



# Epidemiology of Hepatitis E in Bavaria Germany

K.Hriskova<sup>1,2,3</sup> D.Marosevic<sup>1</sup> K.Katz<sup>1</sup> A.Belting<sup>1</sup> J.J.Wenzel<sup>4</sup> A.Carl<sup>4</sup>

<sup>1</sup> Bavarian Public Health and Food Safety Authority (LGL), <sup>2</sup> Institute for Medical Information Processing, Biometry and Epidemiology - IBE, LMU Munich, Munich, Germany, <sup>3</sup> Pettenkofer School of Public Health, Munich, Germany, <sup>4</sup> National Consultant Laboratory for HAV and HEV, Institute of Clinical Microbiology and Hygiene, University Medical Centre Regensburg

## Introduction

- Hepatitis E virus (HEV) is a non-enveloped, single-stranded RNA virus
- Genotype 3 is the most widespread genotype in Germany
- The prevalence of antibodies against HEV in Germany is 16,8%
- Genotype 3 has a zoonotic character and has been detected in several animal species (e.g. pigs, wild boars, deer and rabbits) and humans

## Objectives

- Describe the population diagnosed with HEV in Bavaria
- Identify the most common subgenotypes of HEV circulating in Bavaria
- Identify the risk factors associated with transmission of HEV genotype 3

