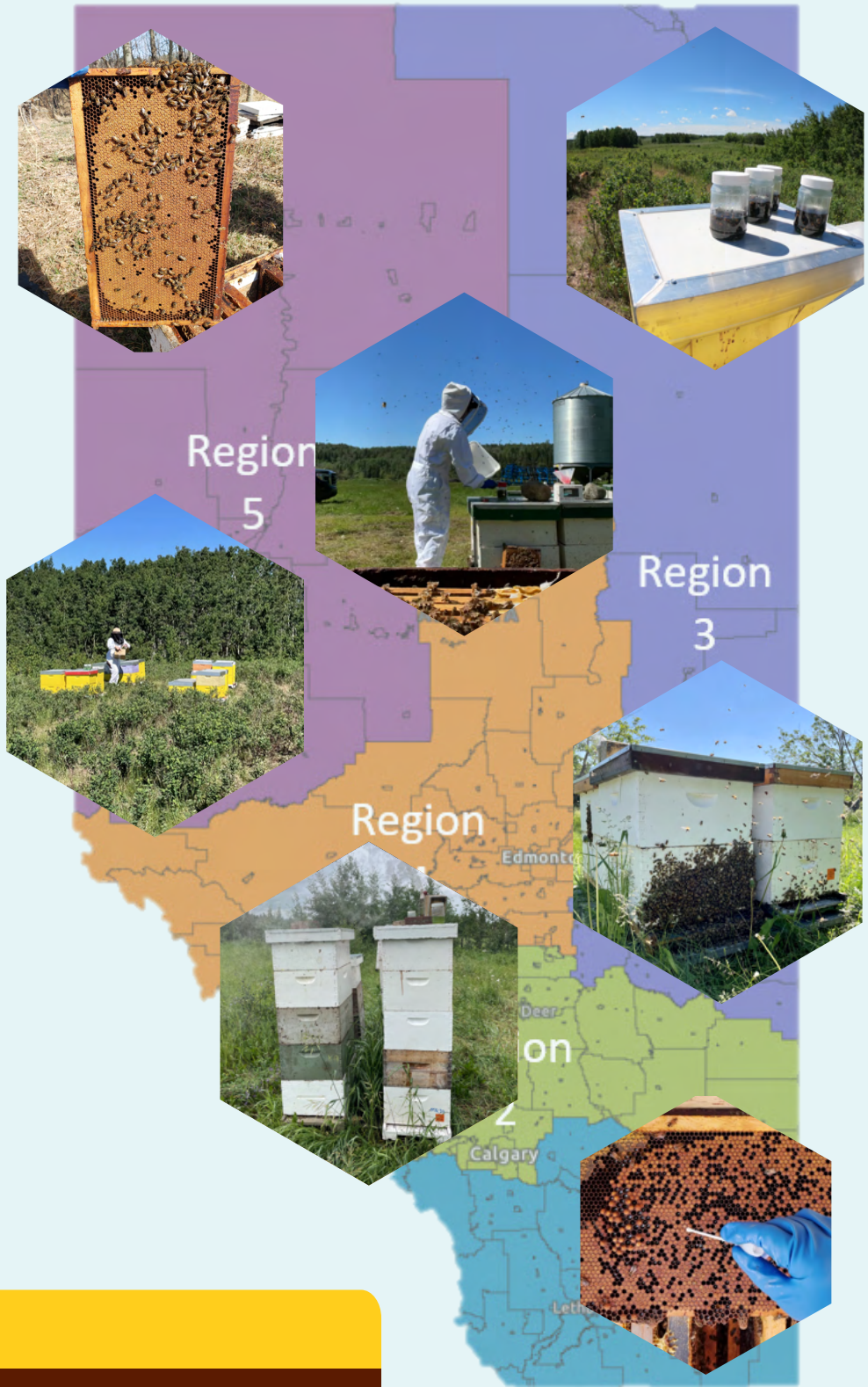
ALBERTA TECH TRANSFER PROGRAM

COLONY HEALTH MONITORING PROGRAM



2021 REPORT

ALBERTA REGIONAL MAP

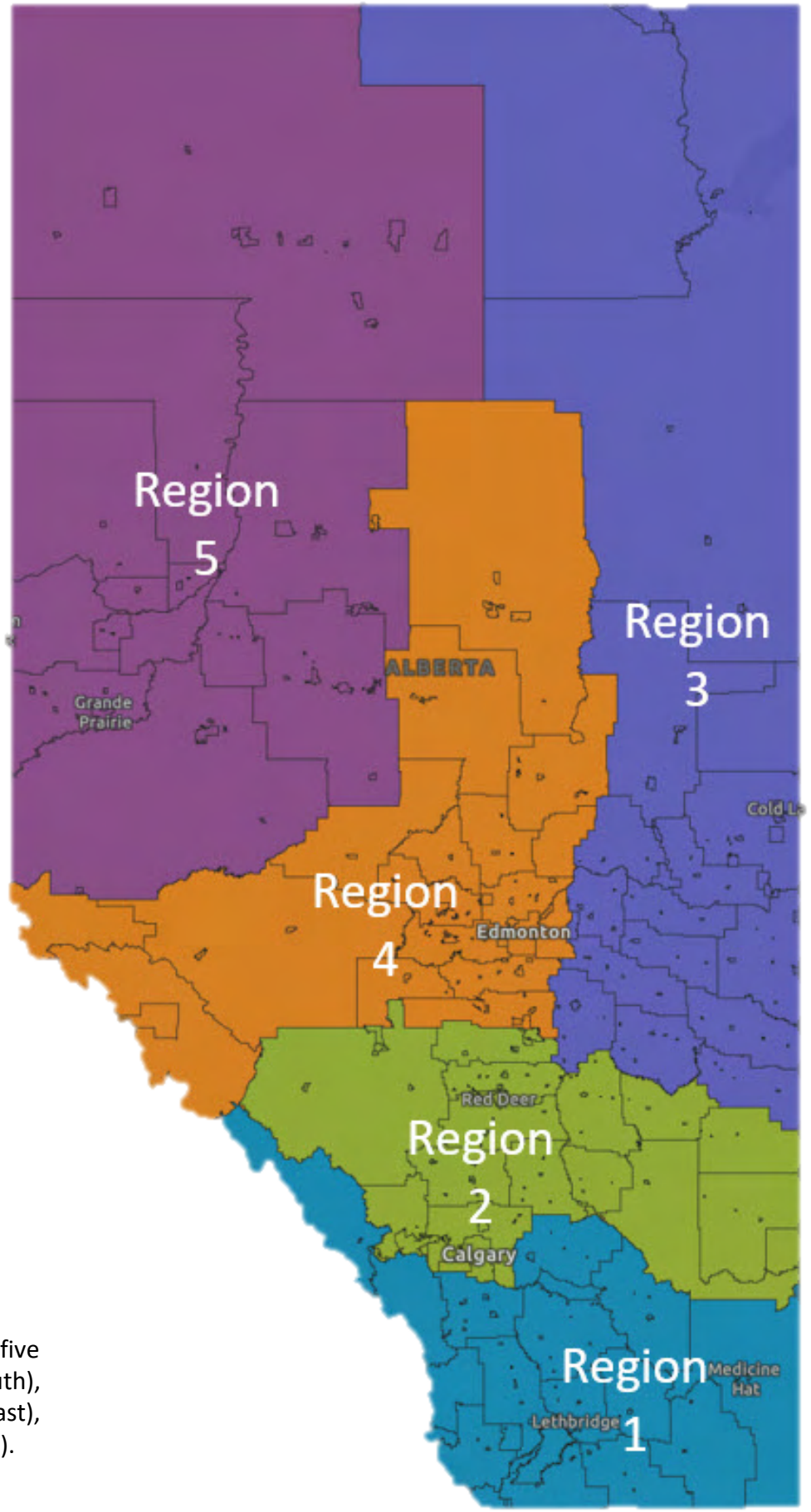


Figure 1. Alberta regional map showing the five beekeeper regions of Alberta: Region 1 (South), Region 2 (North Central), Region 3 (North East), Region 4 (North West), and Region 5 (Peace).

PROGRAM OVERVIEW

Continuous colony monitoring and the implementation of best management practices has been shown to improve bee health, pollination, and honey production, and reduce annual bee losses, use of antibiotics, and overall operating costs for beekeepers. The purpose of the Colony Health Monitoring (CHM) program is to provide temporal monitoring and evaluation of pests and pathogens in the honey bee hive. An effective integrated hive management program includes continuous evaluation and planning steps so that adjustments can be made as necessary to ensure the success of the beekeeping operation. As part of this program, colonies were sampled in early spring and fall for major pests and pathogens, and a sub-group of colonies were also sampled in the summer, during hybrid-seed canola pollination. Additionally, colony management data was collected at the end of the season from beekeepers as a way to provide to beekeepers an evaluation of their pest management practices and pest/ pathogen levels. The long term goal of the colony management data collection is to investigate possible association between management practice and hive pathogen levels.

Apiary sampling occurred 2-3 times a year (spring, summer, fall). Two types of samples were collected from 10 colonies at each apiary: live bee (150 bees) and alcohol wash sample (300 bees). Live bee samples from all 10 colonies in each apiary were combined/pooled into one sample per apiary. Live bee samples were shipped to the National Diagnostic Centre for disease and pest analysis (Nosema, AFB, EFB, and quantification of bee-related viruses). Alcohol wash samples were not pooled. Varroa samples from each colony were assessed locally (for fast data result).

Sample collection and assessment

Table 1. Number of apiaries sampled per region.

		Alberta region				
		Peace	North-East	North-West	North-Central	Southern
Season	Spring	10	15	14	17	28
	Summer	4	4	8	15	24
	Fall	10	15	14	17	28

Table 2. List of samples, sample size, and method of assessment.

Sample	Method of assessment	Sample size
Varroa	Alcohol wash	300 bees per colony
Nosema	Microscopy	Composite sample
AFB	Bacterial culture	of 10 colonies at
EFB	qPCR	approximately 150
Virus	qPCR	bees per colony

