

## **Contextualising samples: Supporting reference genomes for European biodiversity through sample and associated metadata collection-**

### **Review Report**

#### **Title:**

The title clearly reflects the content of the article. However, I suggest replacement of “for” in the title with “of”

#### **Abstract**

The abstract is concise and captures the major points in the article.

55 SSP serves as the sample provider’s entry point... I suggest providers’ reason is that SSP ought to receive several samples; not one sample

#### **I. The Sampling and Sample Processing committee of ERGA**

Introduction clearly demonstrates the motivation for the study.

The introduction builds on relevant recent and past reference research.

76-77 Delete the phrase “one of which is the Sampling and Sample Processing committee (SSP)” It seems to appear slightly early. It can come at the beginning sentence of the next paragraph as follows:

88 The Sampling and Sample Processing committee (SSP) is a working group of volunteer expert ERGA members tasked with developing guidelines 83 to support sampling and sample processing.

#### **Materials and Methods**

This section contains sufficient information that can be replicated in similar researches.

#### **Results**

Data presented in the article are correct and unambiguously presented.

174 ...Widening countries with 44% and 50% of... I suggest ... Widening countries with 44 and 50 % of and

175 However, only 36% or 42% of the... However, only 36 or 42 % of the...

The tables and figures (charts) are clear and self-explanatory. However, the texts in Figure 3 could be made more legible for easier reading.

IV. Sample provision: connecting genome teams with 322 sequencing centres

324 arising from three main categories: biological, logistic, and legal issues. I rather think it should be:

324 arising from **four** main categories: biological, logistic, administrative/policy and legal issues.

### **364 Future taxon-specific best-practice guidelines**

The approach of having different sampling procedures for different taxa is very commendable as it would eliminate complications arising from structural and functional variations between the taxa.

### **490 References**

The listed references are appropriate

### **General Comment**

The article captured very important details associated with an active reference genome community of practice and vividly explained the challenges faced by such a consortium.