ALBERTA TECH TRANSFER PROGRAM

# COLONY HEALTH MONITORING PROGRAM


## 2020 REPORT

# ALBERTA REGIONAL MAP

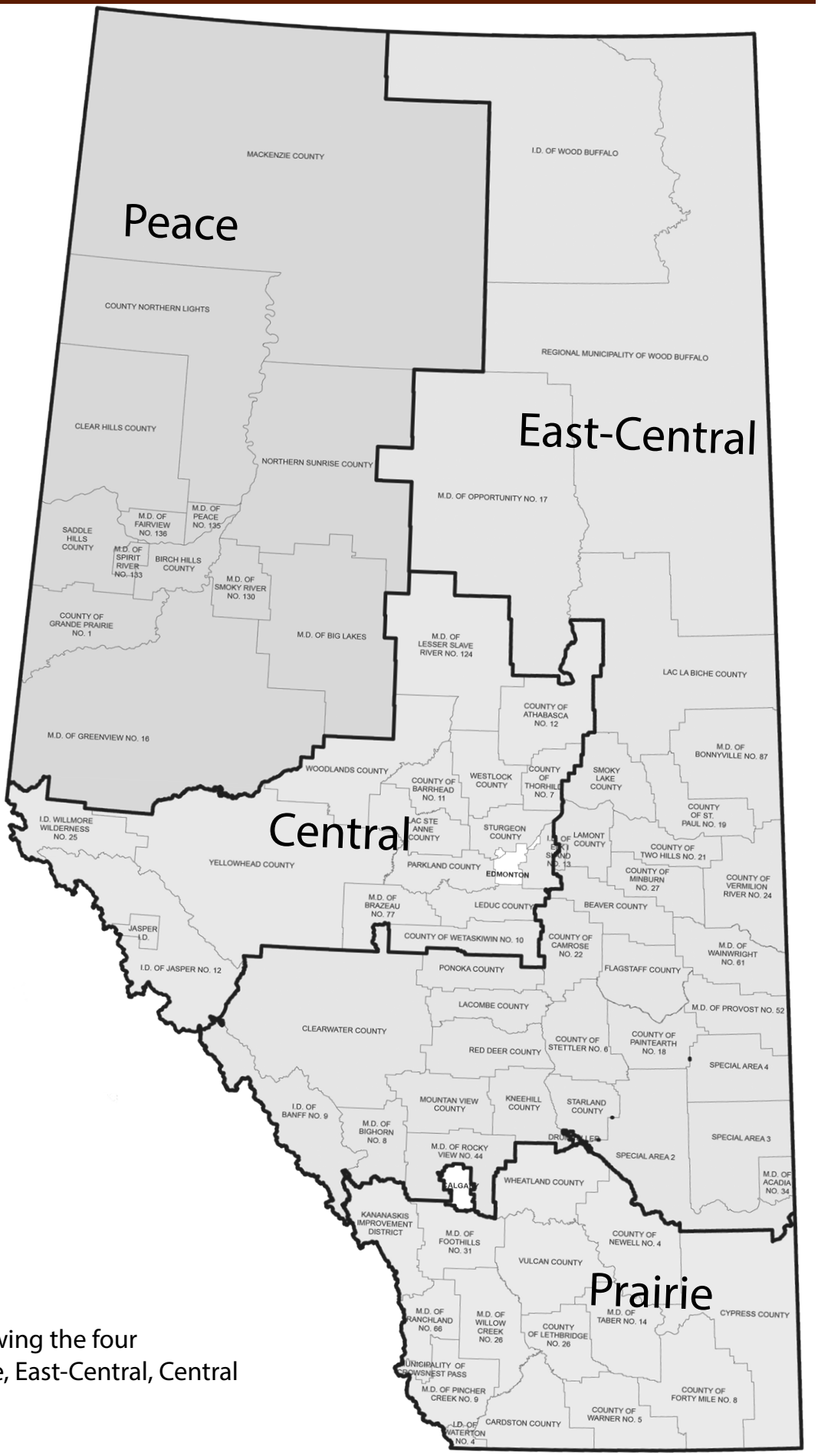



Figure 1. Alberta regional map. showing the four beekeepers' region of Alberta: Peace, East-Central, Central and Prairie.

# 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 each beekeeper 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 | East-Central | Central | Prairie |
| Season | Spring | 10 | 38 | 13 | 26 |
| | Summer | - | 26 | 1 | 26 |
| | Fall | 9 | 41 | 13 | 26 |