RESULTS

Average Nosema Levels

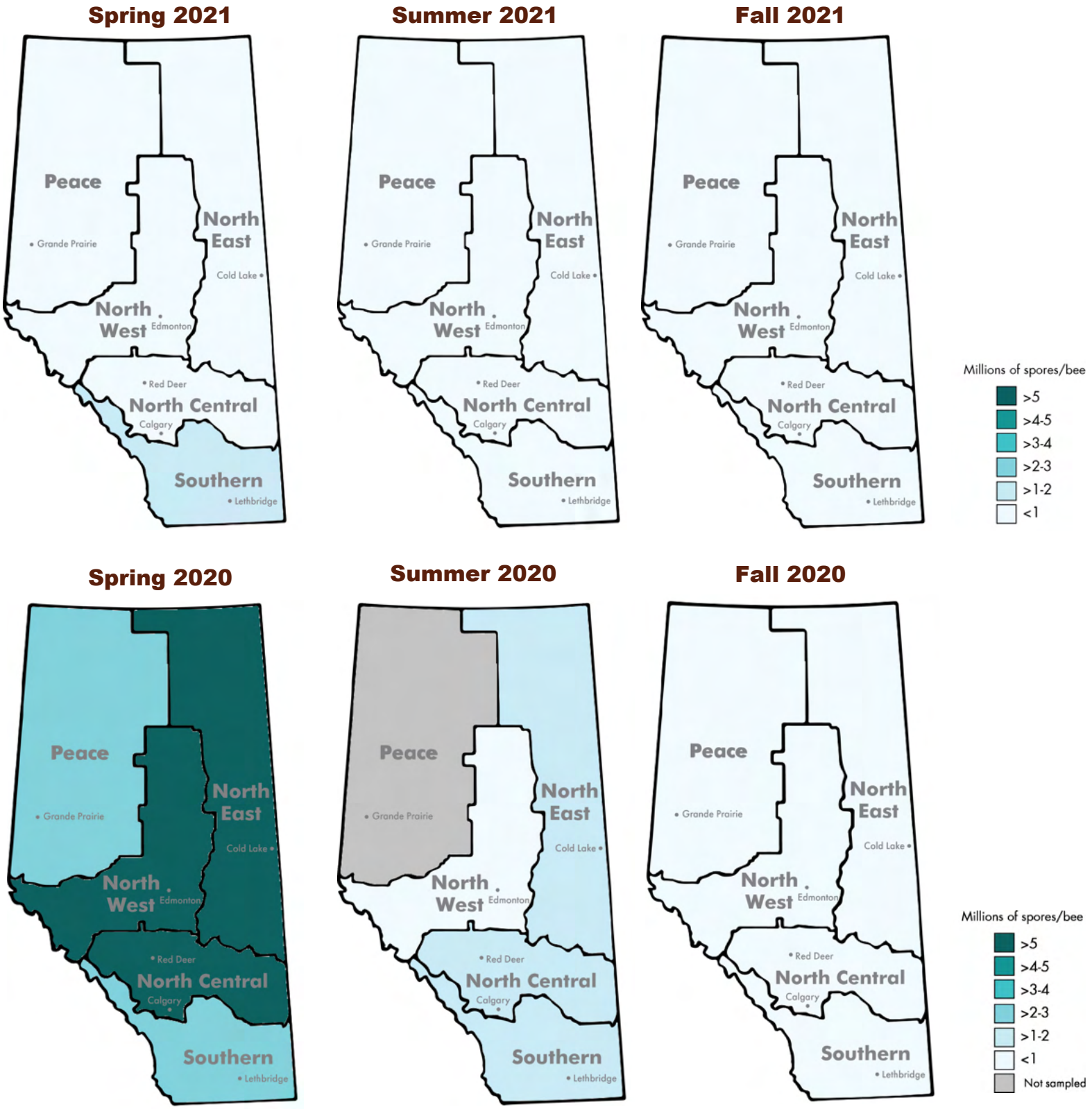


Figure 2. Regional average of Nosema spore count (millions of spores per bee) by season and year.

RESULTS

Average Varroa Infestation Levels

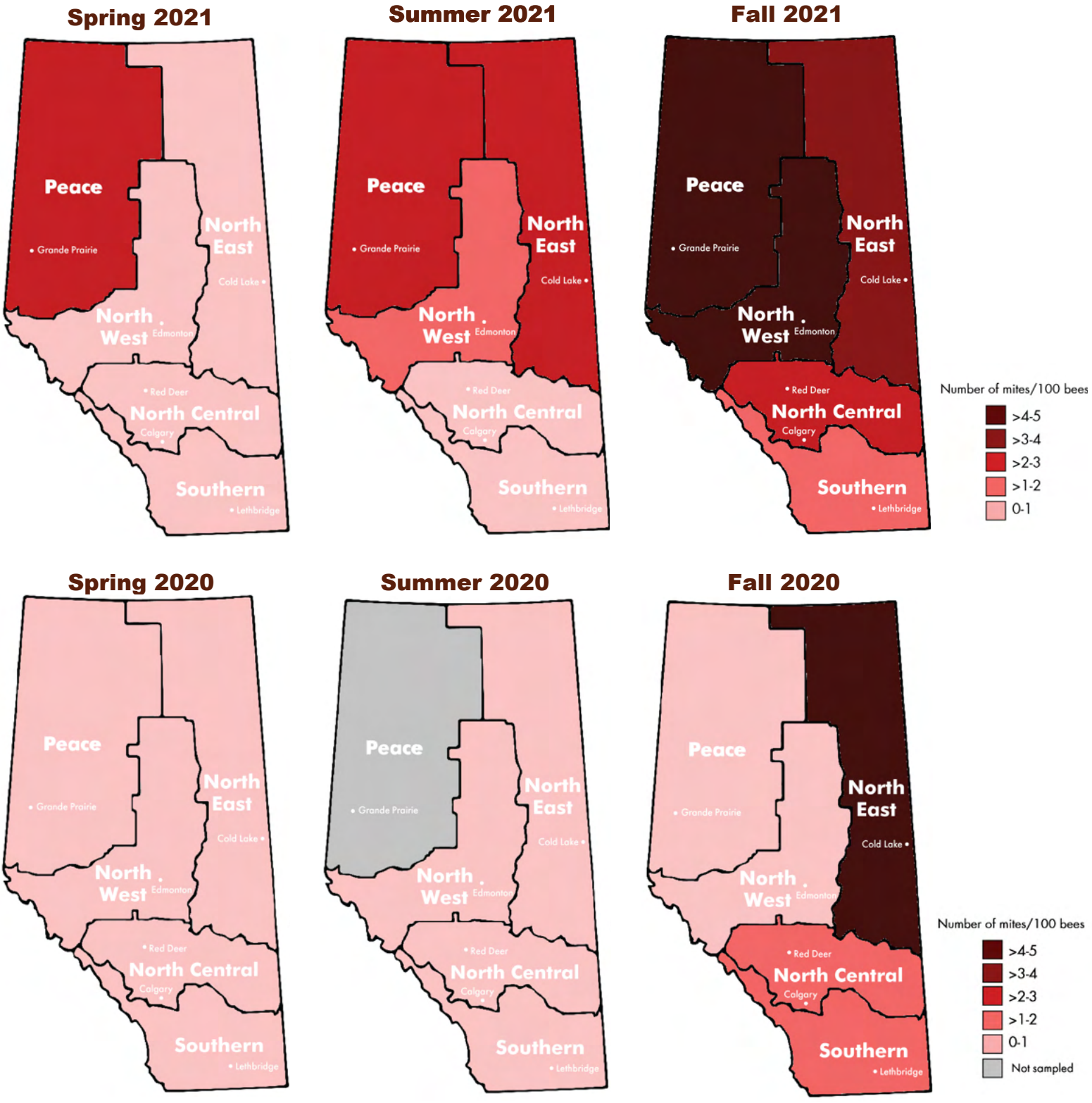


Figure 3. Regional average of *Varroa* mite infestation (number of mites per 100 bees) by season and year, detected using laboratory alcohol washes of adult bees.