## Data Collection HEV cases

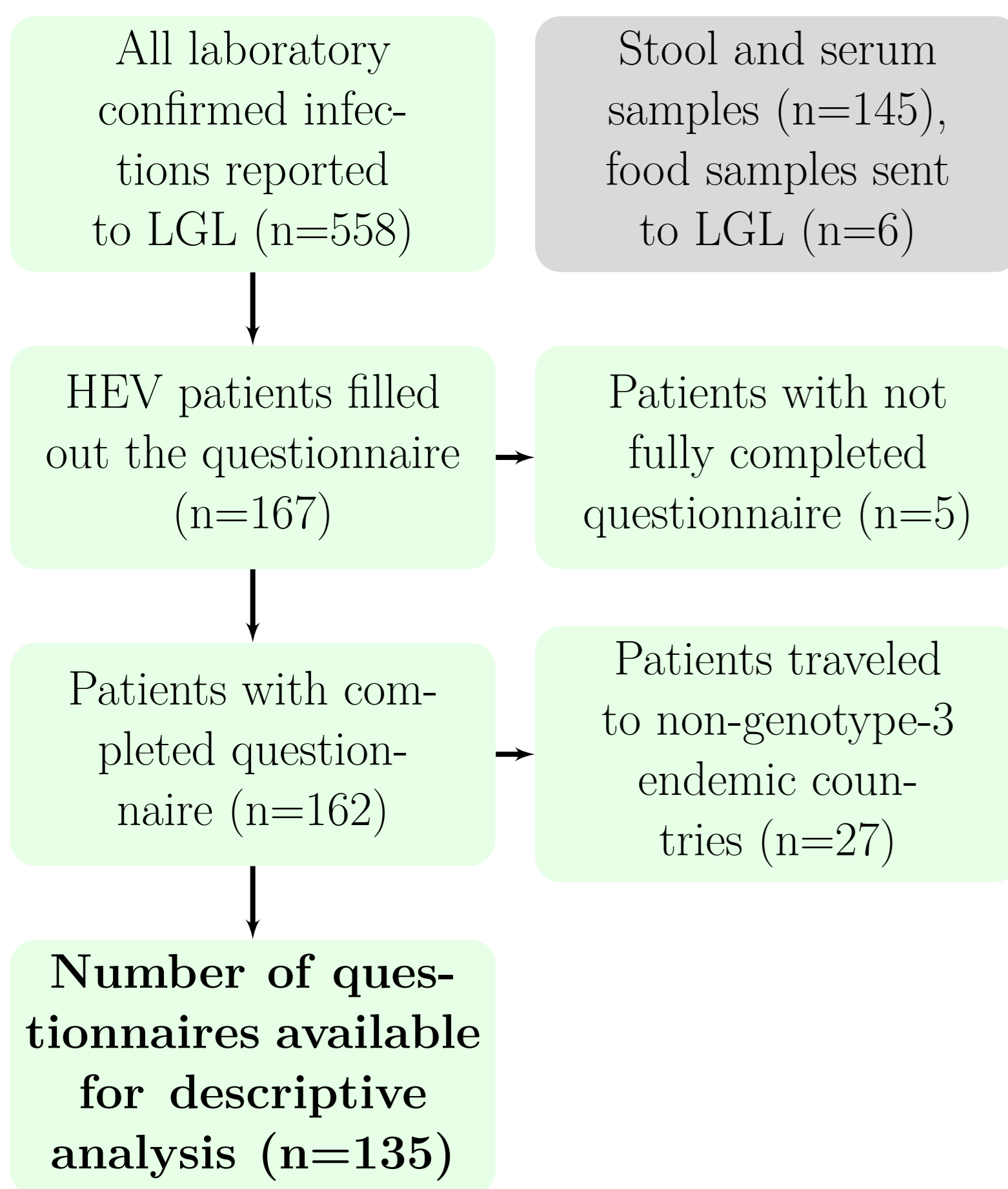


Figure 1: Recruitment of hepatitis E patients

## Data Collection Healthy Population (DEGS1)

**Healthy population**[1] A dataset from RKI (DEGS1) was used to compare food habits of Bavarian HEV cases in 2017 with the general healthy population participating in the RKI survey. Inclusion criteria:

- Food Frequency Questionnaire (FFQ) was filled out
- Living in western federal states
- No previous diagnosis of Hepatitis

## Methods

- Descriptive analysis for Bavarian's HEV cases
- Sequencing to subgenotypes
- Univariable analysis and Logistic Regression

## Results

Gender and age	<ul style="list-style-type: none"> <li>• Women (n=66) mean age 46 years (20-74)</li> <li>• Men (n=69) mean age 47,5 years (20-85)</li> </ul>
Comparison between men and women	<ul style="list-style-type: none"> <li>• No significant difference in the mean age between men and women (t-test and ANOVA)</li> </ul>
Symptoms	<ul style="list-style-type: none"> <li>• Cases with symptoms (n=79/59%)</li> <li>• No significant difference in the presence of symptoms between women and men (Chi-square-test)</li> </ul>

## Subgenotyping

- Stool and serum samples sequenced (n=145)
- Food samples sequenced (n=6). All were negative
- In most of the stool samples the HEV-RNA was not detectable (n=122), because collection of samples was delayed