**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

## *Mite count*

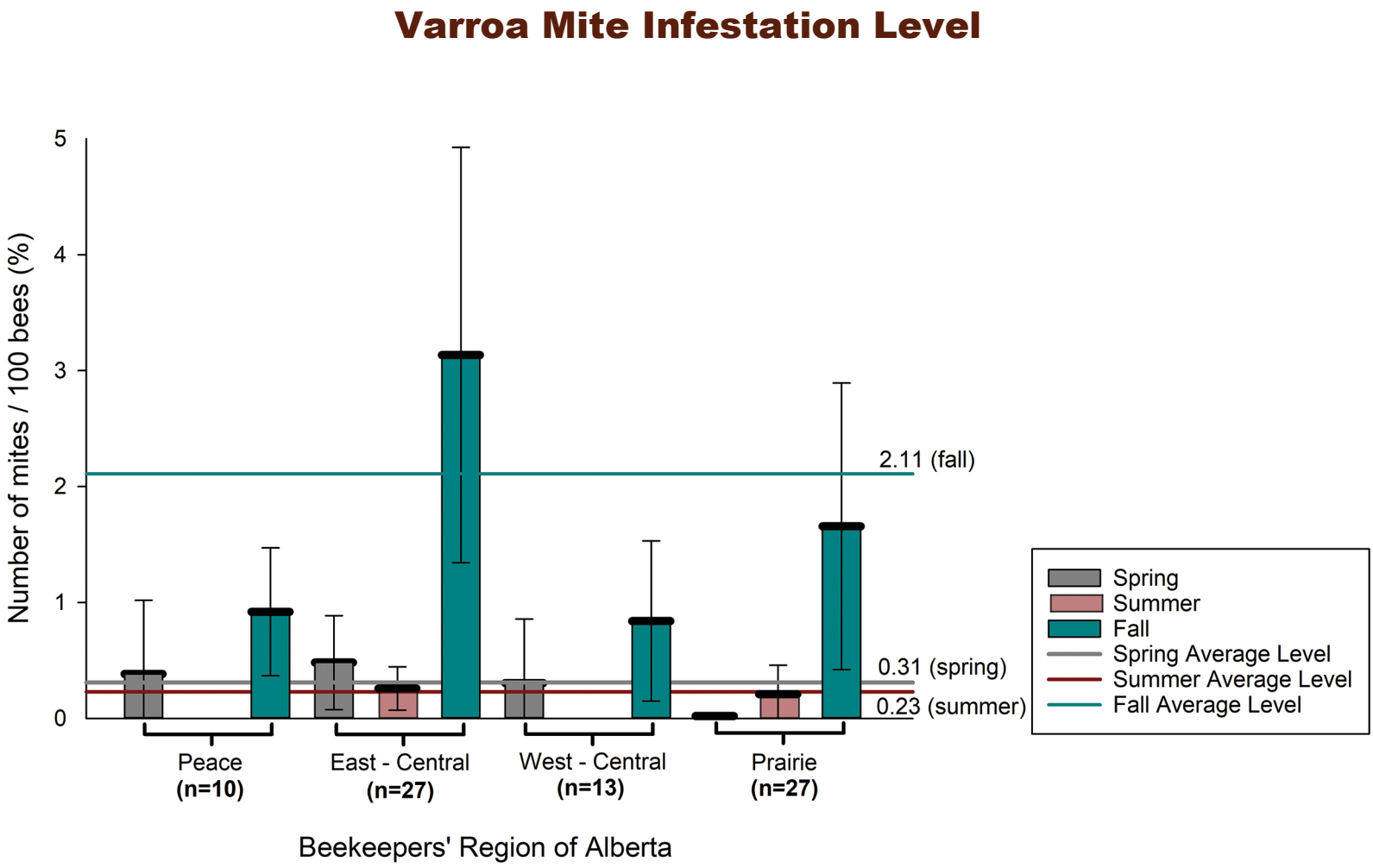



**Figure 2.** Number of mites per 100 adult workers was recorded for each sample and calculated as a percentage of infestation.

# RESULTS

## *Nosema spore count*

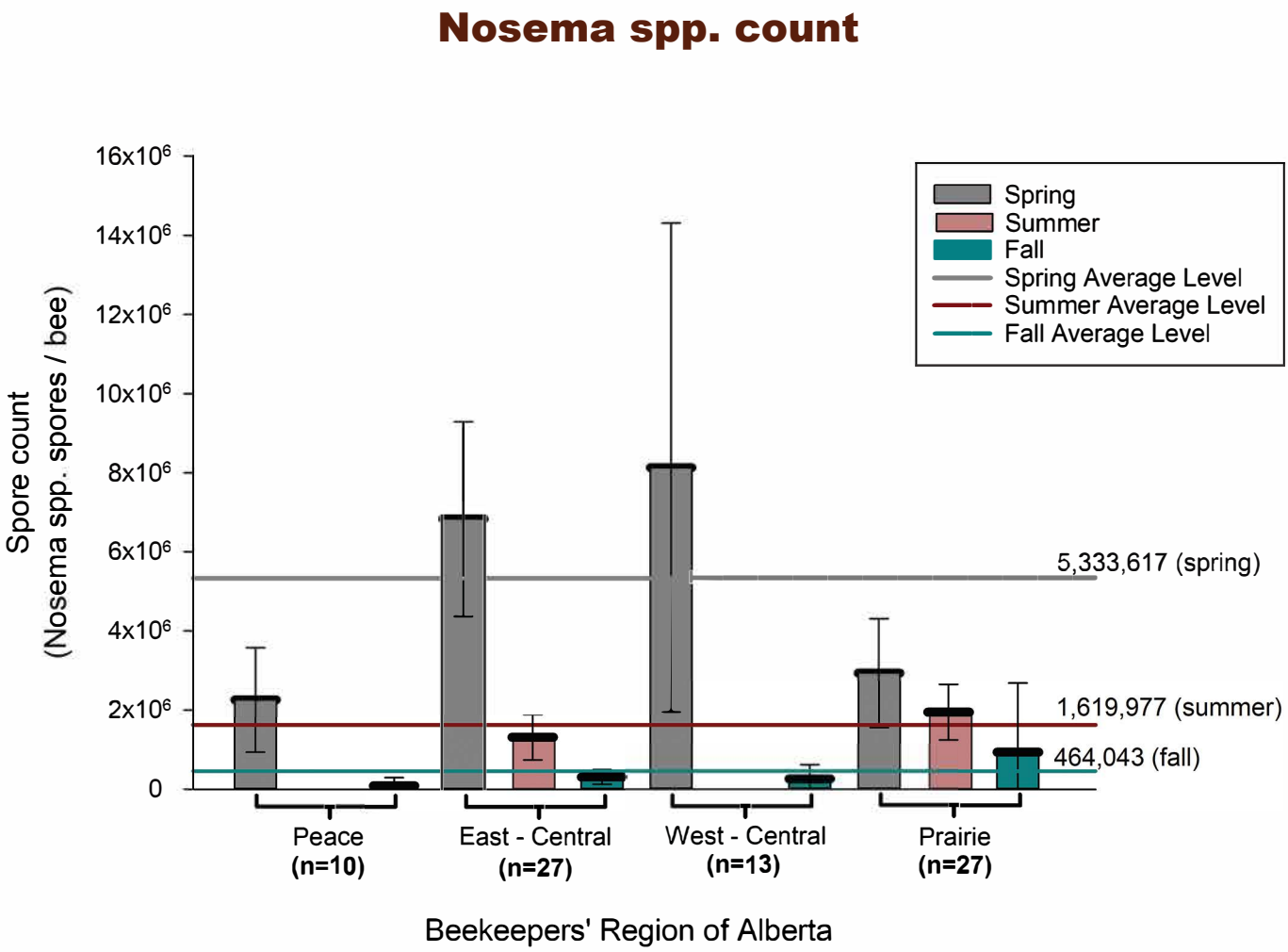



**Figure 3.** Average nosema spore count per bee. Approximately 150 bees from 10 colonies in each apiary were pooled and an aliquot of the homogenized sample was used to assess Nosema spp. infection level.