RESULTS

Average Virus Levels

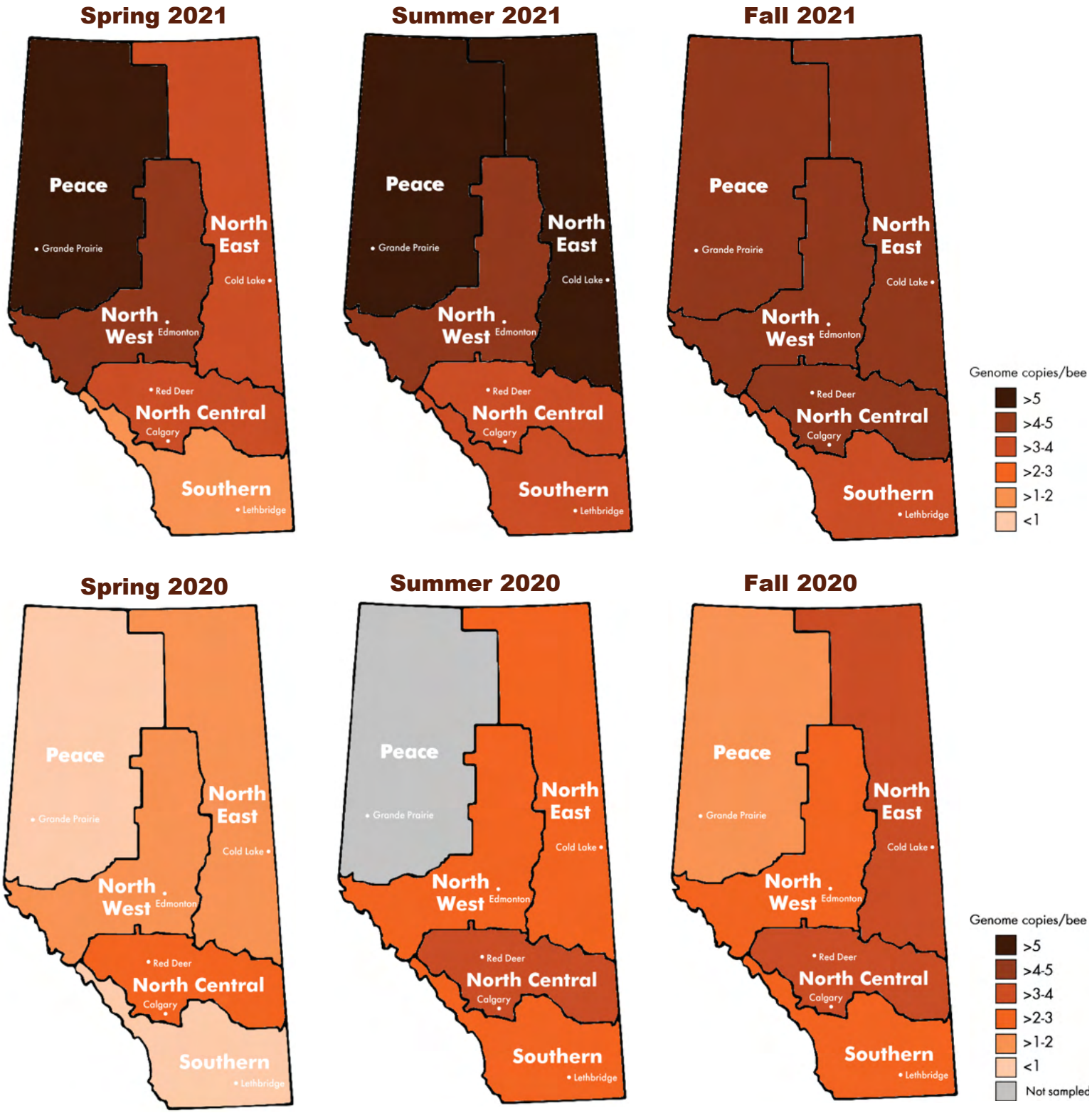


Figure 4. Regional average of overall virus load (genome copies per bee in $\log_{10}$ scale) by season and year, quantified by qPCR. Regional averages were calculated as the sum of genome copies from all viruses (SBV, VDV, DWV, CBPV, BQCV) in each region and divided by the number of samples to calculate the regional average for each season in 2020 and 2021.

RESULTS

Table 3. 2021 regional *Varroa* mite infestation level average, standard error and sample size (apiary).

Season	Region	Average (mite / 100 bees)	Standard Error	Sample size
Spring	Southern	0.03	0.01	28
Spring	North Central	0.07	0.03	17
Spring	North East	0.23	0.05	15
Spring	North West	0.27	0.08	14
Spring	Peace	2.40	1.02	10
Summer	Southern	0.35	0.07	23
Summer	North Central	0.32	0.13	17
Summer	North East	2.99	1.01	4
Summer	North West	1.68	0.54	8
Summer	Peace	2.21	0.69	4
Fall	Southern	1.19	0.31	28
Fall	North Central	2.71	1.15	17
Fall	North East	3.98	1.08	15
Fall	North West	4.62	1.50	14
Fall	Peace	4.19	0.73	10

Table 4. 2021 regional Nosema spore count average, standard error and sample size (apiary).

Season	Region	Average (spores/bee)	Standard Error	Sample size
Spring	Southern	1138392.96	264955.45	28
Spring	North Central	854779.65	333916.23	17
Spring	North East	671875.13	204337.66	15
Spring	North West	577567.14	176230.38	14
Spring	Peace	82031.30	200410.92	10
Summer	Southern	585937.6667	176413.85	23
Summer	North Central	217285.25	96211.26	16
Summer	North East	214844	90913.00	4
Summer	North West	336914.125	162228.23	8
Summer	Peace	39062.5	45105.49	4
Fall	Southern	330636.2857	95904.06	28
Fall	North Central	112592.0588	47827.85	17
Fall	North East	156250.0667	91092.68	15
Fall	North West	66964.35714	45677.22	14
Fall	Peace	667968.9	1004454.32	10

RESULTS

Table 5. Incidence of apiaries positive and negative for American Foulbrood in 2021 and sample size (apiary), per region.

Season	Region	Incidence % Positive	Incidence % Negative	Sample size
Spring	Southern	7.14	92.86	28
Spring	North Central	0.00	100.00	17
Spring	North East	0.00	100.00	15
Spring	North West	28.57	71.43	14
Spring	Peace	0.00	100.00	10
Summer	Southern	0.00	100.00	27
Summer	North Central	12.50	87.50	16
Summer	North East	0.00	100.00	4
Summer	North West	50.00	50.00	8
Summer	Peace	75.00	25.00	4
Fall	Southern	10.71	89.29	28
Fall	North Central	11.76	88.24	17
Fall	North East	0.00	100.00	15
Fall	North West	28.57	71.43	14
Fall	Peace	30.00	70.00	10

Table 6. Incidence of apiaries positive and negative for European Foulbrood in 2021 and sample size (apiary), per region.

