

eDNA vesistöjen tilan seurannassa

Tiina Laamanen, Veera Norros & Kristian Meissner
Energiateollisuuden tutkimusseminaari 7.2.2023



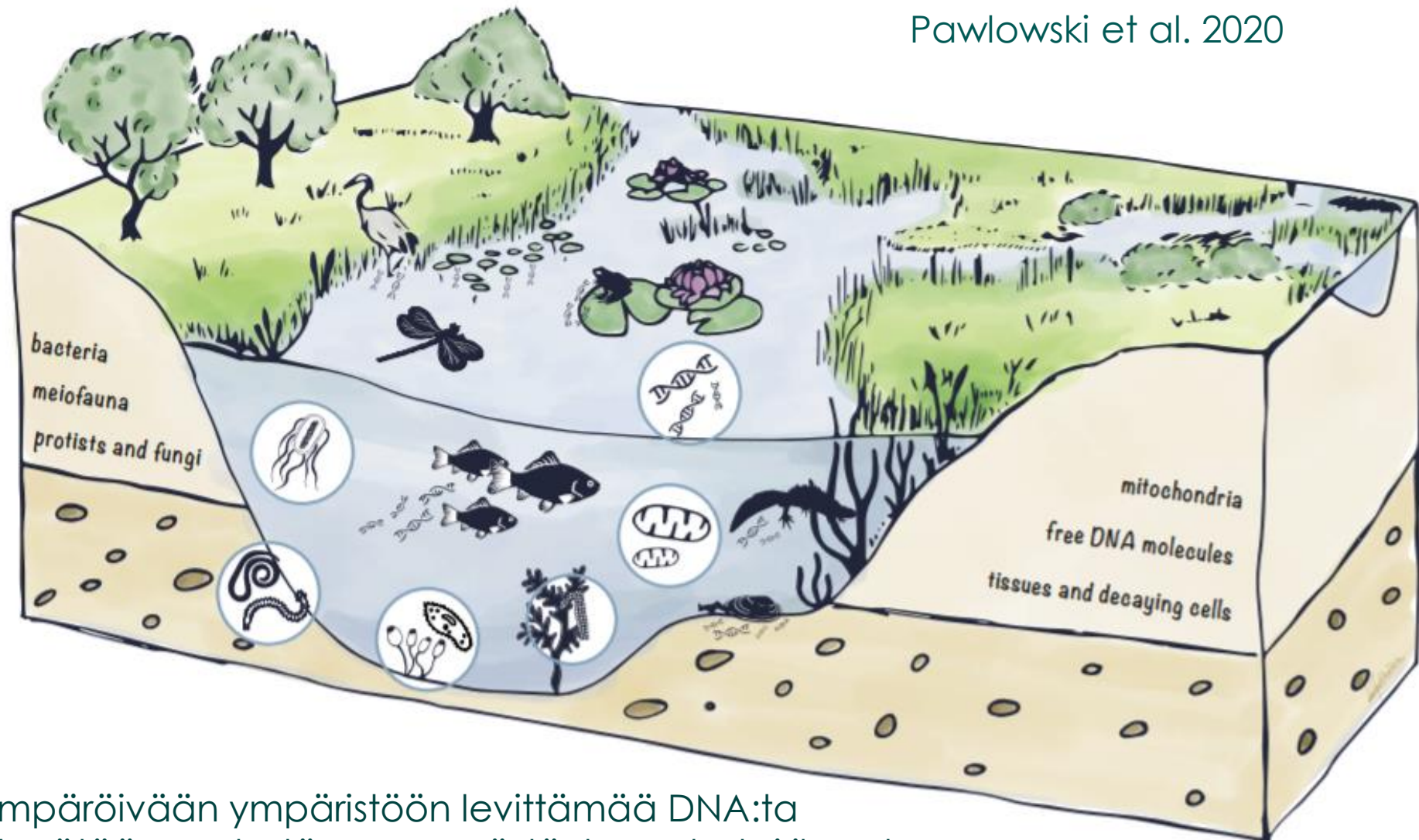
Suomen ympäristökeskus
Finlands miljöcentral
Finnish Environment Institute

Esityksen sisällys

- Lyhyt yleiskatsaus molekyylibiologisiin seurantamenetelmiin
- Menetelmien nykytila, mahdollisuudet ja haasteet
- Menetelmien käyttöönotto Suomessa – mitä seuraavaksi?

Mitä eDNA on?

Pawlowski et al. 2020



- Eliöiden ympäröivään ympäristöön levittämää DNA:ta
- Näytteet kerätään vedestä, maaperästä, lumesta tai ilmasta

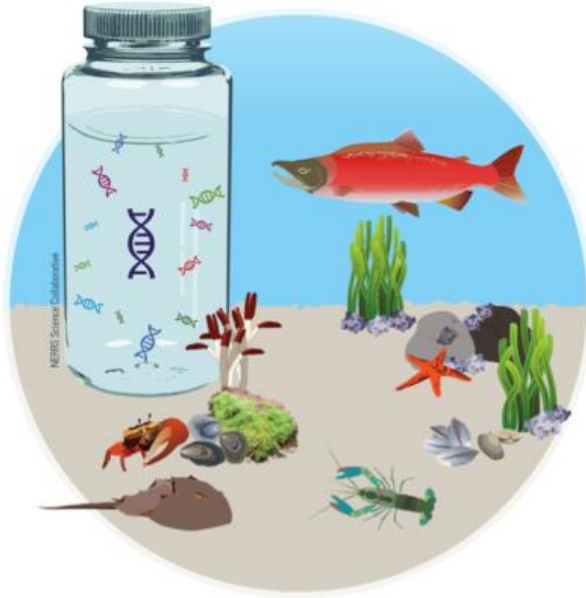
Mitä eDNA on?

