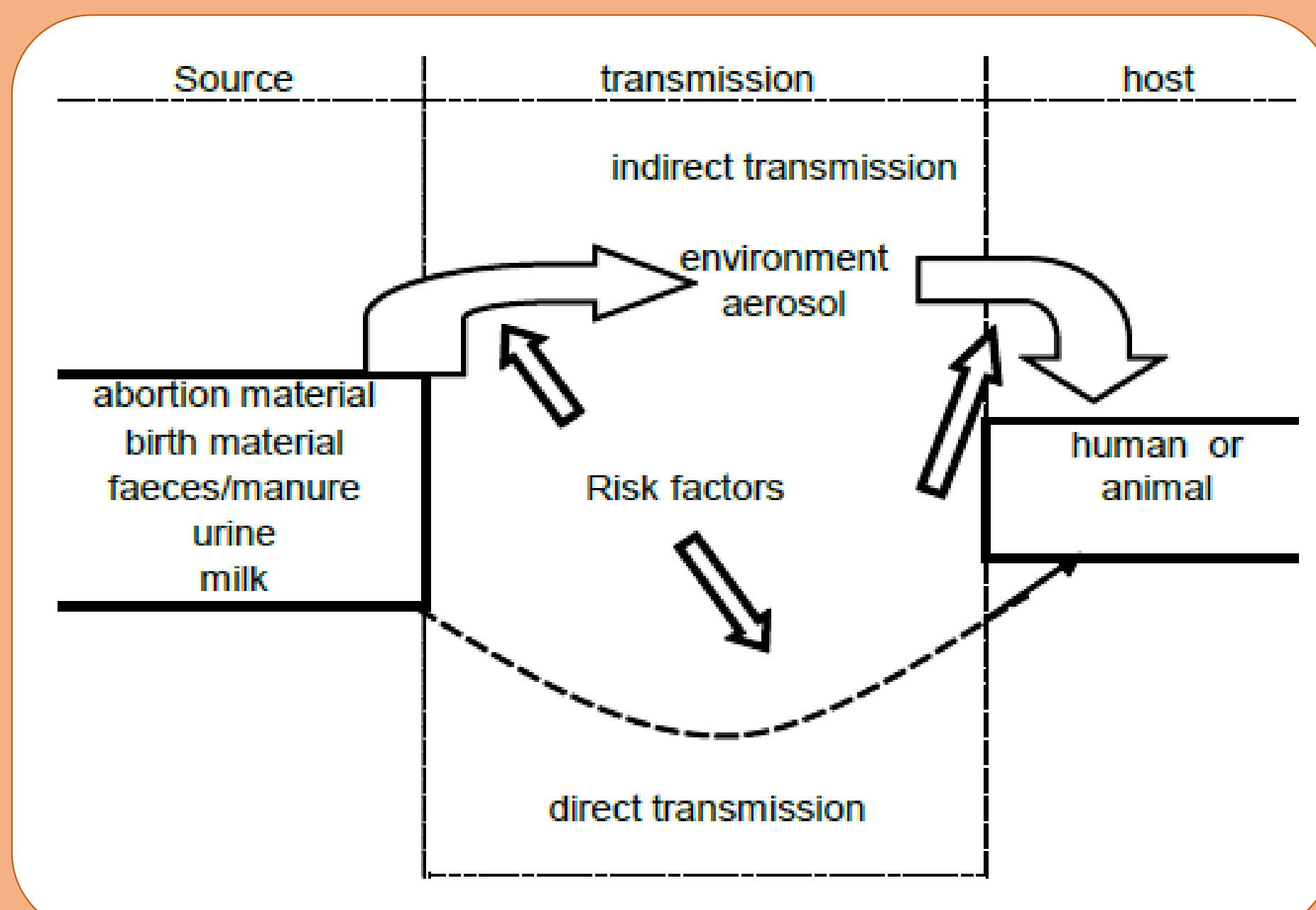


## Introduction:

Q fever is a zoonotic disease caused by the intracellular pathogen *Coxiella burnetii*. Humans become infected mainly by inhalation of aerosols or dust contaminated with *C. burnetii* shed by infected animals. A broad range of species has been identified as a reservoir for *C. burnetii*, but livestock are considered to be the main source of human infection and small ruminants are most frequently involved. *C. burnetii* is highly resistant to environmental conditions, surviving for many months under a range of conditions.

The main entrances of the bacteria in a free herd could be:



- Exposure to contaminated aerosols.
- Exposure to host and reservoir animals. Presence of ticks.
- Environmental factors such wind, drier soils, topography.
- Contaminated manure.
- Workers, fomites.