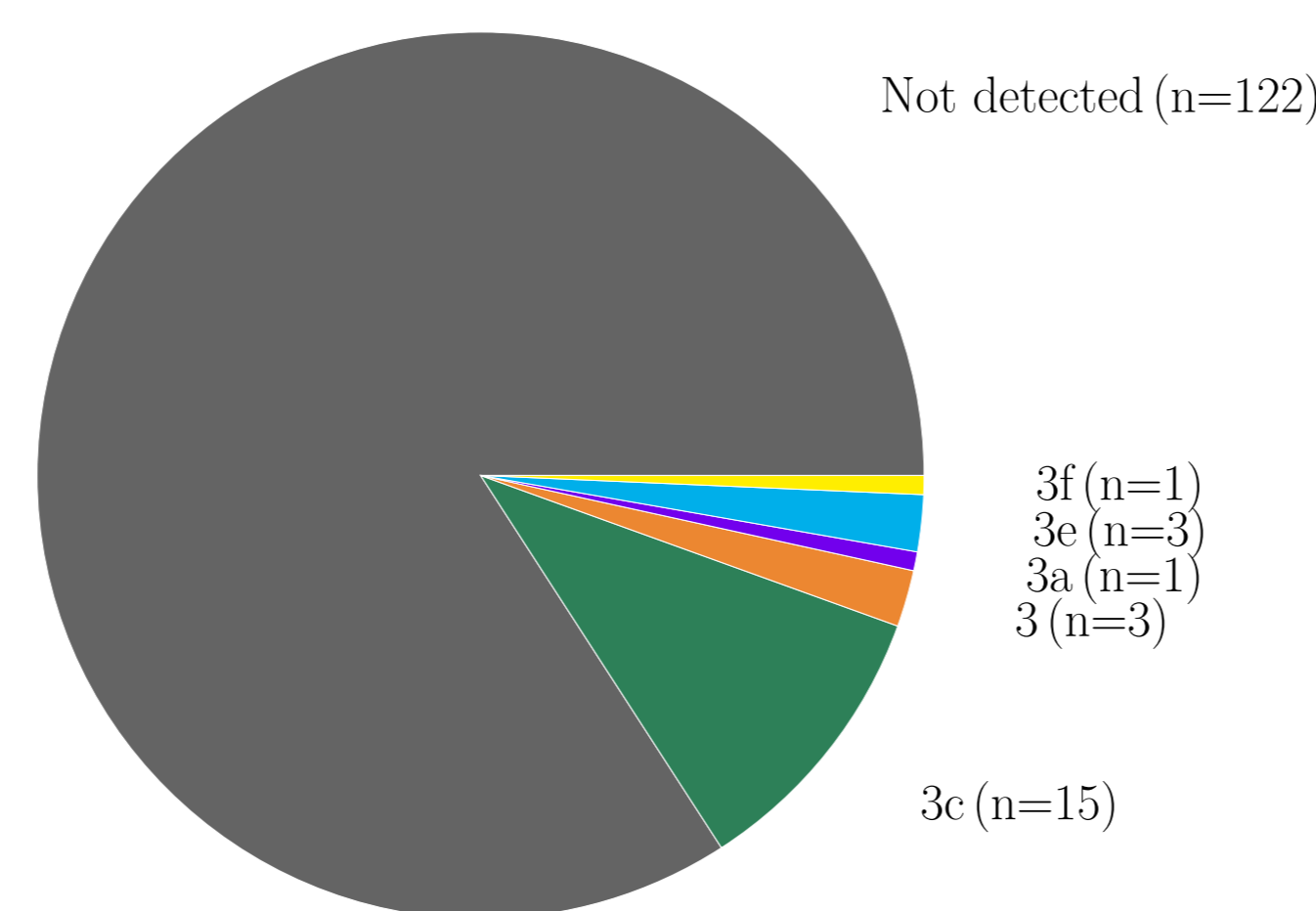


Figure 2: Subgenotype distribution

## Risk factors I

### Positively associated with hepatitis E:

- Consumption of sausages (e.g. salami, liver sausages)
- Consumption of fish (e.g. pollack, trout)
- Owning a cat

### Protective factor for hepatitis E:

- Consumption of raw vegetables

### No association with hepatitis E:

- Consumption of meat like pork, beef and wild meat
- Consumption of ham
- Owning a dog

## Risk factors II

Risk factors	Cases (n = 135)		Healthy population (n = 4.512)		Multivariable Analysis	
	Yes	%	Yes	%	ORs	95% CI
Sausages consumption	133	98,5%	4.037	89,7%	<b>9,6**</b>	1,3 - 70,1
Fish consumption	123	91,8%	3.811	84,8%	<b>2,2**</b>	1,1 - 4,4
Cat possession	39	31,2%	676	15,4%	<b>1,9***</b>	1,3 - 3,0
Raw vegetable consumption	121	90,3%	4.245	95,3%	<b>0,4**</b>	0,2 - 0,8
Meat consumption	131	97,0%	4.326	96,2%	NA	
Ham consumption	120	89,6%	3.828	85,0%	NA	
Dog possession	20	16,1%	608	13,9%	NA	

Table 1: Risk factors. Comparison of the HEV cases and the DEGS1 population (NA - the effect of the variable is not significant; \*\* p-value < 0,05; \*\*\* p-value < 0,01)