# RESULTS

## *American foulbrood prevalence*

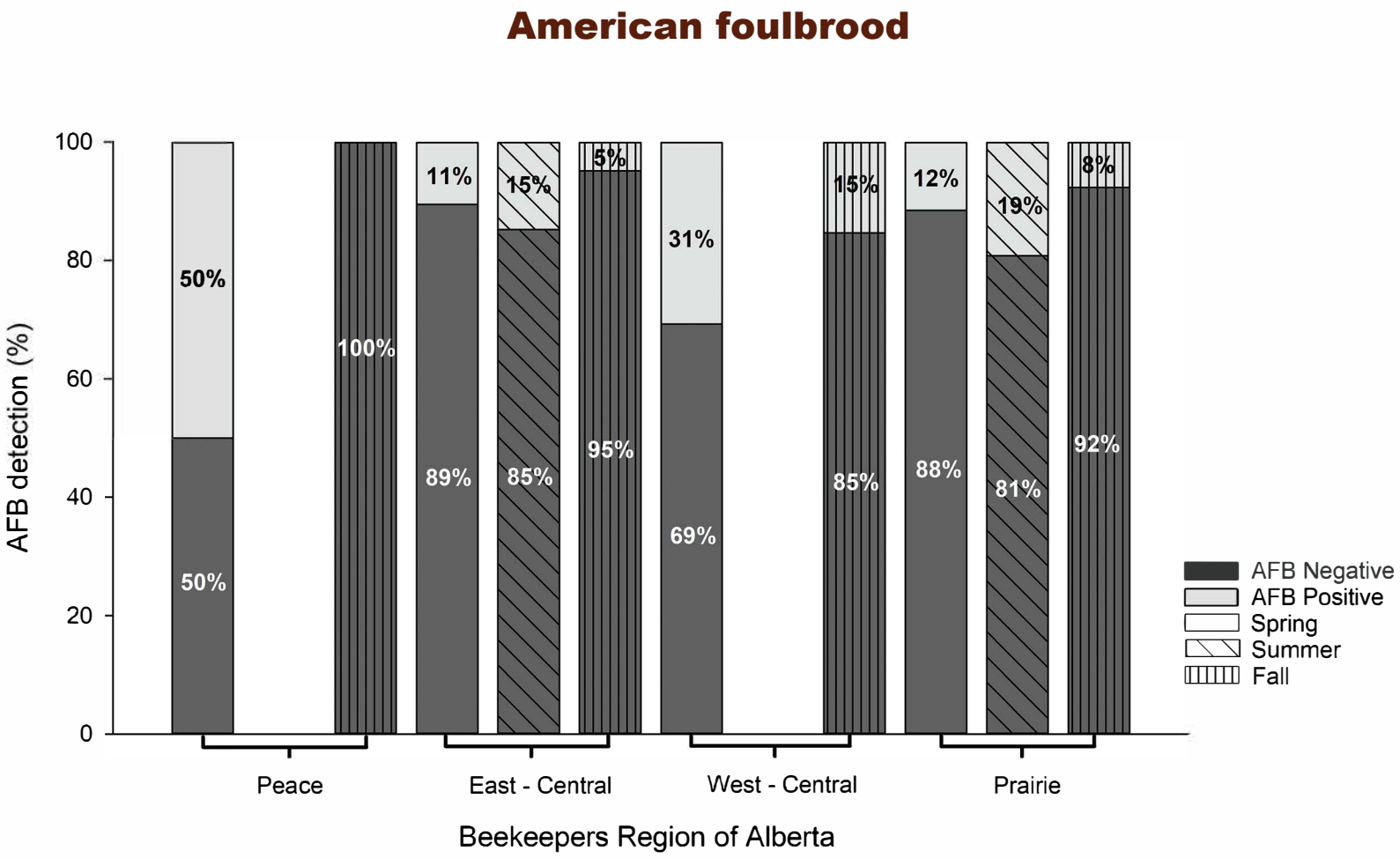



**Figure 4.** Proportion of American foulbrood (AFB) detection calculated by combining the total number of apiaries with detected (positive) presence of *Paenibacillus larvae* (causative agent of AFB) and dividing that by the total number of apiary samples analyzed. The proportion of apiaries with undetected (negative) presence of *P. larvae* was calculated in the same way. The data is expressed as percentage.

# RESULTS

## *European foulbrood prevalence*

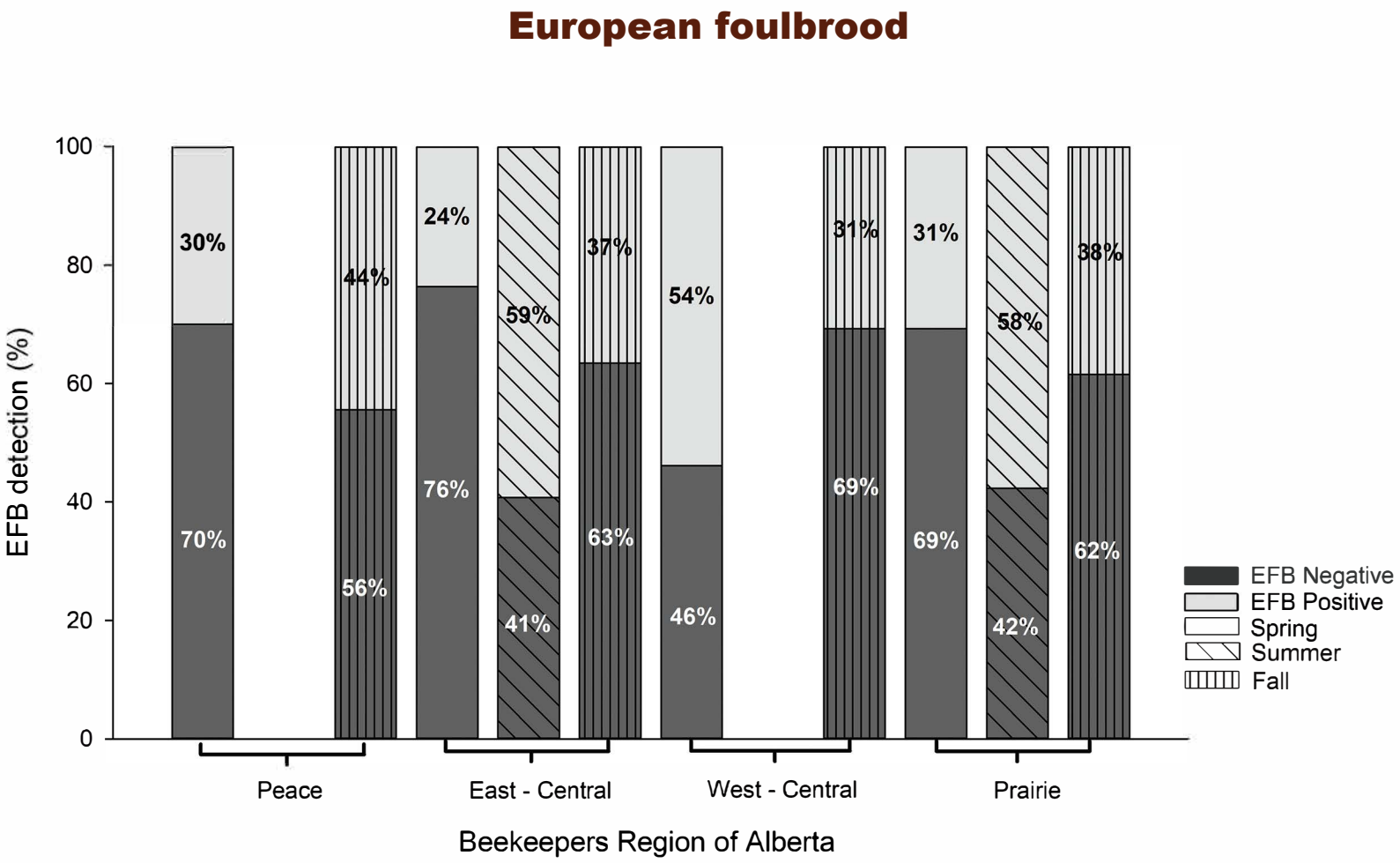



**Figure 5.** Proportion of European foulbrood (EFB) detection calculated by combining the total number of apiaries with detected (positive) presence of *Melissococcus plutonius* (causative agent of EFB) and dividing that by the total number of apiary samples analyzed. The proportion of apiaries with undetected (negative) presence of *M. plutonius* was calculated in the same way. The data is expressed as percentage.

