

RESEARCH ARTICLE

Standardized tissue sampling guidelines for histopathological and molecular analyses of rainbow trout (*Oncorhynchus mykiss*) in ecotoxicological studies

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Abstract

In ecotoxicology, evaluation of toxicities and *no observed effect concentrations* (NOEC) of test compounds in experimental fish is commonly based on molecular-, biochemical- and analytical chemistry analyses of organ/tissue samples and the assessment of (histo-) pathological lesions. Standardization of organ/tissue sampling locations, sample numbers, and sample processing contributes to warrant the reproducibility and inter- and intra-study comparability of analysis results. The present article provides the first comprehensive tissue sampling guidelines specifically adapted to rainbow trout (*Oncorhynchus mykiss*) as a frequently used fish species in ecotoxicological studies. A broad spectrum of ~40 different organs and tissues is covered. Appropriate sampling locations, sample sizes and sample numbers for subsequent routine histopathological evaluation (all organs/tissue) and for molecular analyses (~30 organs/tissues) are described in detail and illustrated with schematic drawings and representative macroscopic and histological images. These field-proven sampling guidelines were developed based on the pertinent literature and practical experience in ecotoxicological fish studies. They are intended to serve as a standard reference for any routine ecotoxicological study using rainbow trout as a test system. A broad application of the featured tissue sampling procedures will help to improve the reproducibility of analyses and to reduce inter- and intra-study variability induced by sampling bias and (normal) inter-sample morphological variation, and will therefore provide a robust basis for reliable characterization of toxicity and NOEC identification of diverse test substances and aquatic pollutants.

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Introduction

In ecotoxicological exposure studies, the rainbow trout (*O. mykiss*) is a frequently used test system to examine toxic effects of diverse surface water pollutants [1–4]. With regard to environmental risk assessment, the experimental results and evaluated toxicological endpoints such as the *no observed effect concentration* (NOEC) are used for the assessment of the ecotoxicological potential of the given test substance and its classification as relevant for the (aquatic) environment, and may therefore provide the basis for the restriction of emissions/discharges or even the ban of hazardous substances [5,6]. Given the far-reaching consequences, the reproducibility of the analyses results, as well as the comparability of the results of different studies examining the same test substance, are essential. The applied mode of sampling and processing of organ/tissue specimens is an important factor affecting the unbiasedness, reproducibility, and comparability of analysis results that must be considered in the experimental design of any study. Here, application of standardized sampling guidelines can contribute to limit the intra- and inter-study variability by definition of organ/tissue-specific sampling locations, sample numbers, sample sizes, and, where applicable, their orientation(s), providing comparable organ/tissue specimens whose representativeness is warranted. Therefore, the use of standardized organ/tissue sampling protocols has become a generally accepted and expected standard in diverse life-sciences disciplines, such as toxicologic pathology or translational medicine, and standardized sampling guides have been established for several experimental animal species [7–14]. For fish of the size of the rainbow trout considered in the present guidelines, such standard sampling guides are missing to date, but they are urgently required in ecotoxicological studies. The present article provides the first comprehensive standardized sampling guidelines specifically adapted to rainbow trout of body weights between 300–2000 g, for the reproducible generation of tissue samples for histopathological examinations and a broad spectrum of molecular analyses.

Experimental fish, ethics statement

For development, demonstration and validation of the methods shown in the present study, eight healthy rainbow trout of both sexes with body weights ranging from 300–2000 g were sacrificed. The use of the fish in this study was performed in accordance with the relevant legal regulations and with permission of the local authorities, and was approved by the institutional ethics committee of the Institute of Veterinary Pathology of the Ludwig-Maximilians-Universität Munich via verbal consent. The fish were obtained from the breeding facility of the Bavarian Environment Agency in Wielenbach, Germany. After initial health status check, fish were sacrificed either by stunning (concussion) and exsanguination or with tricaine methanesulphonate solution (500 mg/l, Tricaine Pharmaq[®] 1000 mg/g, Pharmaq Ltd., United Kingdom) and subsequent brain destruction after circulatory arrest. In none of the examined fish, clinical, macroscopic, and histological examination revealed indications of disease or pathological alterations.