Season	Region	Incidence % Positive	Incidence % Negative	Sample size
Spring	Southern	17.86	82.14	28
Spring	North Central	41.18	58.82	17
Spring	North East	40.00	60.00	15
Spring	North West	50.00	50.00	14
Spring	Peace	50.00	50.00	10
Summer	Southern	48.15	51.85	27
Summer	North Central	37.50	62.50	16
Summer	North East	100.00	0.00	4
Summer	North West	87.50	12.50	8
Summer	Peace	100.00	0.00	4
Fall	Southern	39.29	60.71	28
Fall	North Central	35.29	64.71	17
Fall	North East	46.67	53.33	15
Fall	North West	35.71	64.29	14
Fall	Peace	60.00	40.00	10

RESULTS

American Foulbrood (AFB) Risk Levels

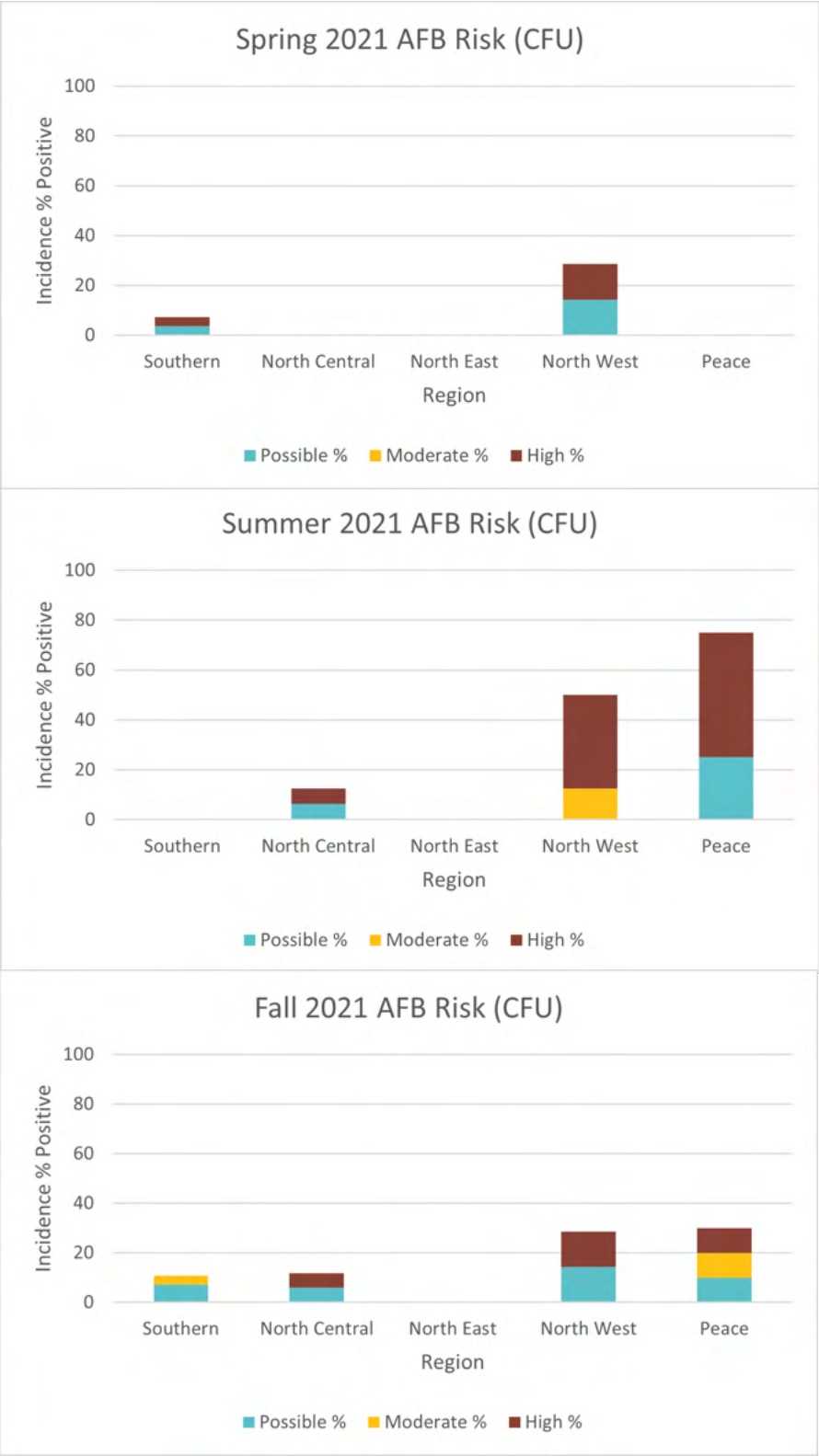


Figure 5. American foulbrood (AFB) risk levels by region and season. Positive samples for AFB were categorized into 3 groups for their propensity to develop clinical symptoms of the disease. Risk levels were designated based on the average number of CFUs (Colony Forming Units): Possible Risk (1-99 CFU), Moderate Risk (100-999 CFU) and High Risk (>1,000 CFU). The proportion of apiaries affected in each region is shown by the bar height.

RESULTS

American Foulbrood Culture Response to Antibiotic Exposure (rAFB)