# RESULTS

## *Absolute DWV count*

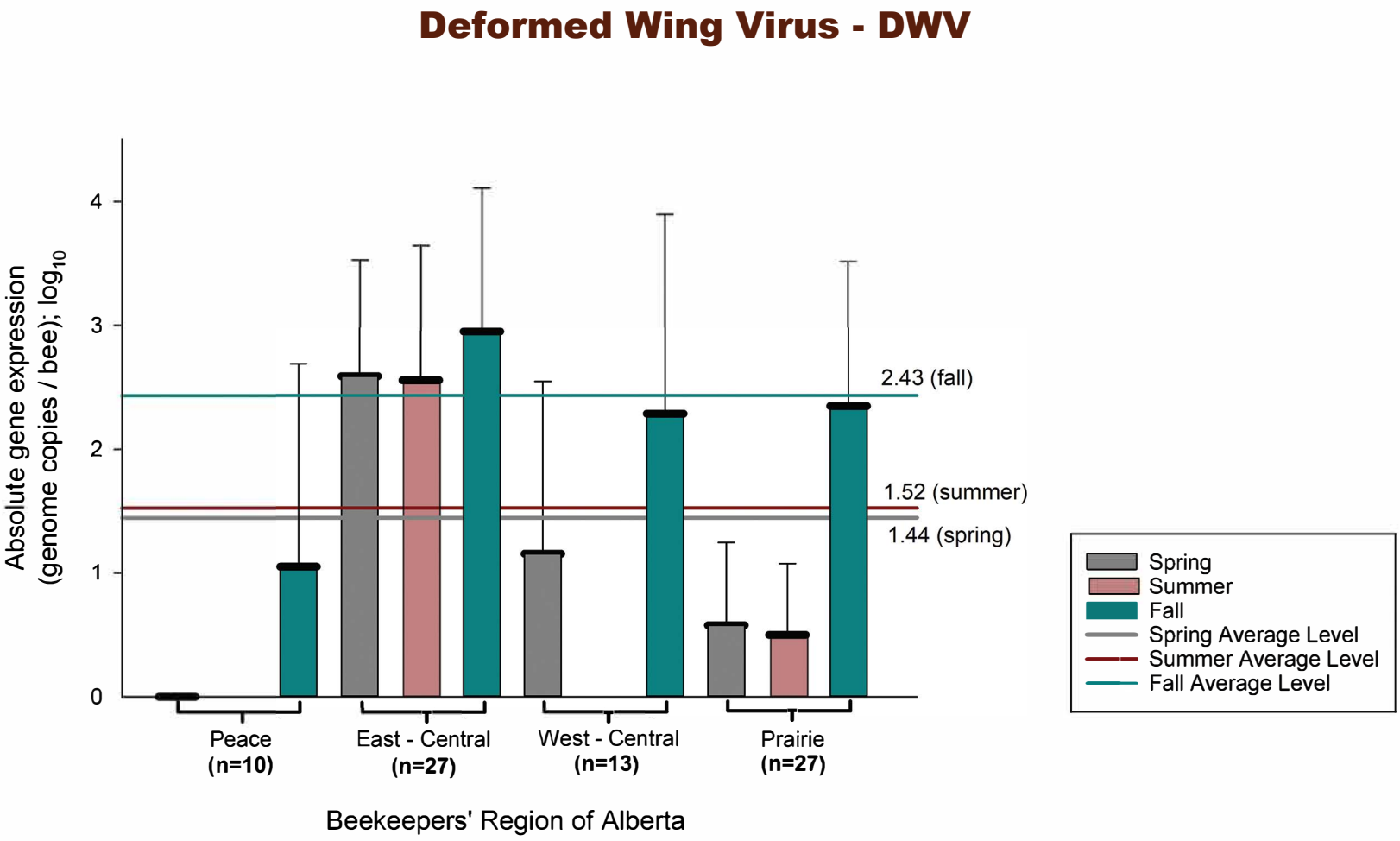



**Figure 6.** Genome copies of DWV per bee. Quantification of DWV was determined by real-time PCR using previously published methods. Virus copy numbers shown here were $\log_{10}$ transformed.

## *Absolute VDV count*

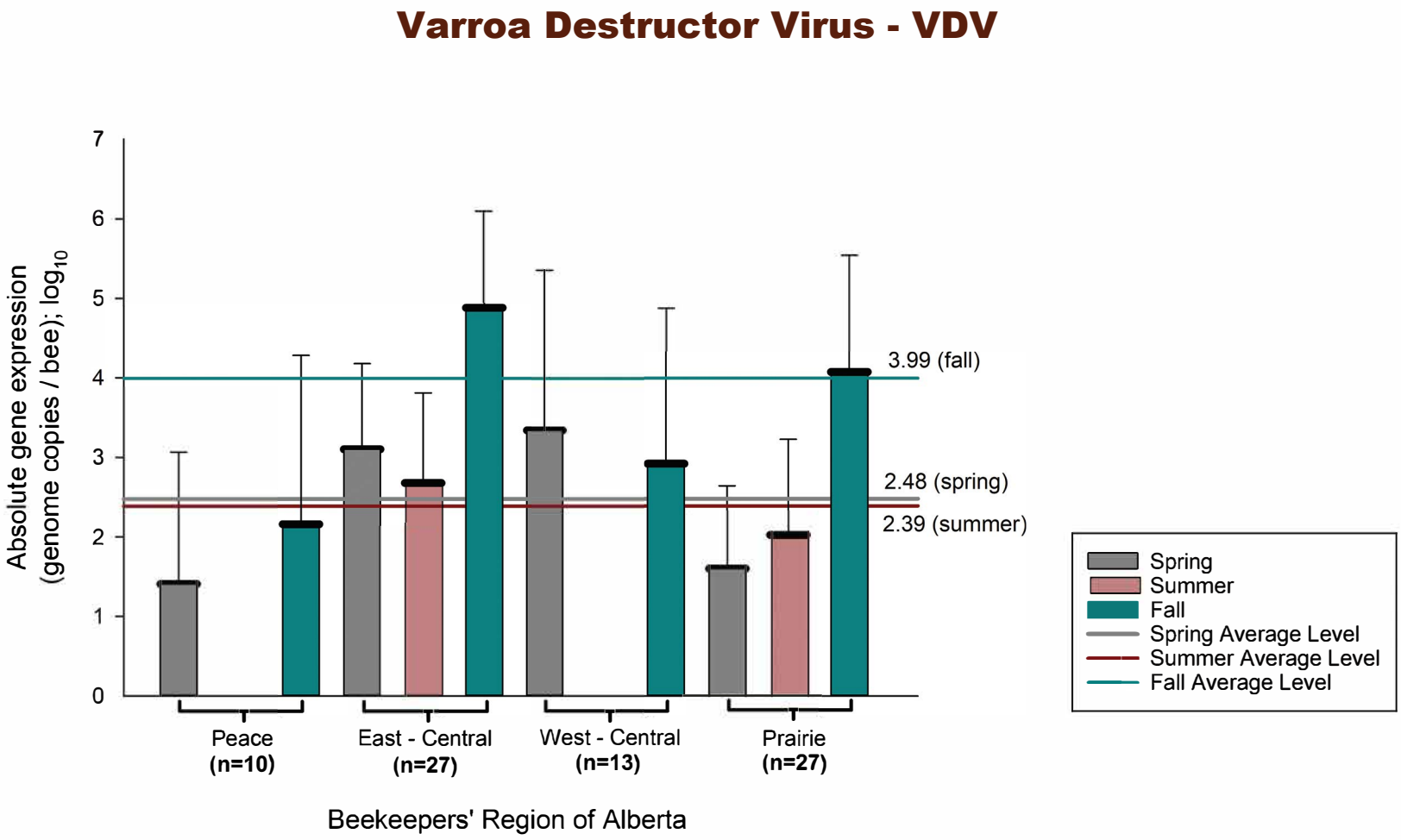



**Figure 7.** Genome copies of VDV per bee. Quantification of VDV was determined by real-time PCR using previously published methods. Virus copy numbers shown here were $\log_{10}$ transformed.