## Conclusion

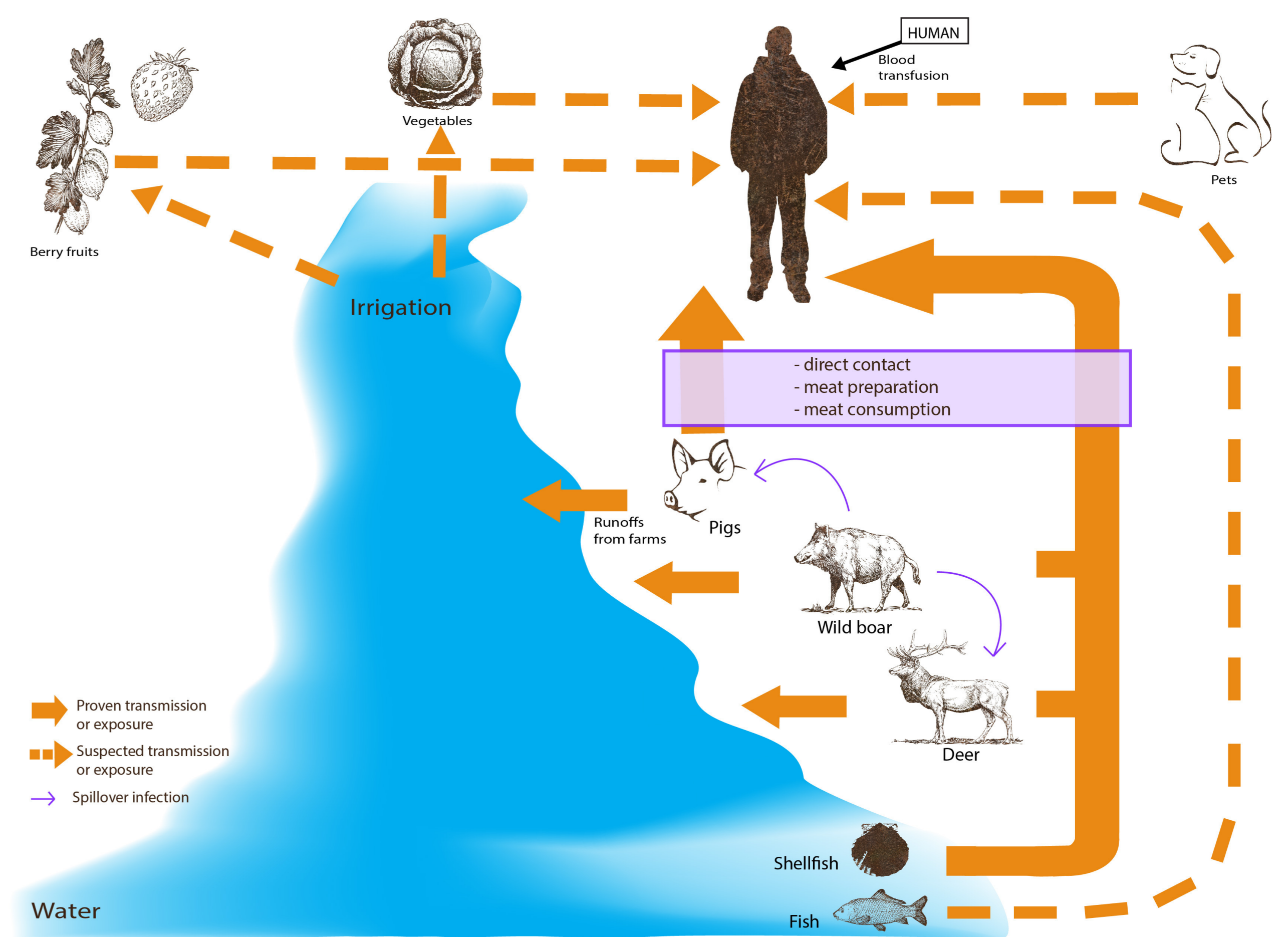


Figure 3: Summary of known and suspected transmission routes of HEV genotype 3 in the literature

- Pigs, wild boar and deer have been identified as reservoir of HEV in Germany
- Runoff from animal manure and faeces, containing HEV, could contaminate irrigation or coastal waters and these could contaminate shellfish and possibly fish
- In our study fish was identified as a new risk factor
- Dogs and cats have been found seropositive for HEV in Germany
- In our study cat ownership was positively associated with HEV
- Furthermore, women with cat ownership have a higher risk than men owning a cat
- It is tempting to hypothesize that women living in a shared household are more likely to care for their pets (feeding and cleaning) and are therefore more exposed

## References

[1] Robert-Koch-Institute. German health interview and examination survey for adults (degs1). Robert Koch Institute, Department of Epidemiology and Health Monitoring, 2015.

## Acknowledgements

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