Rowley et al. 2020

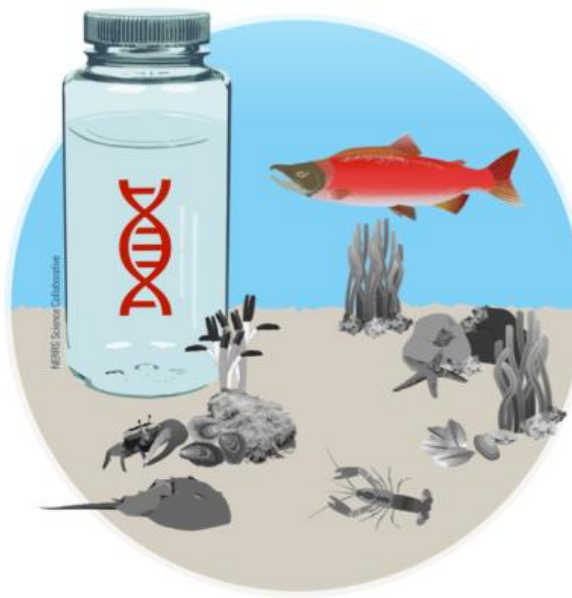
- Muunlaisia näytteitä:
 - Kudos- ja ulostenäytteet ym. → lajintunnistuksen varmistaminen, lajinsisäinen populaatiorakenne tai geneettinen monimuotoisuus
 - Yhteisö- tai bulkkinäytteet (esim. erilaisilla pyydyksillä)
- DNA:n sijaan tai lisäksi menetelmien perusteena voi olla RNA, jolloin saadaan tietoa ilmentyvistä geeneistä

- Eliöiden ympäröivään ympäristöön levittämää DNA:ta
- Näytteet kerätään vedestä, maaperästä, lumesta tai ilmasta

Erilaisia lähestymistapoja



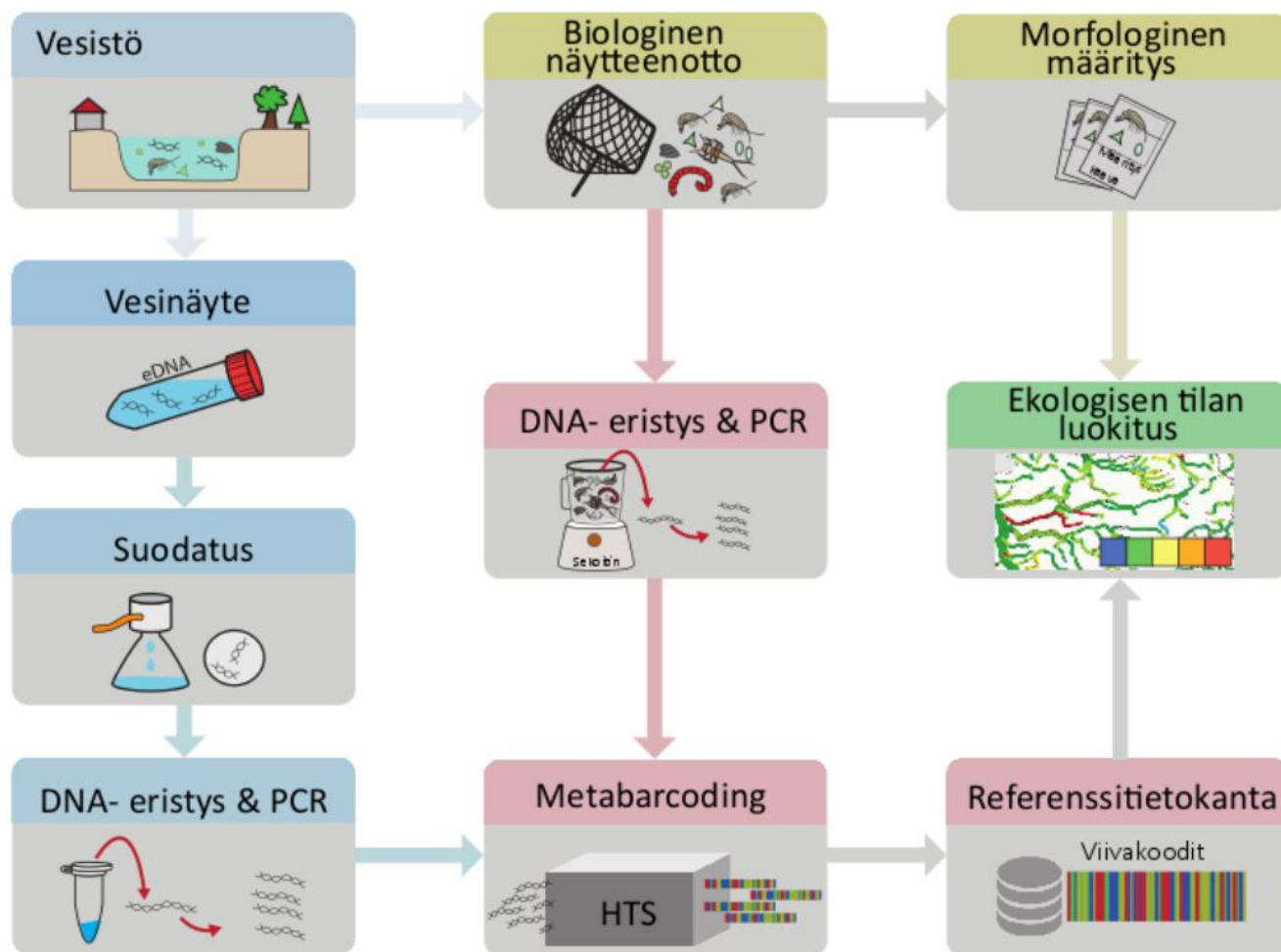
Metabarcoding identifies multiple species in a sample, but may be complex to interpret.



Single species PCR including quantitative (qPCR) digital (dPCR) is generally quicker, cheaper, but limited to identification of a single target organism.