Standardized sampling guidelines for rainbow trout organs and tissues

The present guidelines (**S1 File**) contain sampling protocols for ~40 different organs and tissues (**Table 1**) of rainbow trout of 300–2000 g body weight. For each featured organ/tissue, detailed sampling schedules are provided for the generation of standard formalin-fixed and paraffin-embedded (FF-PE) samples for light-microscopic histopathological evaluation, as well as for the generation of snap-frozen tissue specimens, suitable for a broad spectrum of downstream molecular and biochemical analyses, such as *e.g.*, DNA-, RNA-, protein-, lipid-, and small molecule metabolite analysis as well as analytical chemistry. The samples are taken

Table 1. List of rainbow trout organs and tissues covered by the present sampling guidelines for histopathological examination and molecular analyses.

Organ System	Organ/Tissue	Histo-pathological analyses ¹	Molecular analyses ²	Chapter (Suppl. material)
Respiratory system	Gills	✓	✓	2.1
Cardiovascular system	Heart	✓	✓	2.2
	Blood vessels	✓	-	2.2
Digestive system	Tongue	✓	-	2.3.1
	Teeth	✓	-	2.3.1
	Liver and gallbladder	✓	✓	2.3.2
	Gastrointestinal tract ³	✓	✓	2.3.3
	Pancreas (exocrine & endocrine)	✓	✓ ⁴	2.3.4
	Swim bladder	✓	✓	2.3.5
Adipose tissue	Visceral and subcutaneous adipose tissue	✓	✓ ⁵	2.4
Hematopoietic and immune system	Spleen	✓	✓	2.5
Reproductive system	Testes and ovaries	✓	✓	2.6
Urinary and hematopoietic system	Kidneys (head- and trunk kidney)	✓	✓	2.7
Central nervous system	Brain	✓	✓ ⁶	2.8
	Spinal cord	✓	✓	2.8
Integument	Scaled and non-scaled skin	✓	✓	2.9
Locomotor system	White and red skeletal musculature	✓	✓	2.10.1
	Bone	✓	✓ ⁷	2.10.2
	Cartilage	✓	-	2.10.2
	Fins	✓	✓	2.10.3
Pseudobranchs	Pseudobranchs	✓	✓	2.11
Sensory system	Olfactory rosettes	✓	✓	2.12.1
	Inner ears	✓	-	2.12.2
	Lateral line canal	✓	-	2.12.3
	Eyes	✓	✓ ⁸	2.12.4
Endocrine system	Pituitary gland	✓	✓ ⁹	2.13.1
	Endocrine pancreas	✓	✓ ⁹	2.13.2
	Thyroid gland	✓	-	2.13.3
	Inter- and suprarenal tissue	✓	-	2.13.4
	Corpuscles of Stannius	✓	✓ ⁹	2.13.5
	Pineal gland (epiphysis)	✓	✓ ⁹	2.13.6
	Urophysis	✓	-	2.13.7
	Ultimobranchial gland	✓	-	2.13.8

¹Standard light-microscopic histopathological examinations of sections of FF-PE tissue samples. ²Snap-frozen samples suitable for different downstream molecular, biochemical or analytical chemistry analyses. ³Gastrointestinal tract samples include: Esophagus, stomach, pyloric caeca, mid intestine, and posterior intestine. ⁴The Brockmann body is sampled for molecular analyses of the (exocrine and endocrine) pancreas. ⁵The specimen for molecular analyses of adipose tissue is generated from the visceral adipose tissue (VAT). ⁶Three brain samples for molecular analyses are generated: Telencephalon, diencephalon and mesencephalon, and rhombencephalon. ⁷The vertebral centrum is generated as bone tissue specimen for molecular analyses. ⁸Vitreous humour, cornea, lens, and retina are generated as specimens for molecular eye analyses. ⁹If the study design requires molecular analyses, it is recommended to sample the corresponding organ/tissue in toto.

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from defined anatomical locations, the recommended sample sizes and sample numbers, as well as sectioning directions and sample orientations (if applicable) are indicated. For convenience, hereinafter the broad entirety of downstream analyses such as molecular, biochemical and analytical chemistry analyses are collectively referred to as “molecular analyses”.

