Question 1:

Which are the most commonly used parameters to evaluate viral infection intensity in mice?

○ Body temperature

○ Sneezing / coughing

● Changes in body weight

Explanation:

Mice do not develop fever after viral infections they rather show a drop in body temperature. Additionally, mice are not able to sneeze or cough. Body weight is an easily accessible parameter that reflects the course of disease (in most cases).

○ A and B

○ A and C

Question 2:

Which of the following are two distinct types of genetic approaches?

● Reverse and forward

Explanation:

Reverse genetics comprises techniques of the introduction of wanted mutations into the mouse genome. For this hypothesis-driven approach, prior knowledge about the gene of interest is essential. Forward genetics describes unbiased approaches utilizing natural variation in the mouse species for which no prior knowledge of the causative gene is needed.

○ Forward and backward

❍ Straight and reverse

❍ Straight and backward

Question 3:

Human genomes are characterized by extensive natural variation that have accumulated over time through which mechanisms?

❍ Mutation events

❍ Gene flow

❍ Sexual reproduction

● All of the above

Explanation:

Mutation events, gene flow as well as sexual reproduction increase the number of genes / gene variants available in the genetic pool and therefore add to natural variation.

Question 4:

Which of the following methods is NOT used to increase the likelihood of mutations in male mice?

❍ Treatment with chlorambucil

❍ Radiation treatment

● Treatment with poisonous substances

Explanation:

Poisonous substances do not alter DNA sequences and therefore do not increase the likelihood of mutations.

❍ Utilization of transposons

Question 5:

Which of the following are examples for transposon approaches?

❍ Cinderella

● Sleeping beauty

Explanation:

The approach is named after the transposase that is utilized, in this case "Sleeping Beauty (SB) transposase".

❍ Piggybag

❍ Snow white

Question 6:

The size of chromosomal regions identified through QTL mapping depends on which factors?

❍ Number of recombination breakpoints

❍ Number of analyzed phenotypes

❍ Genetic complexity of the region

❍ All of the above

● A and C

Explanation:

The number of recombination breakpoints determines the mapping resolution whereas the genetic complexity influences the number of genes that are present in a certain chromosomal location.

Question 7:

Which of the following mouse strains is NOT included in the eight founder strains of the Collaborative Cross?

❍ A/J

❍ PWK/PhJ

● BALB/c

Explanation:

Which strains are included into the set of eight Collaborative Cross founder strains was a community driven effort. BALB/c mice are often used in biological research but were not included.

❍ 129S1/SvImJ

❍ NZO/HlLtJ

Question 8:

The genetic diversity present in the Collaborative Cross is comparable to the diversity in humans. What percentage of the Mus musculus species is captured in the Collaborative Cross?

❍ 75%

❍ 100%

❍ 85%

● 90%

Explanation:

The Collaborative Cross captures 90% of the genetic variation present in the mouse species and is therefore comparable to the genetic diversity found in humans.

Question 9:

A common observation in studies utilizing pre-CC lines is that the phenotypic range is...

❍ Equal to the range observed in the parental strains

● Greater compared to the range observed in the parental strains

Explanation:

Due to the fact that genes were "scrambled" in new ways the phenotypic range was always greater compared to the range observed in the parental strains.

❍ Smaller compared to the range observed in the parental strains

❍ Not correlated with the range observed in parental strains

Question 10:

Which of the following resources is NOT one of the resources typically used to narrow down mammalian QTL regions?

❍ Sanger SNP browser

❍ BioGPS

● QTLmagic

Explanation:

There is no such resource as QTLmagic for the analysis of mammalian QTLs.

❍ Pubmed

Question 11:

Which of the following genes was identified to play a major role in human susceptibility to norovirus infection?

❍ IFITM3

● FUT2

Explanation:

At the gut surface, FUT2 controls the secretion of ABO histo-blood group antigens (HBGAs) which are the presumed receptors for caliciviruses (including norovirus). IFITM3 is associated with viral replication in influenza A virus infections, IL28B is associated with spontaneous clearance of hepatitis C virus infections and HLA-B is associated with viral load in human immune deficiency virus 1 infections.

❍ IL28B

❍ HLA-B