5 *Figure 1. Metabarcoding and single species PCR are common eDNA analytic methods.*

Erilaisia lähestymistapoja

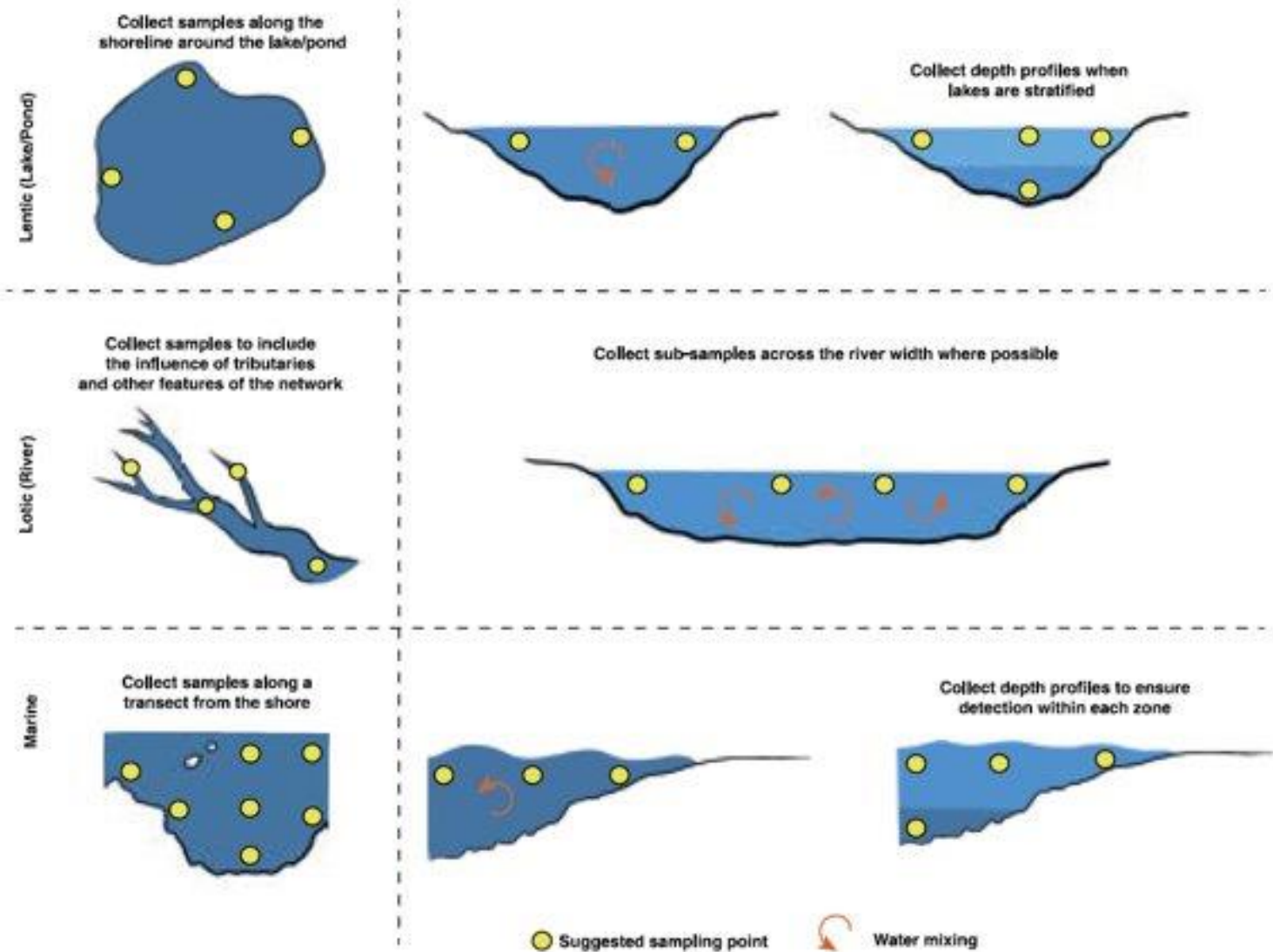
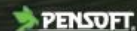


Näytteenoton suunnittelu

Bruce et al. 2021

A practical guide to DNA-based methods for biodiversity assessment

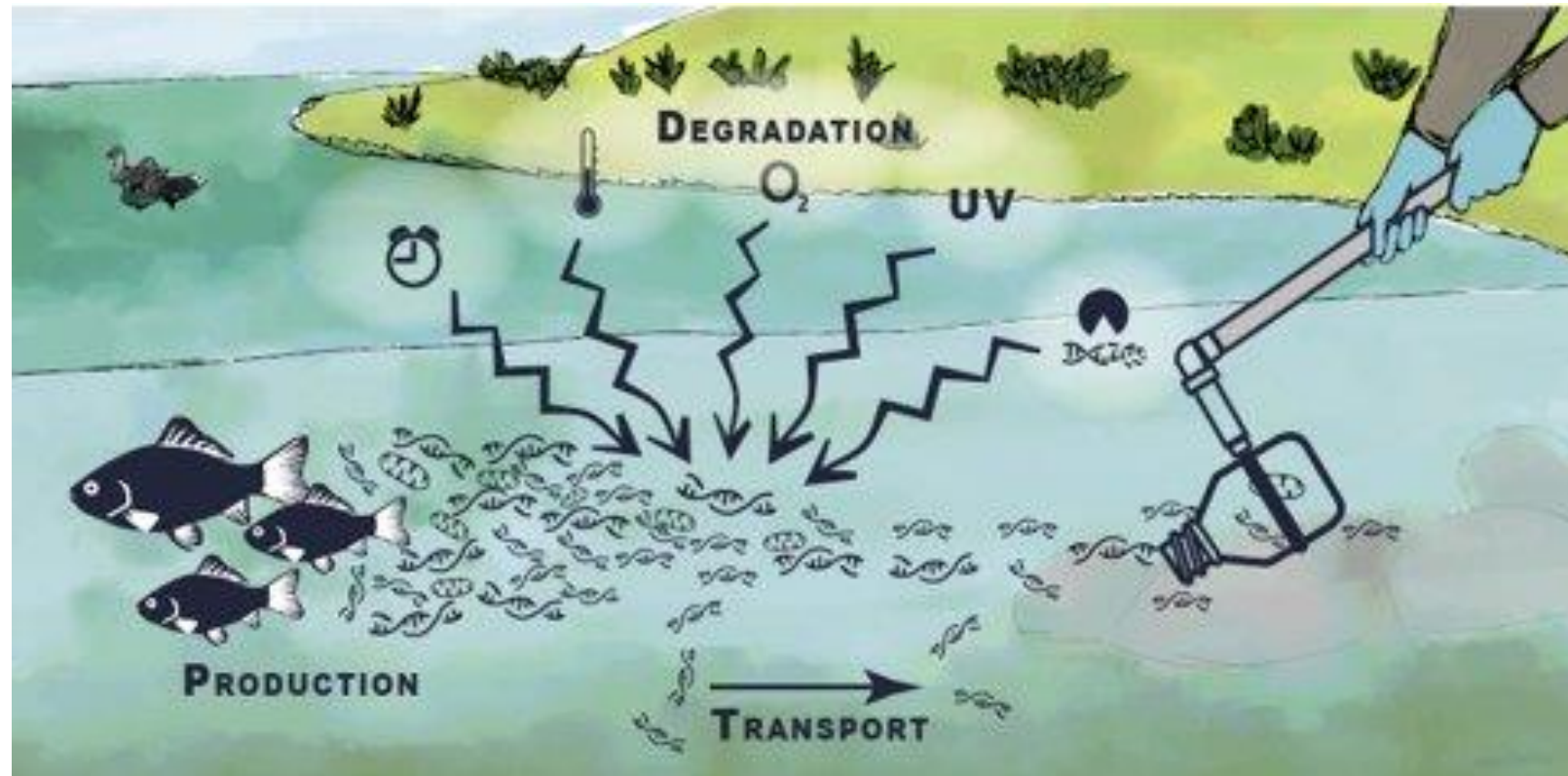
Kat Bruce, Rosetta C. Blackman, Sarah J. Bourlat, Micaela Hellström, Judith Bakker, Iliana Bista, Kristine Bohmann, Agnès Bouchez, Rein Brys, Katie Clark, Vasco Elbrecht, Stefano Fazi, Vera G. Fonseca, Bernd Hänfling, Florian Leese, Elvira Mächler, Andrew R. Mahon, Kristian Meissner, Kristel Panksep, Jan Pawlowski, Paul Luis Schmidt Yáñez, Mathew Seymour, Bettina Thalinger, Alice Valentini, Paul Woodcock, Michael Traugott, Valentin Vasselon, Kristy Deiner