2.5 Spleen

Relevant anatomical features/preparation

The rainbow trout's spleen is situated in the left lower abdomen, attached to (and often embedded in) the visceral adipose tissue (Figure 32). It is a soft, dark-red, compact organ whose size can vary due to antigen exposure (e.g., bacterial or viral infections) or changes in the splenic erythrocyte reservoir volume (e.g., due to stress) [2, 95]. In rainbow trout, additional smaller accessory spleens may be present [4]. In physiological state, the spleen margins are sharp-edged [3]. In teleost fish, the spleen functions as a hematopoietic organ (i.e., site of erythropoiesis) and erythrocyte reservoir [2, 36, 42]. In rainbow trout, the spleen also has immunological function by acting as an "antigen trap" and by removing aged or infected blood cells by phagocytosis [2-4]. A thin, fibrous capsule is surrounding the spleen matrix composed of the red and white pulp, which are not as distinctly separated as in mammals [2, 36, 42]. A distinct feature of the spleen of teleost fish is the melanomacrophage centers (MMC), typically located next to splenic blood vessels [2-4].

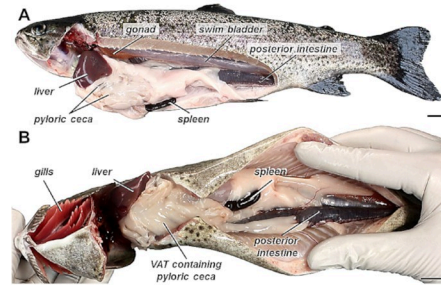


Figure 32. Photographic illustration of the viscera in situ. A. Lateral aspect of the viscera of a rainbow trout after removal of the lateral body wall and excision of the gills. B. Ventral aspect of the viscera of a rainbow trout after opening of the abdominal cavity by a transverse section in the ventral midline. The spleen is attached to and partly embedded in the visceral adipose tissue (VAT). Bars = 1 cm.

At necropsy, the spleen is removed from the abdominal cavity together with the gastrointestinal tract (GIT) and the visceral adipose tissue (VAT) after excision of the gills and the liver. The abdominal cavity is opened by transverse section in the ventral midline, the liver is dissected and the GIT is excised by severing the cranial esophagus and cutting out the vent (urogenital papilla). The connection between the visceral aspect of the spleen and the visceral adipose tissue is separated. After sampling for molecular and histopathological analyses (Figure 33B) and transfer of the histopathology sample to neutrally buffered 4% formaldehyde solution, the remaining caudal pole of the spleen is also preserved (i.e., immediately transferred to an adequate fixative), to ensure that sample material is available for new/expanded scientific issues arising from the analyses.

Fig 1. Illustration of the spleen sampling protocol as a representative example of the rainbow trout sampling guidelines. Each sampling protocol contains a brief summary of the relevant trout-specific anatomical, functional and histological features and recommendations for dissection/preparation (**Relevant anatomical features/preparations**), a brief instruction on the general examination procedure (e.g., weighing, macroscopic examination) (**General examination parameters**) as well as sample locations/numbers/sizes and subsequent sample processing steps and storage conditions for histopathological and molecular analyses (**Sampling scheme for routine analyses of the rainbow trout spleen**). For histopathological analyses, the protocols additionally contain recommendations on sample section plane orientations. The protocols further include an estimate of time required for sampling (**Time requirements**) and a concluding comparison of the proposed sampling scheme with previously published ecotoxicological studies using (rainbow) trout (**A comparison of the proposed sampling scheme for routine analyses with previously published studies**). Each protocol is illustrated with comprehensible schematic drawings and representative macroscopic and histological images.

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General examination parameters

The dissected spleen is briefly dabbed dry with a laboratory paper towel and weighed to the nearest mg. The spleen is macroscopically examined for pathological alterations, corresponding findings are (photo-) documented. If present, samples of altered tissue locations are taken for subsequent histopathological, molecular or microbiological analysis, as appropriate.