# RESULTS

## *Absolute SBV count*

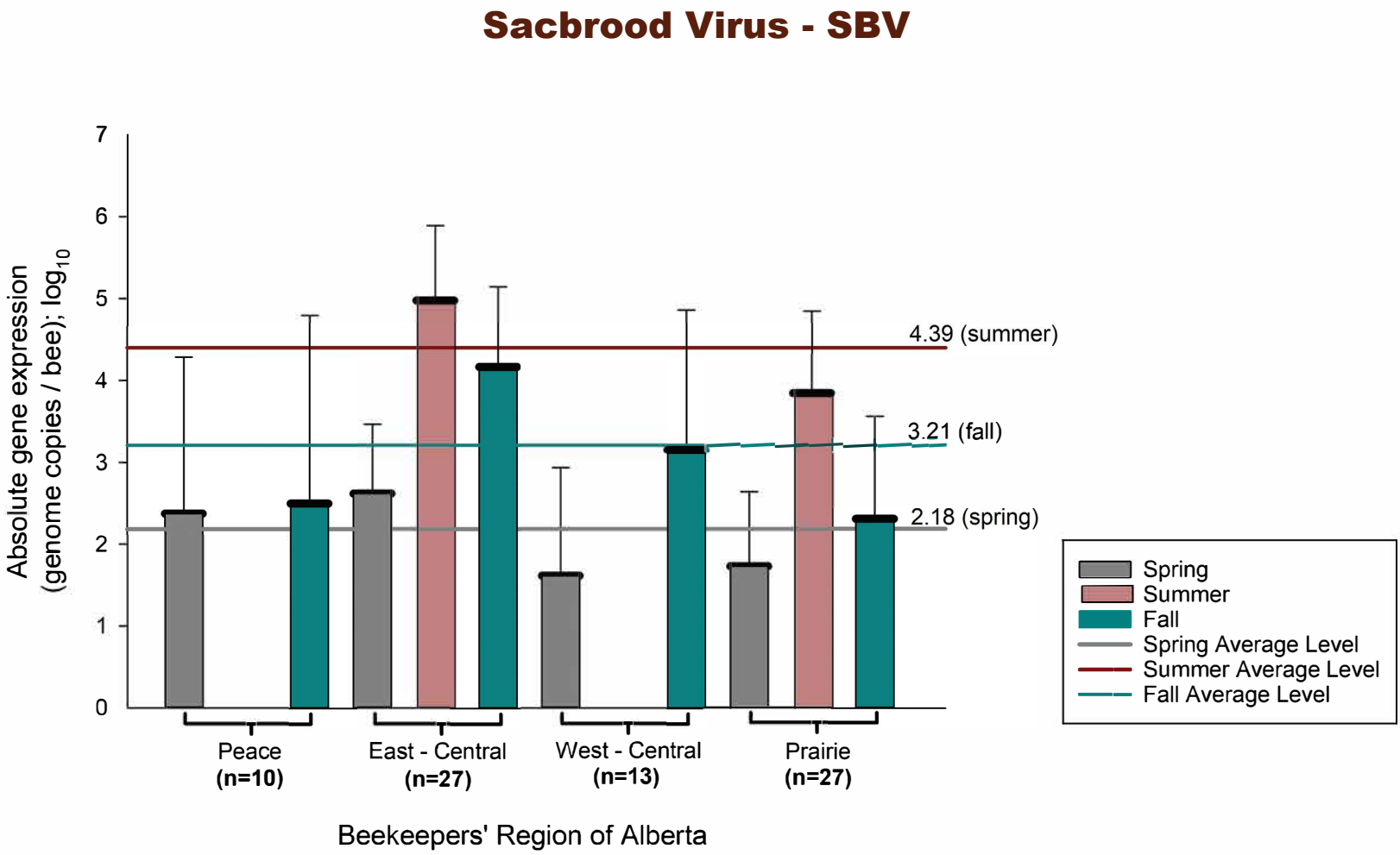



**Figure 8.** Genome copies of SBV per bee. Quantification of SBV was determined by real-time PCR using previously published methods. Virus copy numbers shown here were $\log_{10}$ transformed.

## *Absolute CBPV count*

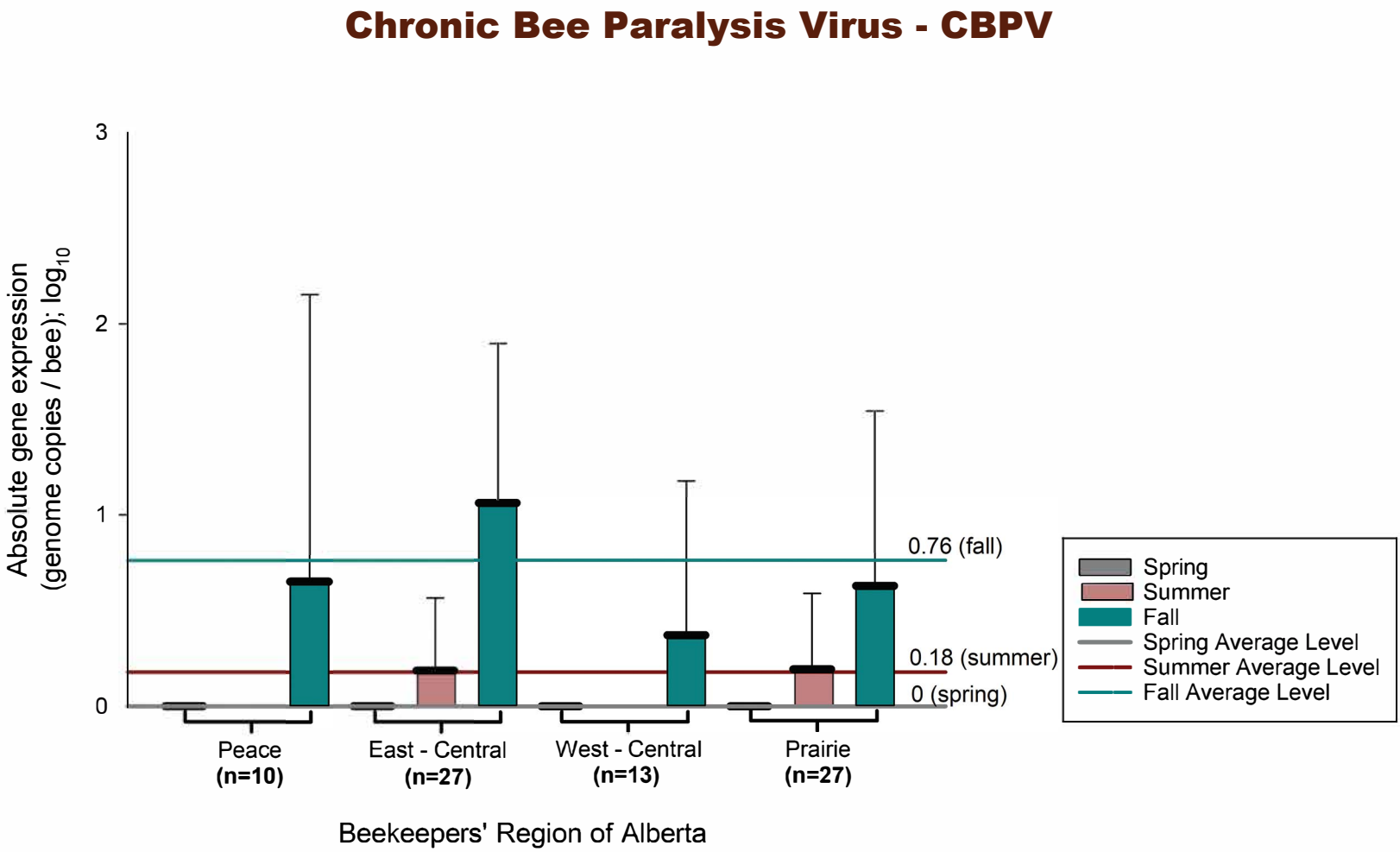



**Figure 9.** Genome copies of CBPV per bee. Quantification of CBPV was determined by real-time PCR using previously published methods. Virus copy numbers shown here were $\log_{10}$ transformed.