eDNA:n kulkeutuminen ja hajoaminen

- eDNA voi kulkeutua yli kymmenestä kilometristä (purot) jpa 100 kilometriin (suuret joet)
- eDNA:n hajoaminen riippuu useista fysiokemiallisista ja biologisista tekijöistä
 - Mm. lämpötila, UV, pH, ionit ja mikrobiaktiivisuus

Pawloski et al. 2020

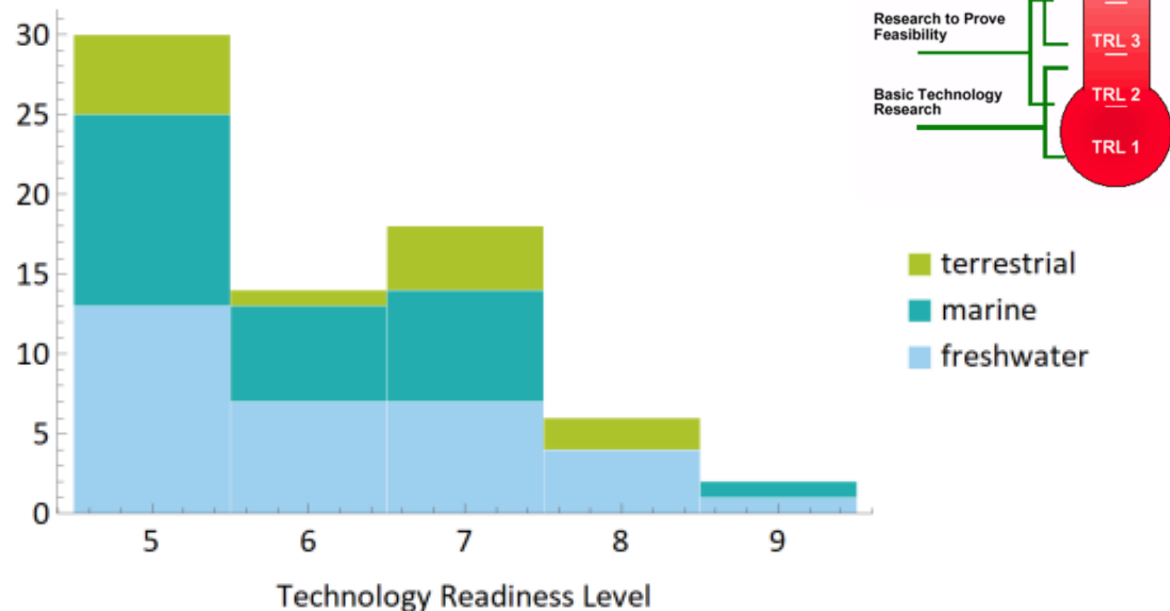




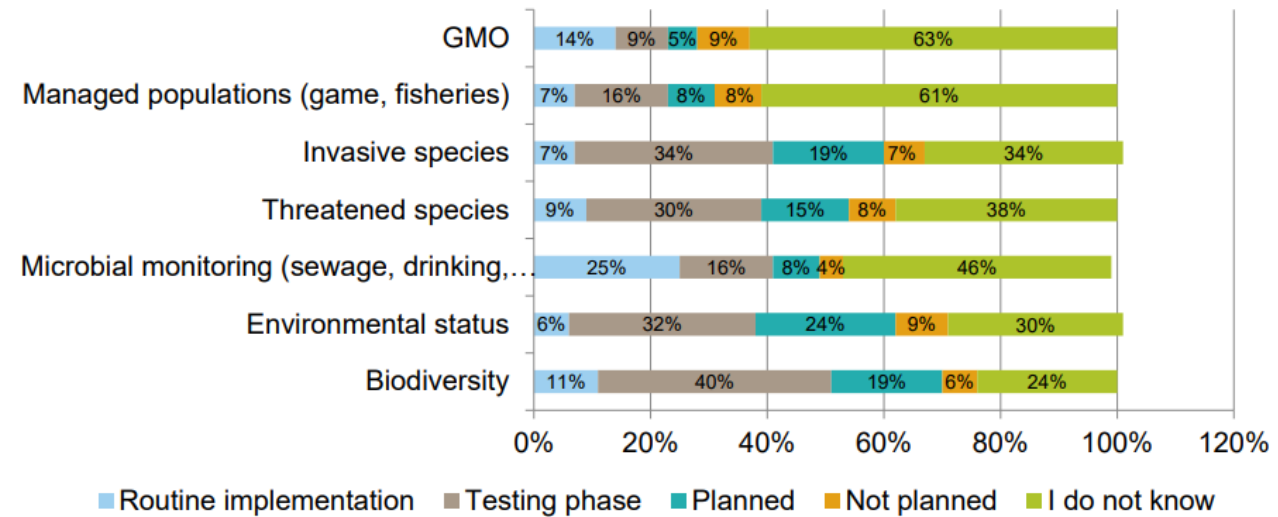
Menetelmien nykytila, mahdollisuudet ja haasteet