Sampling scheme for routine analyses of the rainbow trout spleen

1. Sample for molecular analyses of the spleen

Location: Sampling location is indicated in Figure 33B.
Number of samples: One.
Sample size: Entire cranial portion of the spleen from the cranial margin to the location of the widest organ extension (i.e., the sample location for histopathological analyses).
Remarks: A homogenous sample is cut from the spleen.
Processing: The sample is frozen (liquid nitrogen) and stored at -20°C or -80°C (short-term storage) depending on the intended analysis (chemical or molecular analysis). For prolonged storage of the tissue sample for subsequent RNA- and protein analyses, storage at -150°C is recommended.
Downstream analyses: DNA-, RNA-, protein-, and other OMICS profiling- or targeted analyses requiring cryo-conserved specimen as well as chemical (analytical) analyses.

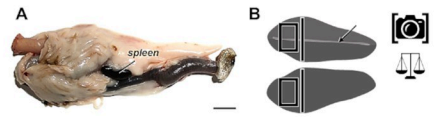


Figure 33. Sampling for histopathological examination and molecular analyses of the spleen. A. Excised gastrointestinal tract and spleen attached to the visceral adipose tissue. The peritoneal attachment at the visceral aspect of the spleen (arrow in B) is dissected using scissors. Bar = 1 cm. B. Schematic illustration of the excised spleen with indicated sampling locations for routine histopathological and molecular analyses (upper image: visceral aspect; lower image: parietal aspect). The sampling location of the specimen for molecular analysis (black rectangles), as well as sampling location and orientation of the specimen for histopathological examination (black lines) are indicated. Lines in the upper and lower image indicate the identical sampling locations and section plane orientations for routine histopathological and molecular analyses. Both samples contain the spleen capsule.

2. Sample for histopathological examination of the spleen

Location & orientation of sections: Sampling location and orientation is indicated in Figure 33B. A transverse splenic tissue section is cut from the spleen at the location of the widest organ extension.
Number of samples: One.
Section plane size: The sample size depends on organ size/diameter, thickness of the tissue sample is ~0.2 cm.
Fixation & embedding: FF-PE.

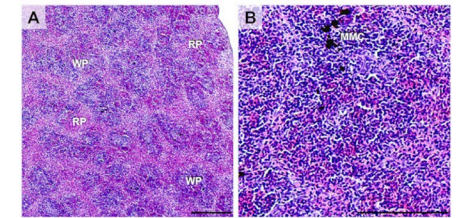


Figure 34. Histology of the rainbow trout spleen. A. Transverse section of rainbow trout spleen parenchyma, enclosed by a thin splenic capsule (a part of the splenic capsule is apparent in the upper right corner). The parenchyma is composed of the red (RP) and white (WP) pulp. B. Transversely sectioned spleen parenchyma. A feature of the rainbow trout spleen is the presence of melanomacrophage centers (MMC), composed of pigment-laden macrophages which are involved in the spleen's immunological function. FF-PE. HE. Bars = 100 µm.

Time requirements

2-3 minutes are to be scheduled for dissection of the GIT and the attached spleen, macroscopic examination of the spleen, sampling and further processing of the histological and molecular samples. This estimate does not include the time needed for killing the fish, dissection of gills/liver, prearrangement of sampling instruments and materials, or the further processing of fixed/frozen specimens.

A comparison of the proposed sampling scheme for routine analyses with previously published studies

Previously published ecotoxicological studies examining rainbow trout spleen either sample the whole organ [95-98] or examine spleen subsamples without distinct information regarding sample number and size [99, 100]. The sampling location for histopathological analyses of the rainbow trout spleen is chosen in accordance with the study by Schwandt et al. [101], where a tissue sample from the middle of the spleen is generated for histological examination. Due to the homogenous composition of the splenic parenchyma, the number and sizes of tissue samples as well as the sampling locations proposed in the present guidelines are regarded to provide sufficiently representative tissue specimens for the examination of most of the qualitative splenic tissue alterations and molecular analyses of the rainbow trout spleen.

A brief introduction summarizes the general necropsy- and tissue sample processing methods and explains the pictograms and symbols used to illustrate the sampling locations and sample types for the different downstream analyses, the sectioning directions and sample orientations, as well as subsequent sample processing steps and storage conditions.