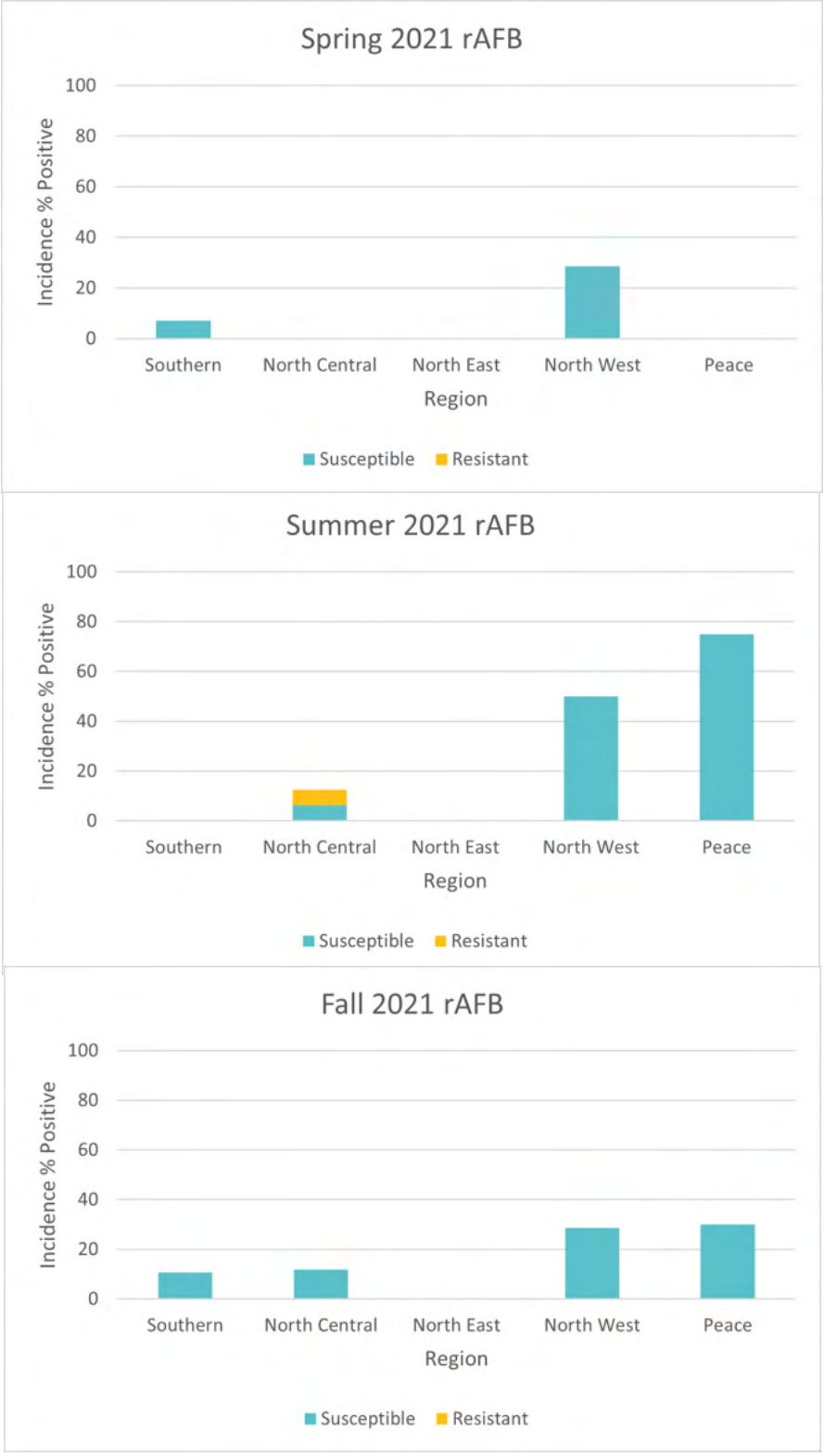
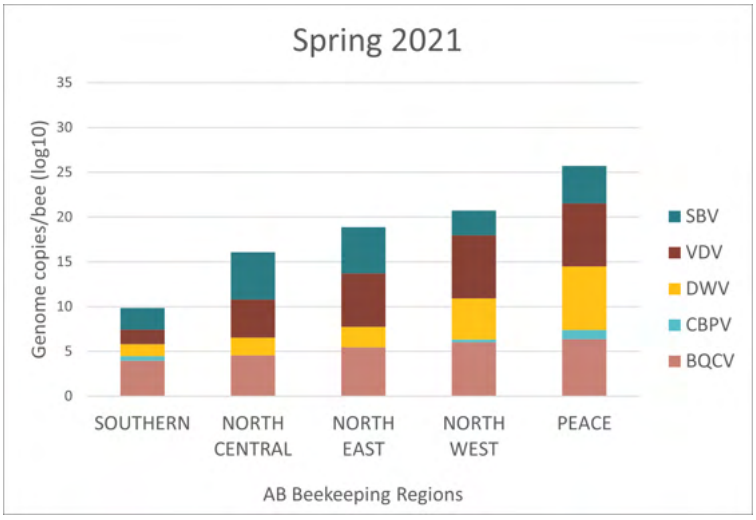
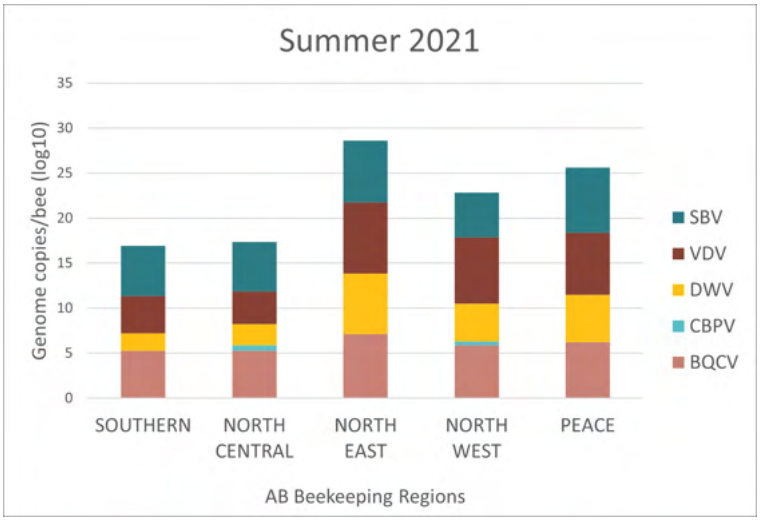


Figure 6. American foulbrood (AFB) culture response to antibiotic exposure. Positive samples for AFB were further analyzed for resistance or sensitivity to Oxytetracycline (OTC). The graph shows the proportion of positive samples that were sensitive or resistant to OTC. The proportion of resistant (yellow) and susceptible (blue) samples in each region is shown by the bar height.

RESULTS

2021 Virus Levels by Region and Season





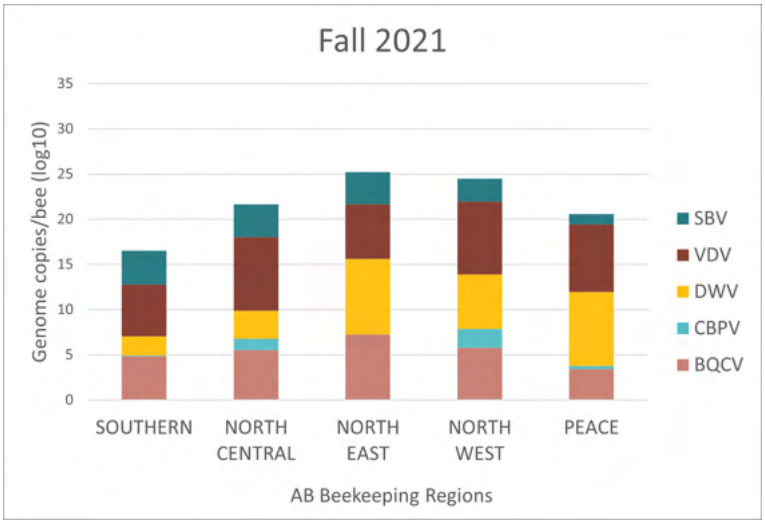


Figure 7. Average virus level (genome copies/bee), by season and region. Regional averages for each virus was calculated as the sum of genome copies, for that specific virus, in each region and divided by the number of samples to calculate the regional average for each season. The regional abundance of each virus is shown by the bar height of its colour-coded segment. Sacbrood Virus = SBV, Varroa Destructor Virus = VDV, Deformed Wing Virus = DWV, Chronic Bee Paralysis Virus = CBPV and Black Queen Cell Virus = BQCV.