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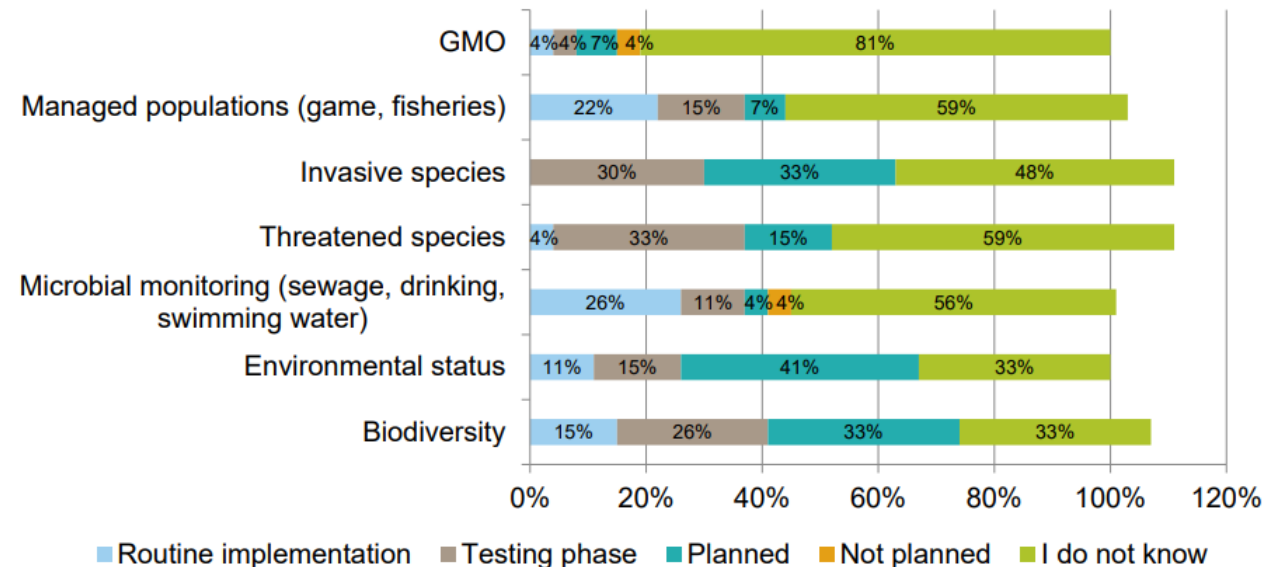
Menetelmiä on kehitetty laajasti eri eliöryhmille mutta niitä ei ole vielä otettu rutiinikäyttöön



A) International status of implementation (excluding Finland)



B) National status of implementation



CONSERVATION			SUSTAINABLE USE			GENES
	Threat status	Protection and restoration	Species	Habitats	Ecosystem functioning	Genetic diversity
NBSAP objective by 2035	The level of threat to species and habitats is no longer increasing.	The coverage of protected areas has reached 30%, one third of which is strictly protected. Restoration measures cover 15% of degraded habitats.	Populations of declined indicator species groups of different habitats have increased [20%].	The quantity and quality of habitats under land use pressure have increased [10%].	The capacity of ecosystems to provide central ecosystem services has improved [10%].	Genetic diversity has not decreased (effective population sizes of species have not decreased).
Possibilities offered by MoMM	- Improved detection of threatened species by eDNA-based targeted monitoring (e.g. from water, soil, sediment, air, stomach contents, honey). Sampling feasible also for citizen scientists without taxonomic expertise. - Delimitation of populations of closely related species - Detection of hybridization	Assessment of the impact of restoration using DNA-based community composition (taxonomy-based/taxonomy-free) or presence of indicator species.	- Monitoring of some poorly detectable groups feasible only with MoMM - eDNA-based targeted monitoring of indicator species. Sampling feasible also for citizen scientists without taxonomic expertise. - Cost-efficient monitoring of whole communities (incl. estimates of relative abundances) based on metabarcoding	- Assessment of habitat quality using DNA-based community composition e.g. in soil, water or air (taxonomy-based/taxonomy-free). - Assessment of habitat quality by DNA-based detection of indicator species and groups (e.g. microbes, fungi). - Assessment of habitat quality based on gene expression (eRNA)	- Inference of functional composition: DNA-based community composition and trait data - Assessment of ecosystem functioning based on gene expression (eRNA)	- Monitoring genetic diversity of target species (key/umbrella species, threatened species) - Estimation of effective vs. census population size - Delimitation of populations within species / assessing population structure
Challenges / limitations of MoMM	- Limited information on species abundance - Indirect observation (DNA transported e.g. by water or air) - Gaps in reference sequence libraries	- Representative sampling (high local variability in soil; DNA transported e.g. by water or air) - Sufficient reference data needed to establish DNA-based habitat quality measures.	- Comparability of MoMM-based and traditional abundance data - Standardized methods crucial for reliable and consistent monitoring	- Representative sampling (high local variability in soil; DNA transported e.g. by water or air) - Sufficient reference data needed to establish MoMM-based habitat quality measures.	- Representative sampling (high local variability in soil; DNA transported e.g. by water or air) - Sufficient reference data needed to establish MoMM-based measures for ecosystem functioning.	Estimating genetic diversity is by necessity species specific, and therefore significant investments are needed to increase the number of species with sufficient genomic knowledge