The sampling protocols for the individual organs/tissues (see Fig 1 for a representative example) each contain particular information about the following subjects:

- Relevant trout-specific anatomical, functional, and histological organ/tissue features.
- Practical recommendations for the preparation/dissection of the respective organ/tissue.
- Recommended sampling locations, sample numbers, and individual sample sizes for histopathological and molecular analyses.
- Recommended section plane orientations of samples for histopathological analyses.
- Specific tissue processing methods for subsequent histopathological and molecular analyses.
- Comprehensible schematic illustrations and representative histological images.
- Estimates of the time requirement for sample collection.
- A comparison of the proposed sampling scheme with previously published ecotoxicological studies using (rainbow) trout.

Discussion

In ecotoxicological exposure studies, test item related findings indicating toxicity/adverse effects on organ/tissue level (with a dose/effect relationship) are commonly assessed by a variety of analyses of organ- and tissue samples, taken from susceptible species exposed to defined concentrations of the test compound over a specific period of time. The wide range of analyses includes *e.g.*, clinical-chemical analyses, hematological investigations, molecular and biochemical analyses as well as histopathological evaluation [2,15,16]. With regard to environmental risk assessment, the experimental results serve for the assessment of the ecotoxicological potential of the given test substance and its relevance for the (aquatic) environment. Toxicological end points based on the experimental results, such as the NOEC of the test substance, are an important part of the scientific basis for the definition of the *predicted no effect concentration* (PNEC) [2,5,16,17]. The PNEC has an important and legally anchored role in the environmental risk assessment and authorization of anthropogenic substances, such as chemicals or pharmaceuticals [18–21] as well as in the restriction of environmentally relevant priority substances in the water bodies (mainly surface waters) of the European Union [6,22] and may therefore provide the basis for emission/discharge limitations or even the ban of hazardous substances [5,6]. Usually, ecotoxicity data derived from standard biotests on aquatic organisms (including fish) (*e.g.*, OECD test guidelines) are used for the environmental risk/hazard assessment of a chemical test substance [1,20–23]. The test item related effect data collected in these biotests (*e.g.*, mortality or reproductive abnormality) are not always sufficiently sensitive to reliably determine the potential adverse contaminant effects on fish health. Non-standard biotests, such as histopathological, molecular or biochemical studies, have proven to be sensitive tools for detecting (sublethal) contaminant effects in fish and therefore can significantly contribute to the environmental risk assessment of test items [2,15,16,23–25].

A review of previously published ecotoxicology studies on various test substances using rainbow trout (RBT) reveals that tissue sampling locations and examined sample numbers are, if mentioned at all, generally considerably variable (S1 File). In parallel, it becomes evident that the methods and results of different studies examining identical test compounds are occasionally remarkably divergent, as there is no valid guideline to use. Prime examples are the NOECs determined in different studies analyzing the (histo-) morphological effects of the exposure of RBT to diclofenac (an analgesic which is regularly detectable in surface waters), which differ over multiple orders of magnitude from 0.1 µg/l to 320 µg/l [17,26–30].

Insufficient reproducibility and comparability of analytical results in ecotoxicology studies may result from underreporting of a study as well as from various confounding variables, such as different exposure concentrations and -systems, different ages, sexes or genetic background of the examined fish, or differing technical procedures applied in necropsy and sample processing [17,23,30]. Additionally, histopathological diagnoses, and particularly the use of ordinally scaled grading systems for assessment of the severity of histopathological lesions (such as +, ++, +++), may also considerably vary between different observers and studies due to the subjective nature of histopathological interpretation and the sampling- and observational bias [17,31–34]. This is especially relevant, if only subtle alterations are present, which do not manifest in all individual fish of a cohort (*e.g.*, due to exposure to low concentrations of a test substance). In this context, the general experience in life science disciplines examining test animals (mammalian and fish species) is, that standardization of the locations, as well as numbers, sizes, and orientations of samples generated from distinct organs/tissues for routine histopathological and molecular analyses is useful to limit sampling bias, to streamline the experimental study designs, and thus to strengthen the reliability and comparability of the analysis results [7,8,10,29–31,33]. Therefore, standardized sampling guides have been