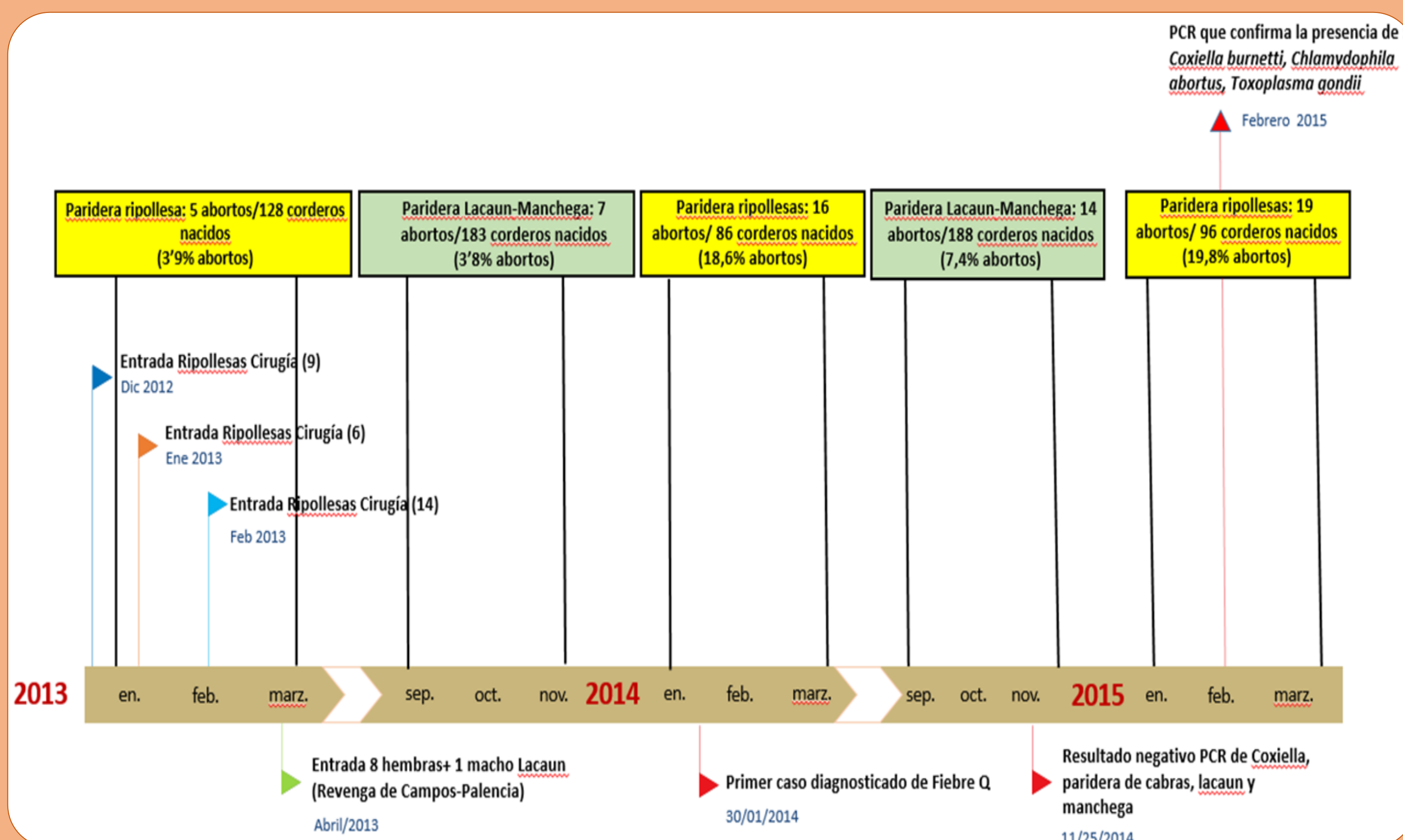
**Figure 1:** General scheme of the transmission cycle of fever Q.

## Materials and methods:

An epidemiological survey was designed to collect information about general characteristics of the farm, aspects related to the management of animals and the performance measures against fever Q outbreak.

The epidemiological survey was conducted by personal interview to the veterinary service responsible farm. They provided the necropsy and PCR's results and an Excel document with the serology results of every animal of the farm. Another survey was recently done recently to a update the rate of abortions.

For the statistical analysis, the Epi Info 7 software was used, the chi-square test was performed and the relative risks and confidence intervals were calculated.



**Figure 2:** Timeline, there are represented the most important events in 2013, 2014 and the first quarter of 2015 in UAB's farm.

