SPECIES SELECTION FOR LARGE-SCALE GENOME PROJECTS –

AN AUTOMATED PROCESS BASED ON

EXPLICITLY BOTTOM-UP DEFINED CRITERIA Torsten H. Struck

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Species selection for genome projects

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Why select species?

Large scale genome consortia









- More species to be sequenced than funding allows
- Develop criteria and strategies on how to select species
- ERGA/BGE choose a bottom-up approach involving SSP



Compile and assess individual selection criteria

- Definition and possible impact
- Decide on relevant ones
- Group into different stages and categories

Four stages in the selection process:

- Exclusion (3 criteria)
- Prioritization (11 criteria in 6 categories)
- Feasibility (11 criteria)
- Permits (3 criteria)



Develop different ranking processes (models)

• Determine importance of different categories





Reference or complete genomes per phylum



- Number of species with chromosome-level or complete genomes per phylum
- Y-axis is logarithmic
- Retrieved from GoaT on July 28th 2023.

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Develop different ranking processes (models)

- Determine importance of different categories
- 8 different models applying different ranking orders, but same weights within each category

Level	Model #7
1 st	Taxonomic representation
2 nd	Country representation & Certainty
3 rd	JEDI
4 th	Applicability & Novel leader



Test the different models using simulated and empirical data

Assess if the desired effect occurs



Presentation of selected models and results at ERGA council with representatives from each European country

- Vote on the preferred species prioritization process
- Ranking process #7 with 89.7%
- Implementing an additional ranking step favoring both countries and individual researchers with 43.6%
- Implement the additional ranking after stage 2 with 44,8%



The species selection process of BGE for community sequencing (2 rounds)



The selected species after stage 3 (round 1)

Wirenia	argentea	Mollusca	Norway
Hydrurus	foetidus	Ochrophyta	Norway
Tetrastemma	longissimum	Nemertea	Spain
Marifugia	cavatica	Annelida	Croatia
Proasellus	hercegovinensis	Arthropoda	Croatia
Diadema	setosum	Echinodermata	Greece
Alexandrium	minutum	Miozoa	France
Tritomurus	scutellatus	Arthropoda	Slovenia
Herpes	porcellus	Arthropoda	Hungary
Hydroglyphus	hamulatus	Arthropoda	Sweden
Omalisus	fontisbellaquei	Arthropoda	Czechia
Protonethes	ocellatus	Arthropoda	Montenegro
Hermodice	carunculata	Annelida	Spain
Phorcus	turbinatus	Mollusca	Spain
Alpioniscus	balthasari	Arthropoda	Croatia
Gammarus	oceanicus	Arthropoda	Poland
Gluvia	dorsalis	Arthropoda	Spain
Phyllidia	flava	Mollusca	Spain
Xylophaga	dorsalis	Mollusca	Spain

Eunicella	cavolini	Cnidaria	France
Triaenophorus	nodulosus	Platyhelminthes	Finland
Distaplia	bermudensis	Chordata	Italy
Cistus	crispus	Spermatophyta	France
Mytilopsis	leucophaeata	Mollusca	France
Pyrrhula	murina	Chordata	Portugal
Androsace	saussurei	Spermatophyta	France
Arnica	montana	Spermatophyta	Germany
Graellsia	isabellae	Arthropoda	Spain
Ailoscolex	lacteospumosus	Annelida	Spain
Botrylloides	israeliense	Chordata	Italy
Erebia	palarica	Arthropoda	Spain
Anodonta	cygnea	Mollusca	Switzerland
Cedrorum	azoricus	Arthropoda	Portugal
Dysdera	ambulotenta	Arthropoda	Spain
Rosalia	alpina	Arthropoda	Hungary
Trachusa	byssina	Arthropoda	Germany
Alyssoides	utriculata	Spermatophyta	Switzerland
Anisus	vorticulus	Mollusca	Germany



Effect of the selection process

• 11 (round 1) or 14 (round 2) of the originally 22 suggested phyla

The selected species

- 10 out of excluded 11 due to the feasibility check (round 1)
- 3 excluded and 5 included due to the feasibility check (round 2)



Effect of the selection process

- 16 out of 25 countries (round 1), 18 out of 29 countries (round 2)
- Again, mostly due to the feasibility check



All non-excluded species



Effect of the selection process

- Only one individual researcher with 2 species (round 1), one with 3 species, three with 2 species (round 2)
- One species one researcher



38 selected species

All non-excluded species



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Effect of the feasibility check

Round 1: 110 of 230 species considered not-feasible (47.8%) Round 2: 103 of 268 species considered not feasible (38.4%) Both rounds: 213 of 426 species considered not feasible (50.0%)

Too small or too large

- 19.6% due to small body size or low numbers of nucleated cells
- 23.8% due to large genome size
- 36.2% due to one of the two or both

Too bad condition

- 31.2% not snap-frozen
- 25.0% not possible to preserve within 5 minutes of their death
- 25.4% not possible to maintain a strict cold chain at -70°C

Too challenging to collect

• 17.5% not already collected or not easy to obtain



Conclusions

- Species selection process developed bottom-up with community involvement
- Four stage process with a total of 28 objective criteria
- Tested using simulated and empirical data
- Automated selection process based on a R script
- More research effort is needed to make the sequencing of reference genomes feasible for a much larger part of biodiversity



General applicability

Khrono.no Friday 05.04.2024 - 15:49

OPPTAKSMELDINGEN

Nye opptaksregler skaper debatt om mer karakterpress

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- Men hvor stor mener dere førstevalgsgruppen bør være?

— Det må vi se litt nærmere på. Vi kom ikke i mål med de beregningene nå. Det er også fordi det også er avhengig av hvor mange tilleggspoeng som blir stående igjen når Stortinget har gjort sine vedtak. Vi kunne hatt en mening om det hvis vi visste at det var vårt forslag som gikk gjennom, men hvis det blir justeringer i Stortinget vil kanskje vurderingene bli annerledes. Så dermed kommer vi tilbake til dette, sier Hoel.

- Essentially prioritization process
- Only one model, not several
- Not tested because parliament might make changes
- Testing would provide better basis for judgement if desired political effects will be accomplished



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Thanks for your attention!