RESULTS

2021 Virus Seasonal Change

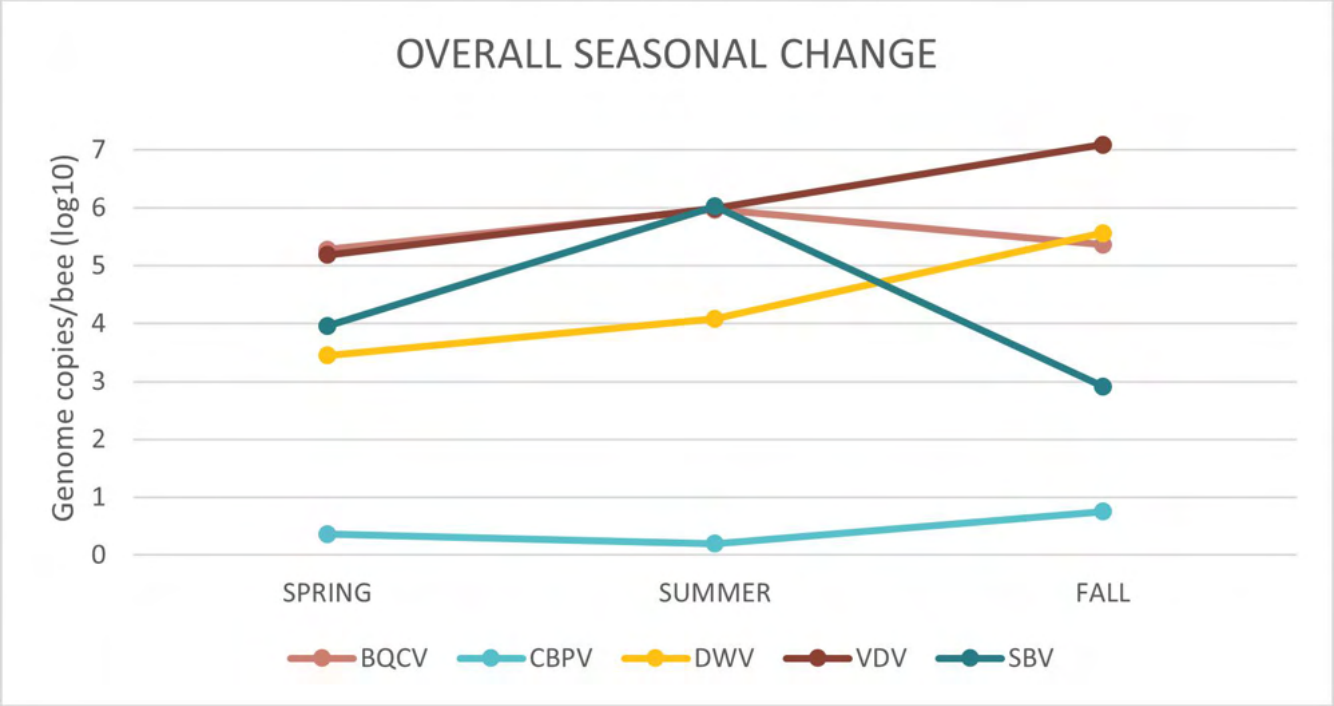


Figure 8. Overall change of each virus shown as the average virus level (genome copies/bee) by season. Virus abundance was calculated as the sum of genome copies, for that specific virus, and divided by the number of samples to calculate the average for each season.