## *Absolute BQCV count*

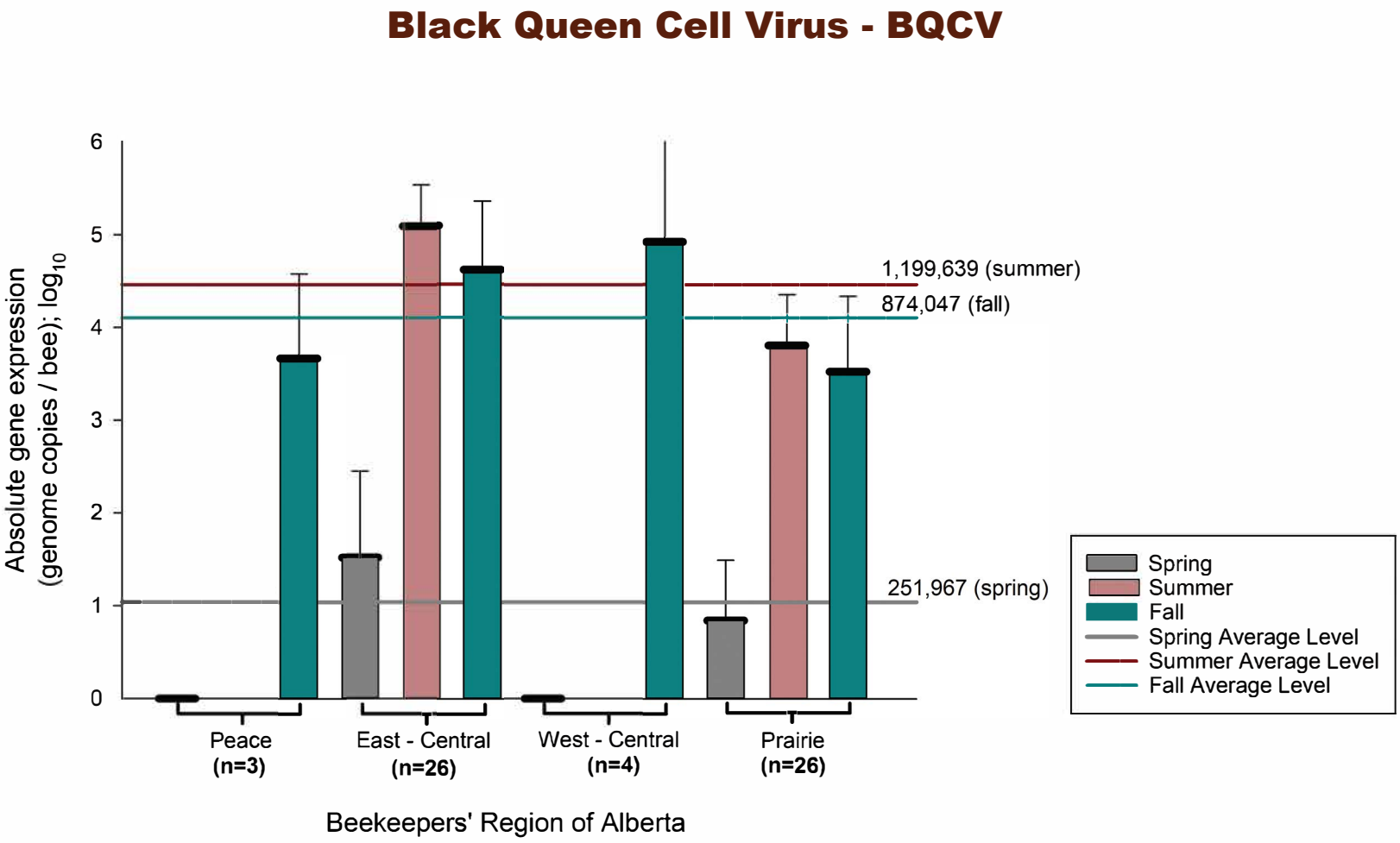



**Figure 10.** Genome copies of BQCV per bee. Quantification of BQCV was determined by real-time PCR using previously published methods. Virus copy numbers shown here were $\log_{10}$ transformed.