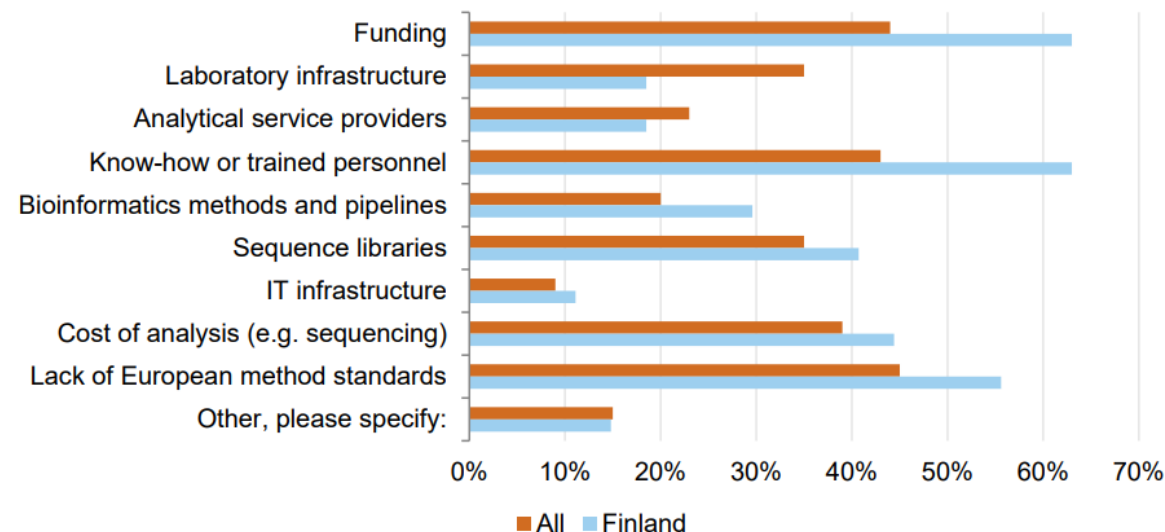
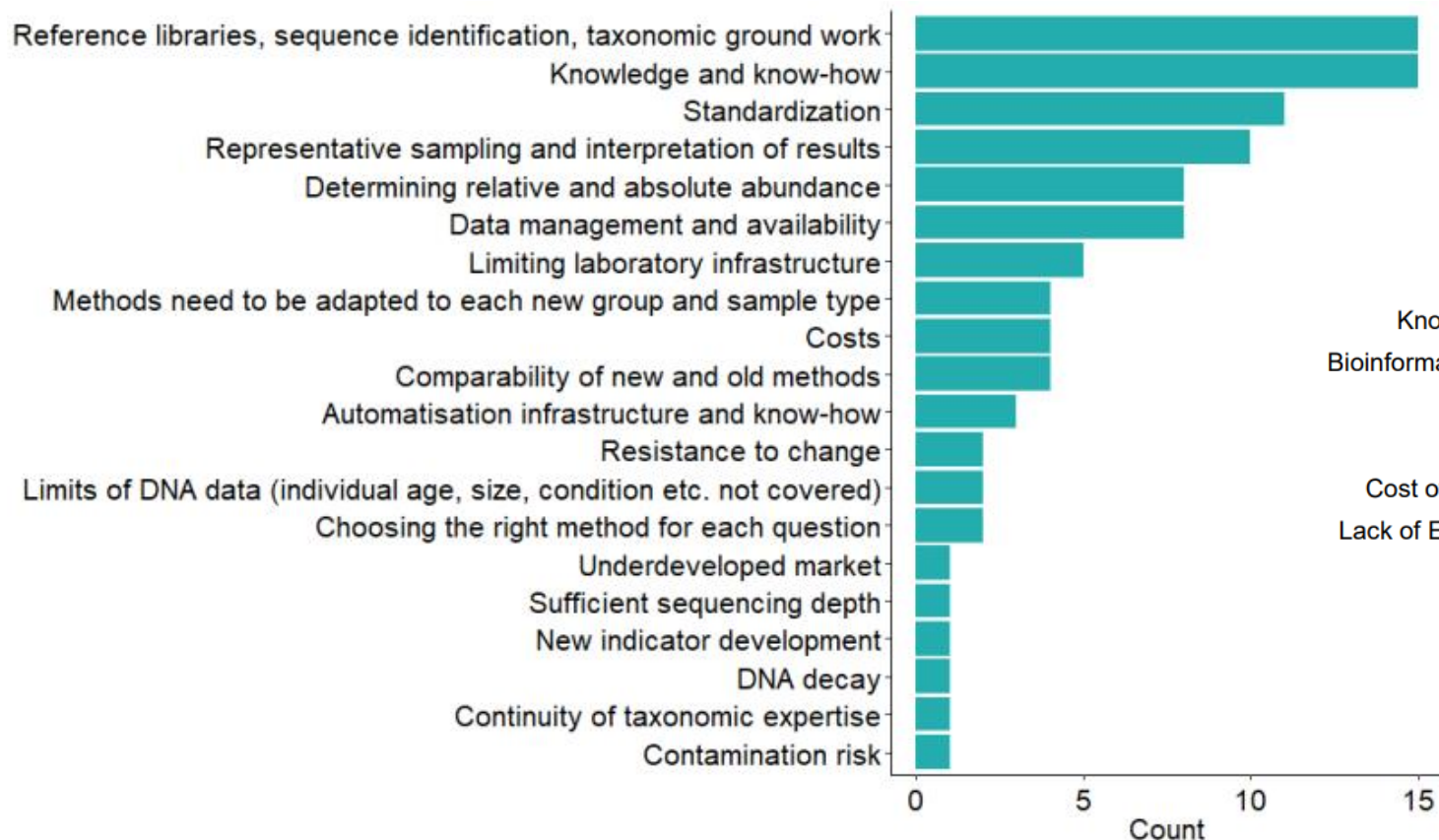
	CONSERVATION		SUSTAINABLE USE			GENES
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NBSAP objective by 2035	The level of threat to species and ecosystems no longer high					Genetic diversity has not decreased (effective population sizes of species have not decreased).
Possibilities offered by MoMM	- Implement threat reduction measures on land, water, air, and marine resources - Feasible scientific taxonomic delimitation of populations - Delimitation of populations within species - Delimitation of populations within species / assessing population structure	- Implement threat reduction measures on land, water, air, and marine resources - Feasible scientific taxonomic delimitation of populations - Delimitation of populations within species - Delimitation of populations within species / assessing population structure	- Implement threat reduction measures on land, water, air, and marine resources - Feasible scientific taxonomic delimitation of populations - Delimitation of populations within species - Delimitation of populations within species / assessing population structure	- Implement threat reduction measures on land, water, air, and marine resources - Feasible scientific taxonomic delimitation of populations - Delimitation of populations within species - Delimitation of populations within species / assessing population structure	- Implement threat reduction measures on land, water, air, and marine resources - Feasible scientific taxonomic delimitation of populations - Delimitation of populations within species - Delimitation of populations within species / assessing population structure	- Monitoring genetic diversity of target species (key/umbrella species, threatened species) - Estimation of effective vs. census population size - Delimitation of populations within species / assessing population structure
Challenges / limitations of MoMM	- Limitations of species-specific measures - Individual-based measures (DNA-based measures by water quality) - Gaps in knowledge of species diversity	- Limitations of species-specific measures - Individual-based measures (DNA-based measures by water quality) - Gaps in knowledge of species diversity	- Limitations of species-specific measures - Individual-based measures (DNA-based measures by water quality) - Gaps in knowledge of species diversity	- Limitations of species-specific measures - Individual-based measures (DNA-based measures by water quality) - Gaps in knowledge of species diversity	- Limitations of species-specific measures - Individual-based measures (DNA-based measures by water quality) - Gaps in knowledge of species diversity	Estimating genetic diversity is by necessity species specific, and therefore significant investments are needed to increase the number of species with sufficient genomic knowledge
		establish DNA-based habitat quality measures.		establish MoMM-based habitat quality measures.	establish MoMM-based measures for ecosystem functioning.	