established for different experimental animal species, including mice, rats, pigs, dogs, monkeys and also small fish species such as fathead minnow (*Pimephales promelas*), zebrafish (*Danio rerio*) or Japanese medaka (*Oryzias latipes*) [7–14]. For data collected in non-standard biotests to be considered in regulatory risk assessment and the derivation of safe concentrations such as the PNEC, ecotoxicological studies must meet some scientific quality criteria for the collection of reliable and reproducible data, and all important information regarding the study design, methodology, test organisms *etc.* should be reported [23,35,36]. Standardized sampling and sample processing protocols help to improve the reporting of ecotoxicological studies and aid to ensure that test results can be reproduced in other studies. This is especially valid for histopathological data, whose interpretation, in addition to the researcher's expertise, *inter alia* depends on the sampling strategy, the sample processing or the chosen section plane. Next to measures like blinded evaluation, the formation of a Pathology Working Group or the use of quantitative morphological analysis methods, therefore the quality, accuracy and reproducibility of histopathological data strongly benefit from standardized, detailed and user-friendly sampling and sample processing protocols, addressing the organ-/tissue-specific properties (*e.g.*, tissue fragility or tendency to autolysis) and (histo-) morphology [31–33].

The sampling guidelines presented here are the first standardized tissue sampling guidelines for routine ecotoxicology studies in RBT. They were specifically designed for RBT of 300–2000 g body weight, which are frequently used in routine ecotoxicological exposure studies and whose size allows the simultaneous generation of samples of multiple organs and tissues. The featured protocols are based on the pertinent literature (specified for each organ/tissue in **S1 File**), as well as on own investigations and practical experience in ecotoxicological studies [16,28,29,37–39]. The guidelines aim to provide a standard reference for the reproducible sampling of appropriate RBT organ/tissue specimens for standard histopathological examinations and molecular analyses. To warrant comprehensible, fast, and reproducible sampling procedures, the sampling protocols schedule the collection of a fixed number of samples with uniform sizes, taken from precisely determined locations and in predefined orientations (if applicable). This sampling regime is considered adequate for the demands of typical ecotoxicological studies, as it facilitates screening of a broad set of different organs/tissues for identification of qualitative histopathological changes and of organ/tissue-specific alterations of *e.g.*, biochemical- or molecular analysis parameters, using robust, standard analysis methods with acceptable sampling efforts. Depending on the objectives and the experimental design of a given study, the number of organs and tissues to be sampled can individually be adjusted. In studies scheduling advanced analyses requiring special sampling regimes (*e.g.*, systematic uniform random sampling) or sample processing procedures (*e.g.*, for electron microscopic analyses), however, additional sampling efforts and different tissue sample processing methods may be necessary. Also, if macroscopically evident lesions are present, additional samples should be taken from the altered sites for histopathology and microbiological/parasitological/molecular *etc.* analyses, as appropriate.

Generally, the appropriate sampling locations and the adequate numbers of samples depend on a variety of different factors. These factors include the size of the tissue samples and scheduled subsequent analysis methods, as well as the composition, heterogeneity and size of the respective organ/tissue, the pattern and extent of pathological lesions, particular susceptibilities of specific organ sites to development of pathological alterations, and biological/individual variances [7]. The proposed sampling locations, sample sizes and sample numbers indicated in the present sampling guidelines were chosen to effectively generate samples that are likely representative for the entire organ/tissue they were taken from, without redundant, time- and work-consuming oversampling. The indicated sample sizes for molecular and histopathological analyses provide sufficient sample volumes/section areas, ensure a fast snap-freezing- or

fixation process, and are adapted to the size of commonly used test tubes or embedding cassettes, respectively.

Conclusions

A broad application of consistent and carefully considered organ/tissue sampling protocols will enhance the quality, significance, and reproducibility of ecotoxicology studies using rainbow trout as test systems. The sampling guidelines presented here provide a robust basis for the generation of standardized rainbow trout tissue samples for routine histopathological and molecular analyses, which will contribute to the validity of inter- and intra-study comparisons of ecotoxicology studies. Due to the provided step-by-step protocol allowing the sampling of all ecotoxicologically relevant organs and tissues from a single rainbow trout, also unnecessary repetition of experiments might be avoided, thus limiting the number of fish sacrificed in ecotoxicological exposure studies.

Supporting information

S1 File. Standardized sampling guidelines for rainbow trout organs and tissues.
(PDF)

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