## *Virus abundance seasonal change*

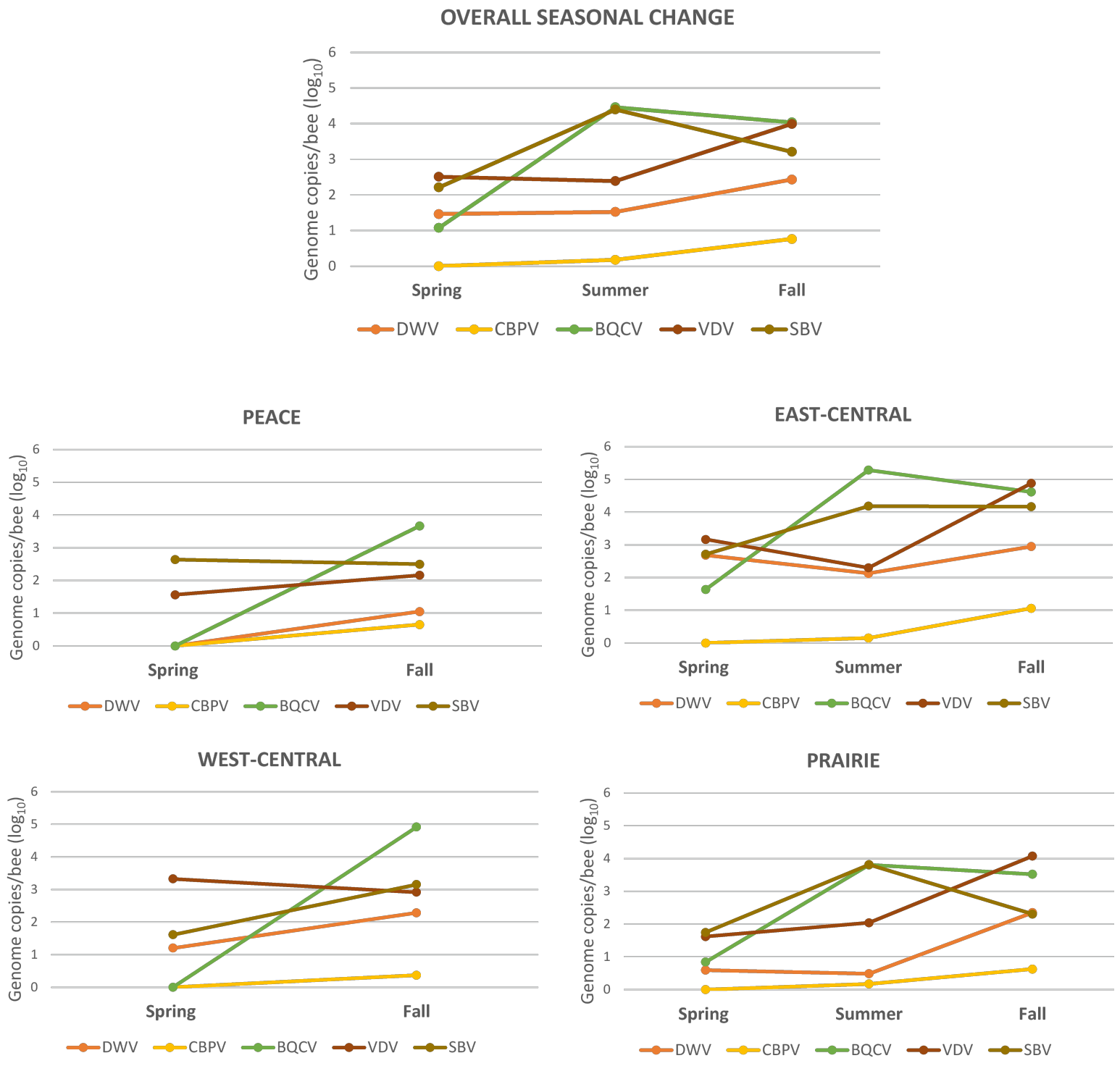



**Figure 11.** Virus abundance at the apiary level. Temporal change of total virus population for each region. The total abundance of each virus was calculated as the sum of the abundance data of all apiaries for each region divided by the total number of apiaries sampled for the specific region.

## *Virus prevalence*

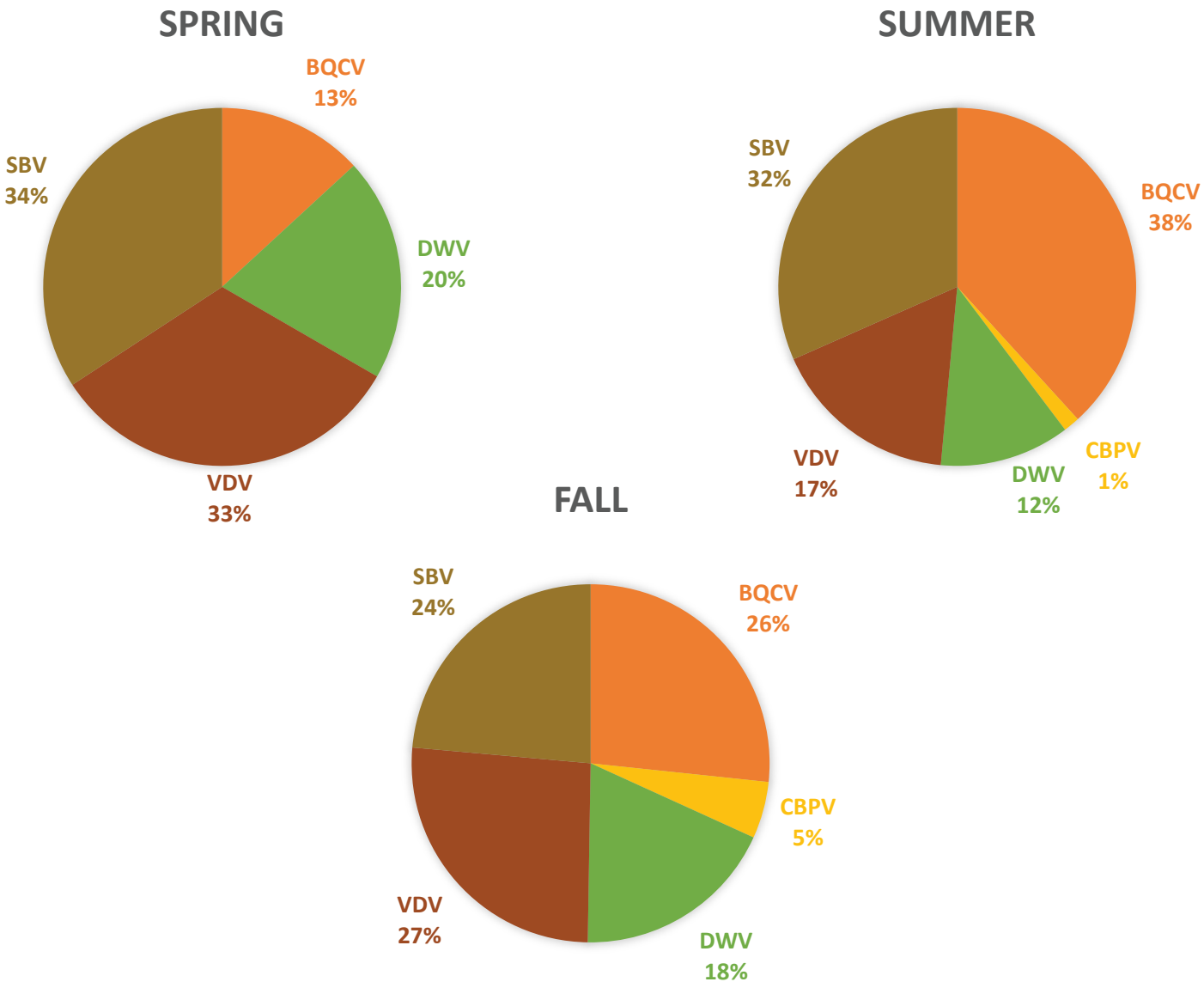



**Figure 12.** Virus prevalence by season. Percentage of the combined population (all regions) with quantifiable levels of Black Queen Cell Virus (BQCV), Chronic Bee Paralysis Virus (CBPV), Deformed Wing Virus (DWV), Varroa Destructor Virus (VDV) and Sacbrood Virus (SBV) during spring, summer and fall.

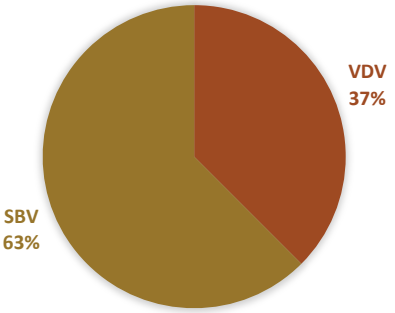
**Figure 13** ***(next page)*****.** Virus prevalence by region and season. Percentage of the population in each region with quantifiable levels of Black Queen Cell Virus (BQCV), Chronic Bee Paralysis Virus (CBPV), Deformed Wing Virus (DWV), Varroa Destructor Virus (VDV) and Sacbrood Virus (SBV) during spring, summer and fall.