Yhteenveto mahdollisuuksista:

- Uhanalaisten lajien tarkempi havaitseminen
- Vaikeasti havaittavien, huonosti tunnettujen ja/tai äärimmäisen monimuotoisten eliöryhmien seuranta
- Kokonaisten eliöyhteisöjen **kustannustehokas** seuranta
- Elinympäristön tilan seuranta eliöstön perusteella (myös ilman lajintunnistusta)
- Kohdelajien geneettisen monimuotoisuuden seuranta
- RNA → ekosysteemien toiminnan seuranta

Tärkeimmät haasteet: rahoitus, osaaminen, standardien puute

Lisäksi: referenssikirjastot, runsaustiedon saaminen, aineiston ja tulosten tulkinta



Menetelmien pilotointi Suomessa

- Tutkimusta ja kehitystä kaikilla ympäristön seurantaan tekevillä laitoksilla
- Rutiinikäytössä yksittäisillä lajeilla populaatioiden levinneisyyden/rakenteen seurannassa
 - Majavat, lohet, susi
- Laajamittaisempia metaviivakoodaukseen perustuvat pilottihankkeita käynnissä
 - Kasviplankton, eläinplankton, pohjaeläimet (GeMeKa & eDNA-monitor)
 - Metsien niveljalkaiset ja sienet (NFI-BIODIV)



Species/group	System	Methods	Stage	Conducted by
Viruses	terrestrial, freshwater, marine	eDNA metabarcoding, qPCR, eRNA (water, air, wastewater, ticks, fungi, plants, insects)	Pilot	THL, SYKE, FMI, Luke, universities
Bacteria	terrestrial, freshwater, marine	eDNA metabarcoding, qPCR (soil, water, air, wastewater, ticks)	Pilot	Luke, SYKE, FMI, THL, RV, universities
Endophytic microbes	terrestrial	eDNA metabarcoding of bacteria and fungi within plant tissues	Pilot	Luke
Benthic diatoms	freshwater	eDNA (biofilm) metabarcoding	Pilot	SYKE / Swedish Univ. of Agricultural Sciences
Phytoplankton	freshwater, marine	eDNA metabarcoding	Pilot	SYKE
Liverworts	terrestrial	Bulk DNA metabarcoding	Pilot	Univ. Turku, MH, SYKE
Vascular plants	terrestrial	eDNA metabarcoding/metagenomics (airborne pollen)	Pilot	FMI
Fungi	terrestrial, freshwater	eDNA metabarcoding/metagenomics (soil, water, air)	Pilot	Luke, SYKE, FMI, RV, universities
Freshwater pearl mussel (EN)	freshwater	eDNA + specific PCR	Pilot	Univ. Jyväskylä, MH
Benthic macroinvertebrates	freshwater, marine	Bulk DNA metabarcoding	Pilot	SYKE
Soil invertebrates	terrestrial	eDNA metabarcoding	Pilot	Luke
Arthropods	terrestrial	Bulk DNA metabarcoding	Pilot	Universities
Glanville fritillary butterfly (EN)	terrestrial	240 SNP panel, whole genome re-sequencing	Pilot (long-term research)	Univ. Helsinki
Noble crayfish (EN), signal crayfish (IAS)	freshwater	eDNA + dPCR	Pilot	Luke, Univ. Eastern Finland
Atlantic salmon (VU), Baltic salmon (VU)	freshwater, marine	An array of 220k SNPs	Routine	Univ. Helsinki, Luke
Fish	freshwater, marine (coastal)	eDNA + qPCR, eDNA metabarcoding	Pilot	Luke, MMM
Common frog, moor frog	freshwater	eDNA + qPCR	Pilot	Luke, Luomus, MMM
Lesser white fronted goose (CR)	freshwater	eDNA + Sanger sequencing	Pilot	Kiljuhanhi LIFE, MH, Univ. Oulu
Bats	terrestrial	DNA from feces + metabarcoding	Pilot	Luomus
Brown bear (NT)	terrestrial	DNA from feces + 96 Single Nucleotide Polymorphism (SNP) panel	Forthcoming pilot (2022)	Luke
European beaver (NT), Canadian beaver (IAS)	terrestrial	eDNA (wood chips) + PCR assays	Routine	Luke
European lynx	terrestrial	DNA from feces + 96 SNP panel	Forthcoming pilot	Luke
White-tailed deer (IAS)	terrestrial	DNA from feces + microsatellites	Pilot	Luke
Wolf (EN) and wolf-dog hybrids	terrestrial	DNA from feces/urine + 96 SNP panel	Routine 2022-	Luke
Wolverine (EN)	terrestrial	14 microsatellites and mtDNA control region (579 bp)	Pilot	Univ. Oulu, Luke