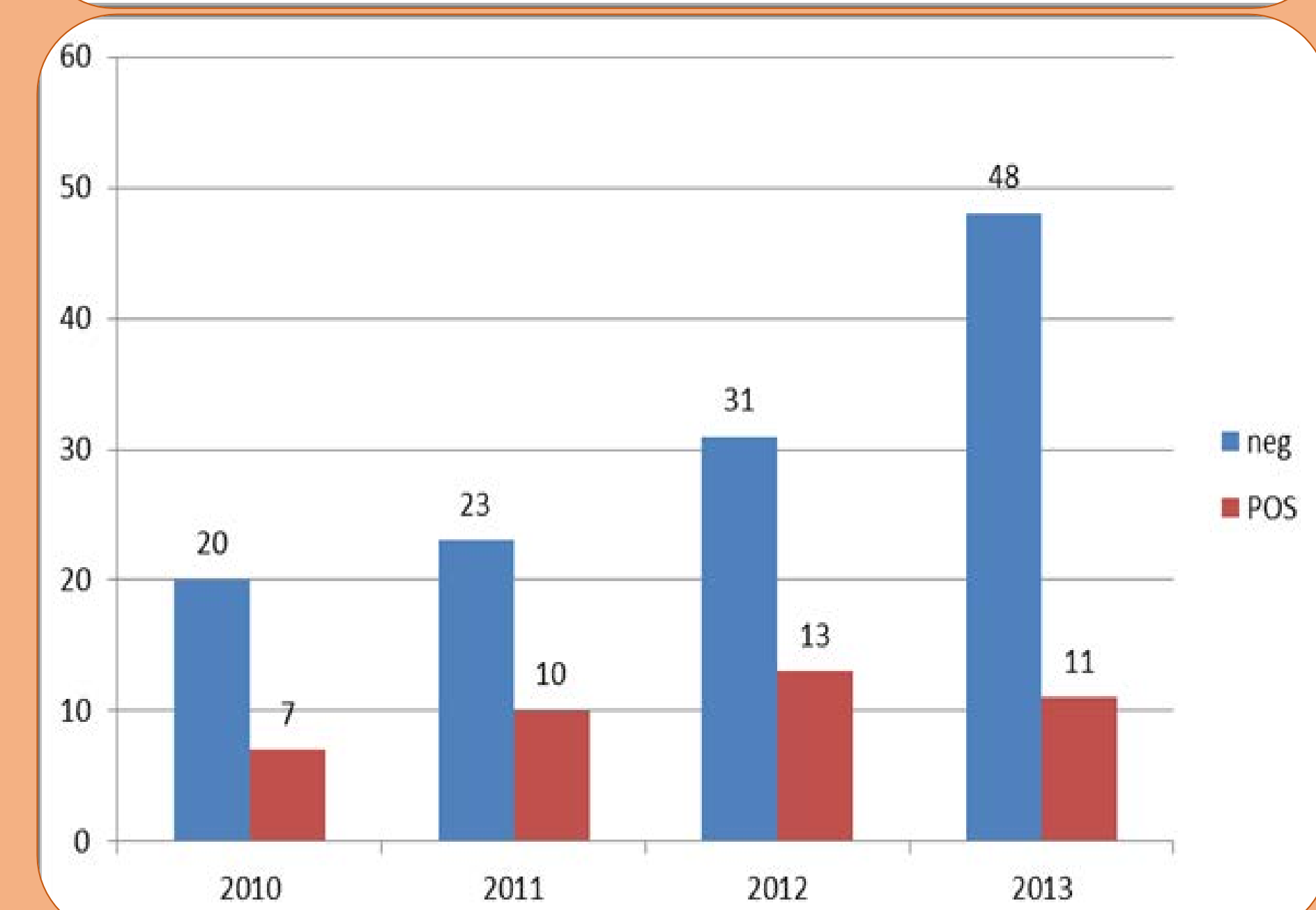
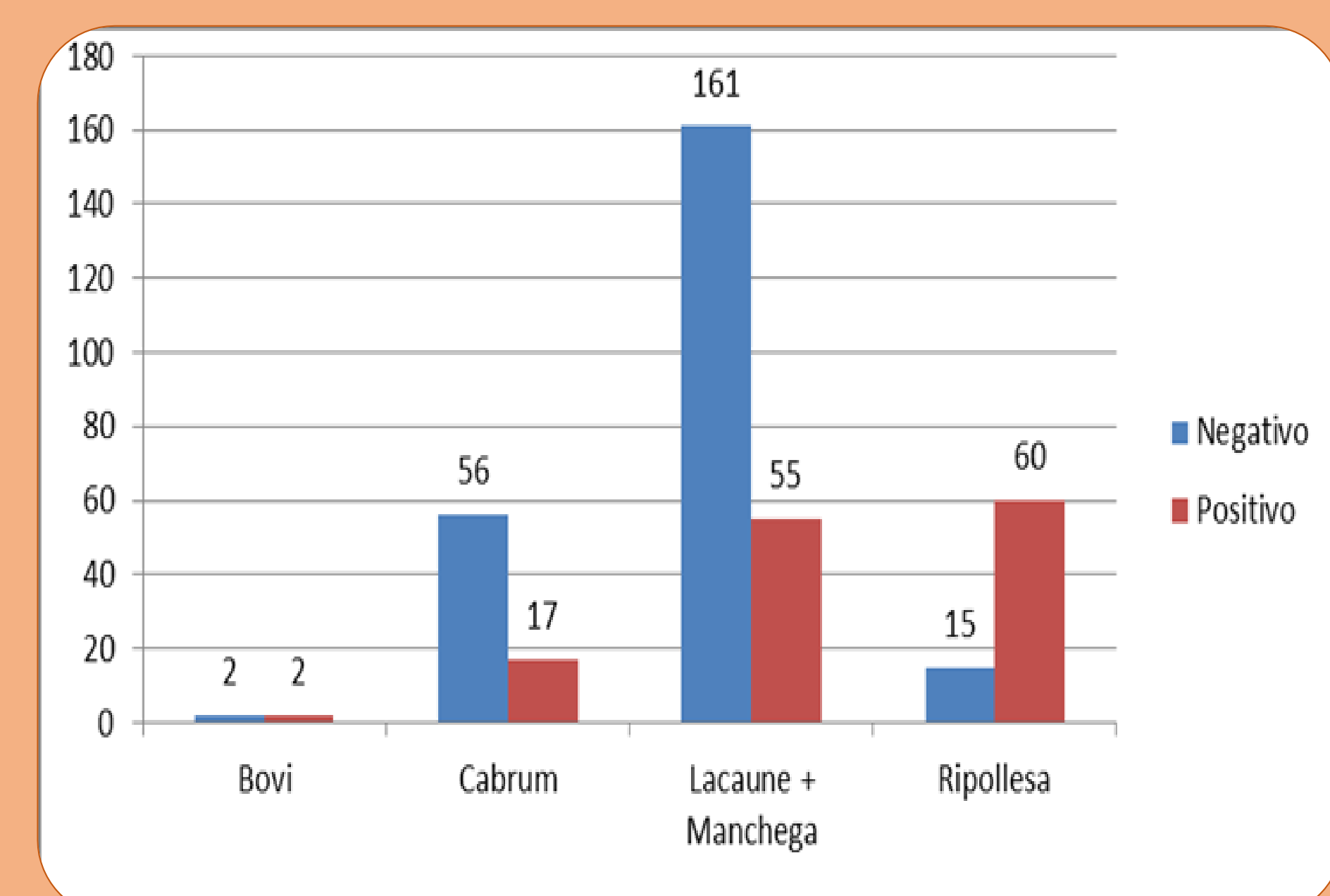
## Results and discussion:

### Descriptive analysis:

The different events that happened in the farm have been represented in a timeline (figure 2). Vaccination has probably reduced the level of shedding of *Coxiella burnetii* and remains as a good control measure. The high percentage of abortions detected recently in Ripollesa is partially explained by an infection with Toxoplasma and Chlamydia.

### Statistical analysis of the ELISA results:

The data analysis has shown that the probability of being positive for Q fever was 3,14 times higher in Ripollesa sheep than Lacaune and Manchega sheep and 3,43 times higher in Ripollesa than in goats (p value <0,05). Possibly this is due to a better management and feeding of sheep intended for milk production. There were no statistically significant differences between the year of birth of the animals.



**Figure 3 and 4:** Serology results organized by specie and breed (up). Serology results organized by year of birth (down).

### Possible origins of the outbreak:

The most likely route of infection of the herd would be (in descending order):

- Entry of infected animals in the herd. The main suspicion are the animals introduced in April 2013.
- Contact with reservoir animals from other species (dogs, cats or wild animals).
- People or fomites.

## Conclusions:

The high percentage of seroconverted animals from different species and ages suggests that *Coxiella burnetii* was circulating time before the detection of the first case. This fact supports the introduction of infected animals as the most likely route of infection of the UAB farm.