RESULTS

2021 Virus Prevalence

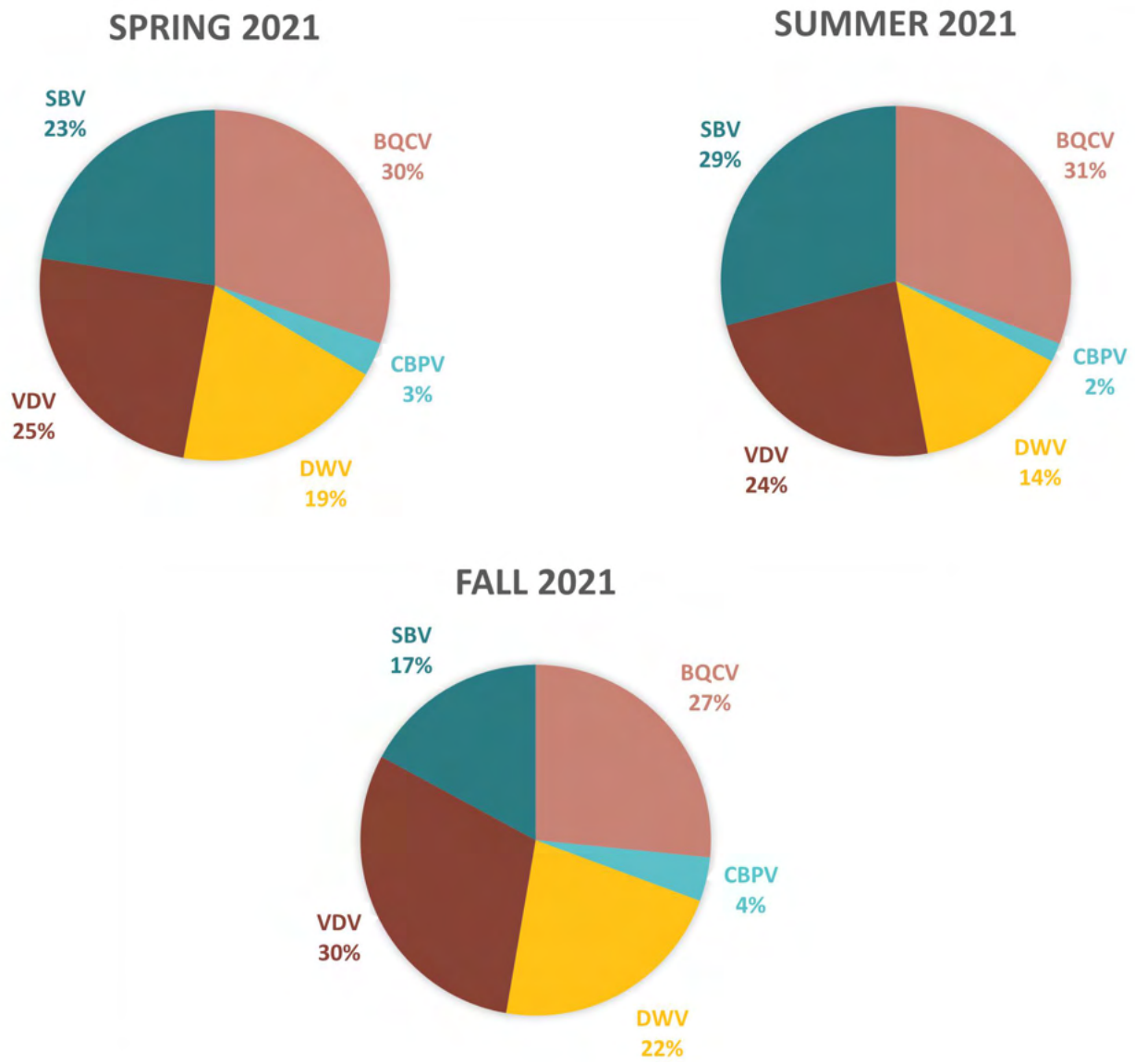


Figure 9. Virus prevalence by season. Percentage of the combined virus population (all regions) with quantifiable levels of Black Queen Cell Virus (BQCV), Chronic Bee Paralysis Virus (CBPV), Deformed Wing Virus (DWV), Varroa Destructor Virus (VDV) and Sacbrood Virus (SBV) during spring, summer and fall.

SUMMARY

The colony health monitoring (CHM) is one of the main TTP programs. The CHM is a disease diagnostic service with the goal to provide the beekeeper colony inspection data and a disease evaluation of their apiary. Beekeepers can then use the data we provide to evaluate their IPM plan and decide if it needs to be adjusted. Our job is not to interfere or police beekeeper's management strategies but to provide guidance.

Historical data can show us seasonal and annual pathogen trends, and by combining years of data into a large dataset, we can then study the relationship among pathogens and how the increase in one pathogen population can affect another pathogen population. This report contains the data we have collected in the past 2 years from participating CHM colonies. Below you will find a summary of the data provided:

Nosema:

- Nosema levels were mostly under 1 million spores/bee throughout 2020.
- Nosema levels were higher in the spring of 2021 compared to the spring of 2020. All regions showed average spore levels above 2 million spores/bee. However, Nosema levels decreased as the 2021 season progressed and fall levels were similar to those in 2020 (less than 1 million spores/bee).

AFB:

- AFB was detected in most regions in 2021. The only region with no incidence of AFB was the North-East.
- A total of 15 samples were found positive for AFB in 2021, compared to 31 in 2020. Only 1 out of 15 samples (6.6%) with detected *Paenibacillus larvae* spores indicated resistance to the antibiotic Oxytetracycline (rAFB). This is a decrease from 25.8% of rAFB samples found in 2020.

EFB:

- In 2021 EFB was detected in all regions in the spring, summer and fall. Similarly to 2020, the highest incidence of EFB was found in the summer. EFB incidence in the summer was 100% in the Peace and North-East regions.

Varroa mite:

- In 2020 the average mite infestation level was under 1% in the spring and summer in all regions. In the fall, the levels were slightly higher but still under the fall threshold of 3%, except in the North-East region.
- In 2021, the average mite infestation level in the spring was above 2% in the Peace, while all other regions showed average levels below 1%. In the summer, the mite infestation level in the Peace was similar to the spring and the North-East and North-West regions showed higher levels, compared to the spring. By the fall, the North-East, North-West, and the Peace regions had average levels higher than the fall economic threshold of 3%. The only region with an average mite level below the fall threshold was the Southern region.

SUMMARY

Viruses:

- Overall virus load was higher in 2021 compared to 2020 during all three seasons.
- Deformed Wing Virus (DWV), Varroa Destructor Virus (VDV) and Chronic Bee Paralysis Virus (CBPV) populations increased from spring to fall while Black Queen Cell Virus (BQCV) and Sacbrood Virus (SBV) populations followed the opposite trend.
- Average viral levels followed average mite population levels closely, and high virus levels were observed in regions with high mite levels.

Several published studies have shown that an increase in the colony varroa mite population can cause an increase in the population of varroa-related viruses. Our data supports those findings and shows that:

- The correlation value between mite infestation level and DWV and VDV indicates a moderate to strong relationship between these two pathogens, 0.4 and 0.5 respectively. In other words, our data shows that there is a moderate to strong association between varroa mite population level and levels of DWV and VDV in the bee population sampled during the 2020 and 2021 CHM program. This also indicates that changes in the mite population level are associated with changes in the DWV and VDV population level.

We took an additional step to understand how much DWV and VDV levels increase with an increase of the mite population level. Our data shows that:

- For every increase of the mite population level by 1%, the DWV population will increase by 4.82% and the VDV population by 6.17%.

MEET THE CHM TEAM

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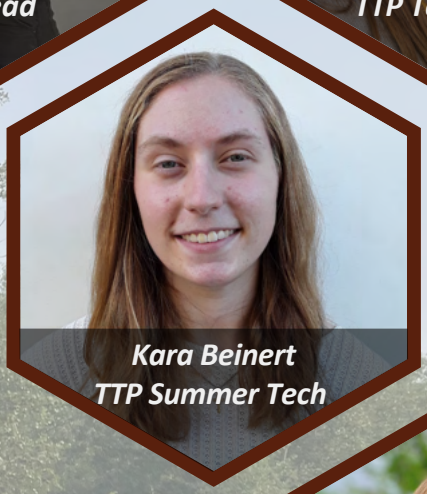

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ALBERTA TECH TRANSFER PROGRAM

The success of this program would not have been possible without the hard work of each CHM team member