Kasviplanktonin eDNA-seurannalle ohjeet

Guidelines for using environmental DNA in Finnish marine phytoplankton monitoring

Improved biodiversity assessment
through method complementation

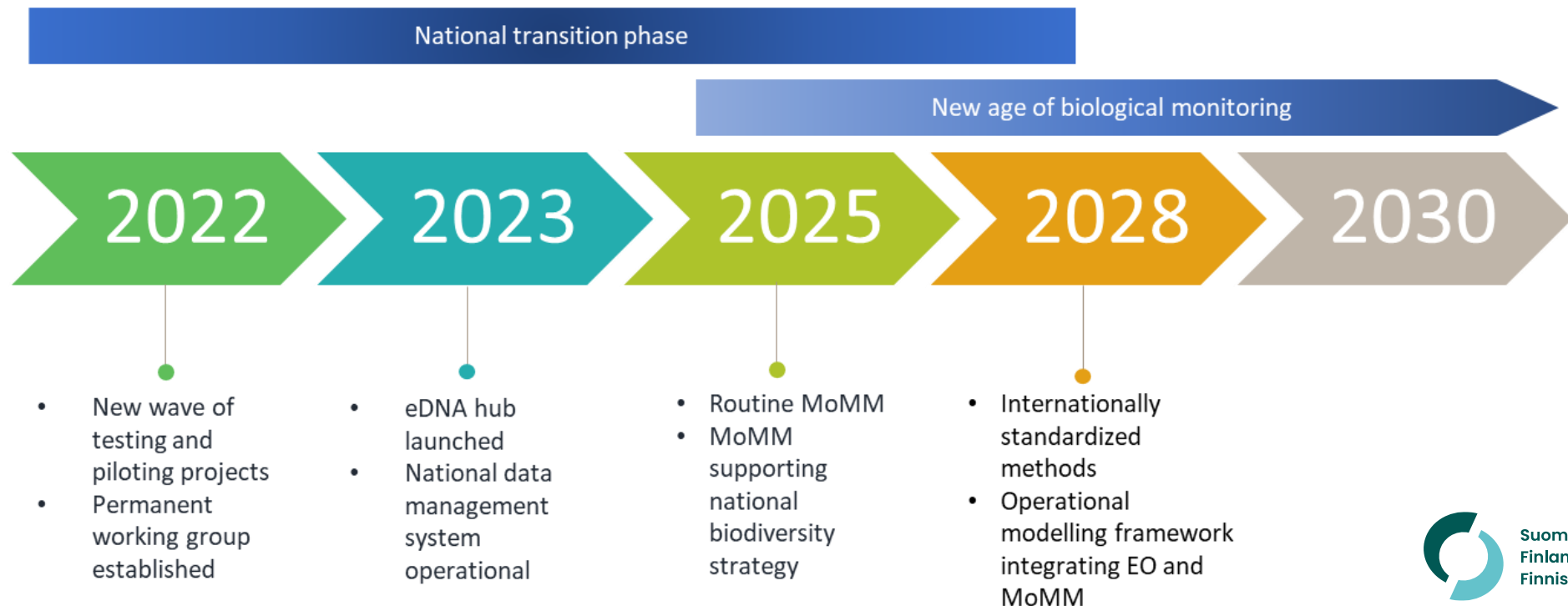
Jacqueline Jerney, Heidi Hällfors, Johanna Oja,
Anna Reunamo, Sanna Suikkanen, Sirpa Lehtinen

Mitä seuraavaksi?



Molekyylibiologiset menetelmät osaksi rutiiniseurantaa

- DNA-menetelmät ovat välttämättömiä kattavamman biodiversiteettiseurannan mahdollistamiseksi
 - Eivät kuitenkaan korvaa perinteisiä menetelmiä!
- ”Siirtymäaikana” tarvitaan entistä laajamittaisempaa ja koordinoitumpaa kehitystyötä sekä standardointia



Miten menetelmien käyttöönottoa ollaan edistämässä?

- Ympäristön seurannan strategian toimeenpano (FIMON)
 - eDNA-menetelmät mukana
- Kansallinen eDNA-ideointitiimi jatkaa toimintaansa (tiina.laamanen(at)syke.fi)
- Kansainvälinen standardointityö etenee
- eDNA-sivusto FEO-portaaliin – tietoa menetelmistä, projekteista, palveluntarjoajista
- DNA-pohjaisen biodiversiteettidatan tiedonhallintaa kehitetään mm. FinBIF-projektissa
 - Kv-datastandardi olemassa ja käytössä GBIF- ja OBIS-tietokannoissa



Kiitos muille eDNA-tiekartan kirjoittajille:

Kristian Meissner, Terhi Iso-Touru, Aapo Kahilainen, Sirpa Lehtinen, Katileena Lohtander-Buckbee, Henrik Nygård, Taina Pennanen, Marja Ruohonen-Lehto, Päivi Sirkiä, Sanna Suikkanen, Mikko Tolkkinen, Eeva Vainio, Sannakajsa Velmala, Kristiina Vuorio and Petteri Vihervaara

Linkkejä:

eDNA-tiekartta: <http://hdl.handle.net/10138/342992>

Yleistajuinen lentolehtinen: <http://hdl.handle.net/10138/345765>

Kasviplanktonohjeet: <http://hdl.handle.net/10138/351131>

SSUNGA-työpajan asiantuntijoiden kannanotto <http://hdl.handle.net/10138/350750>

Jos sinulla herää kysyttävää, tavoitat meidät:

tiina.laamanen(at)syke.fi, veera.norros(at)syke.fi & kristian.meissner(at)syke.fi



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