# RESULTS

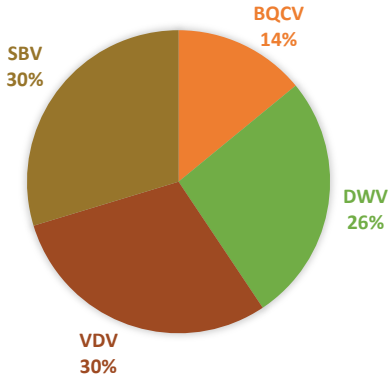
## *Virus prevalence (by region)*

### SPRING

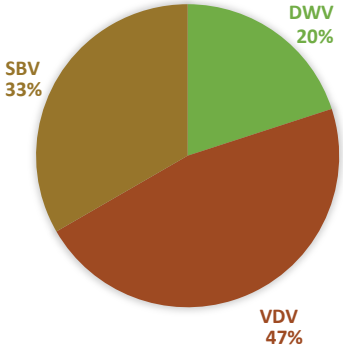
#### PEACE



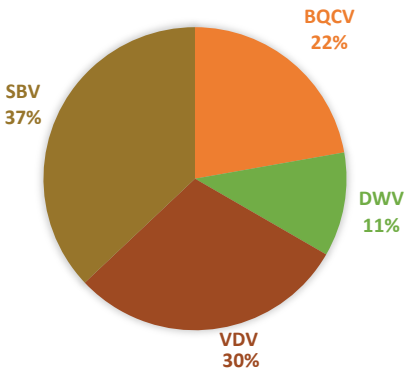

#### EAST-CENTRAL




#### WEST-CENTRAL

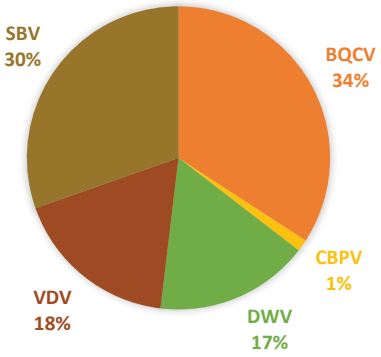



#### PRAIRIE

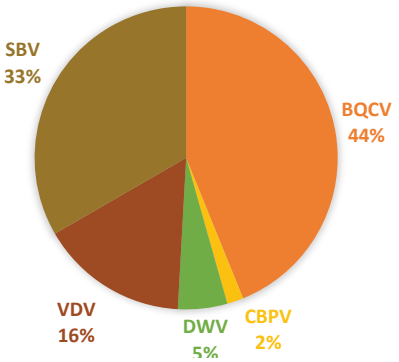



### SUMMER

#### EAST-CENTRAL

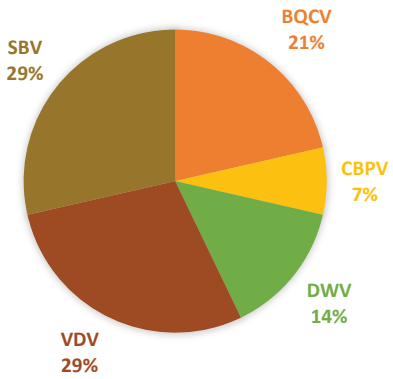



#### PRAIRIE

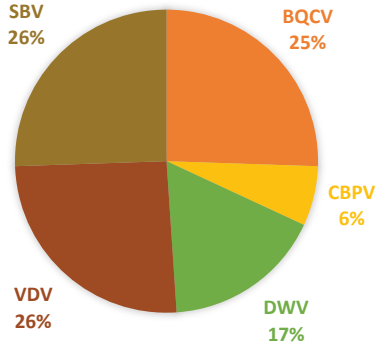



### FALL

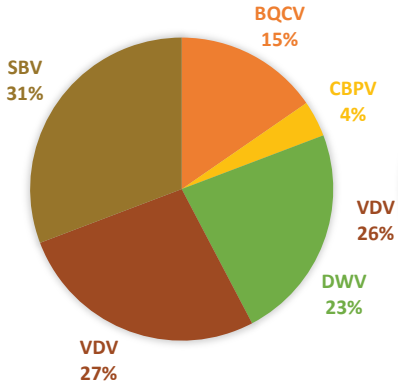
#### PEACE




#### EAST-CENTRAL




#### WEST-CENTRAL

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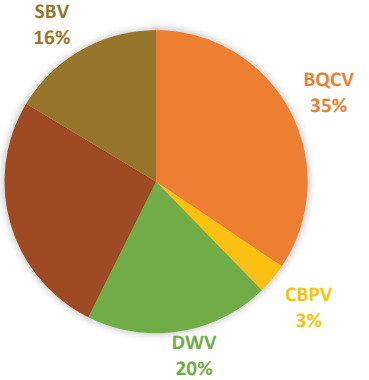


# SUMMARY


❖ Average spring mite infestation level was below the spring economic threshold (1%) in all four regions, with infestation levels ranging from 0 – 5.5%.

❖ Average mite infestation level numbers increased from spring to fall in all four regions. Fall mite infestation levels ranged from 0 – 21%, with the average level in the east-central region staying above the fall economic threshold (3%).

❖ Higher levels of Nosema were detected in the spring compared to the summer and fall. Nosema spring levels ranged from 0 – 37,000,000, while the highest spore/bee detection in the summer and fall were 6,000,000 and 2,000,000, respectively.

❖ AFB was detected in the spring and fall in all regions, except in the Peace, where AFB was only detected in the spring. Eight out of 31 samples (25.8%) with detected *Paenibacilus larvae* spores indicated resistance to the antibiotic Oxytetracycline (fall and spring combined).

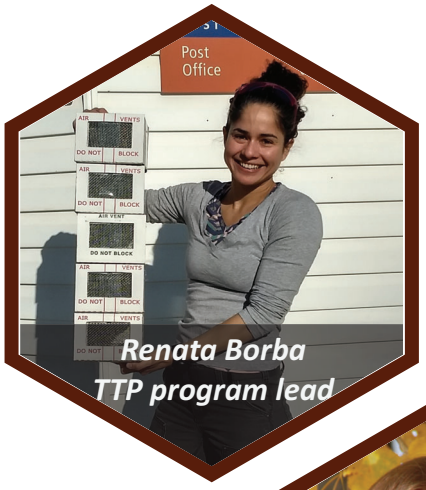
❖ EFB was detected in all regions during all three sampling periods. The highest incidence of EFB was found in the summer in colonies from the East-central (59%) and the prairies (58%).

❖ Overall, virus level increased from spring to fall, which is in accordance with previously published data.

❖ Varroa Destructor Virus (VDV) was the most abundant and prevalent virus in the spring and fall among all regions.

❖ Chronic Bee Paralysis Virus (CBPV) was not detected in the spring. As the season progressed, CBPV prevalence increased from 0% in the spring to 1% and 5% in the summer and fall, respectively.

# MEET THE CHM TEAM

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*TTP summer tech*

*Aaron Toma*
*Program support*

*Cameron Sande*
*Sampling tech*

*Elena Battle*
*Sampling tech*

*Rhonda Thygesen*
*TTP volunteer*

*Emily Olson*
*CHM collaborator*

*Ali Panasiuk*
*CHM collaborator*


*Cass Docherty*
*CHM collaborator*

*Jason Lang*
*CHM collaborator*

*Wyatt Carson*
*CHM collaborator*

ALBERTA TECH TRANSFER
PROGRAM

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