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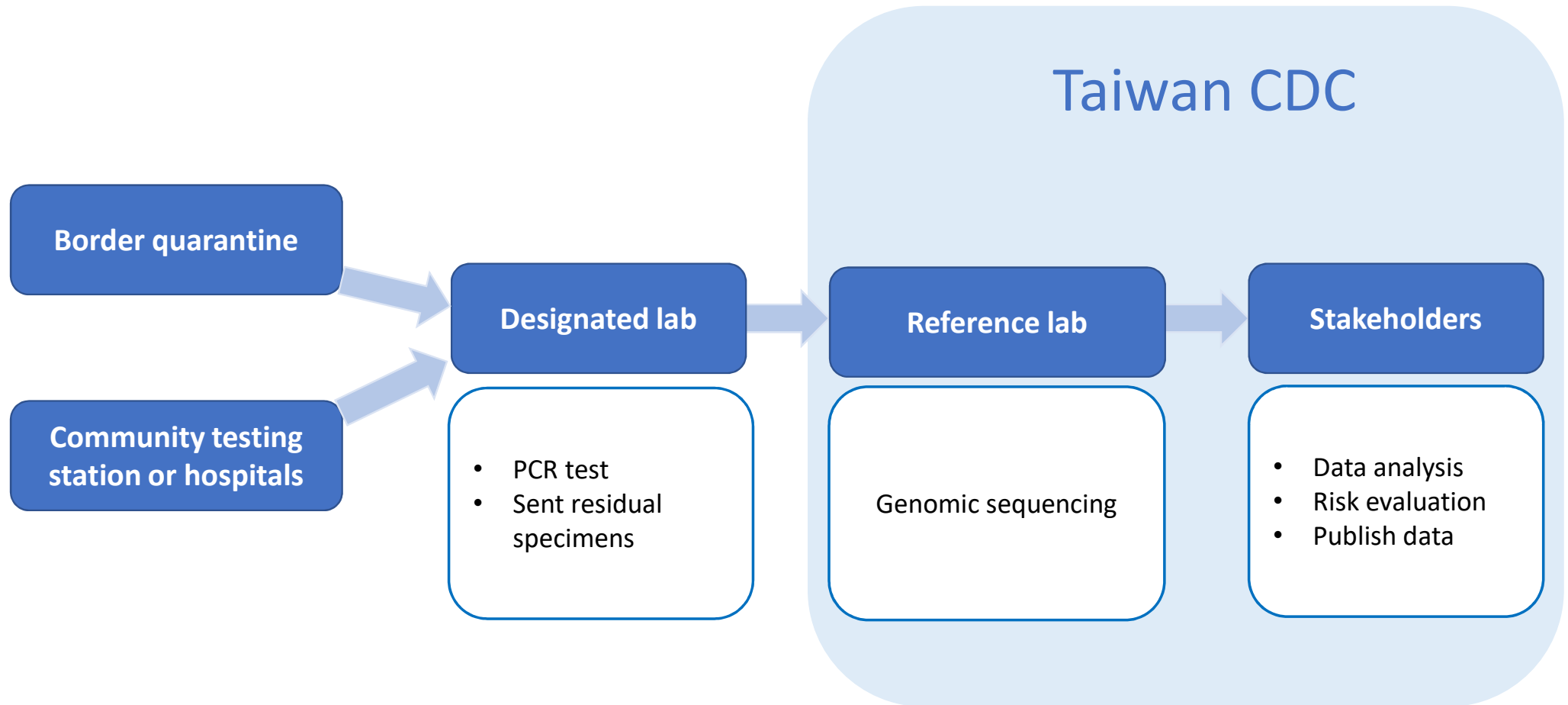
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Evaluation of the SARS-CoV-2 genomic surveillance system— Taiwan, 2021–2022

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Taiwan SARS-CoV-2 genomic surveillance system



Objective

To evaluate whether the genomic surveillance could:

- Provide timely monitoring
- Detect changing situation of SARS-CoV-2 variants
- Represent the situation in Taiwan

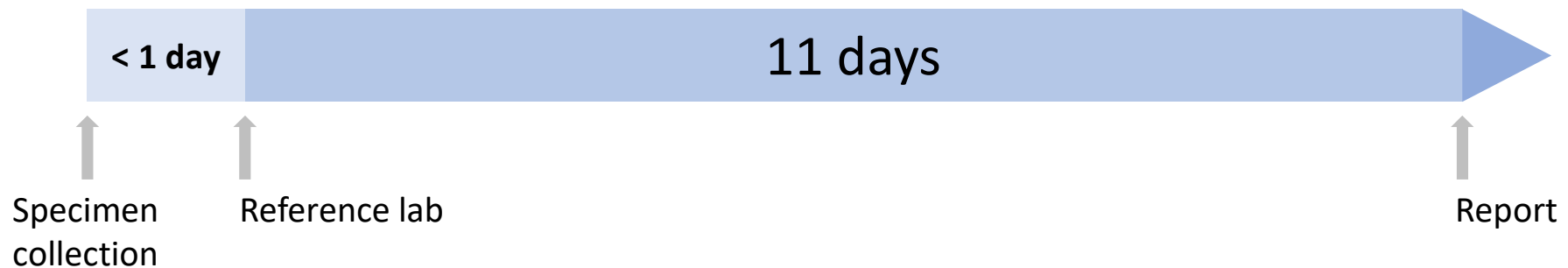
Methods (2021/6–2022/12)

Study group: locally-acquired cases

Data collection: interview stakeholders, COVID-19 database

Attribute	Parameter	Analysis
Timeliness	interval between specimen collection and genomic sequencing report	compared with other countries' data on GISAID website
Sensitivity	median number of genomic sequencing per week	evaluated whether the number was adequate to detect a change in the proportion of a certain variant from 1%–10% according to European CDC's guideline
Representativeness	proportion of re-infection in genomic sequenced cases	compared with proportion of re-infection in locally-acquired cases

Timeliness



- Median interval between specimen collection and genomic sequencing report: **11 days** (interquartile range: 9–14)
- GISAID: four countries with median days from specimen collection to deposition < 11 days
- The SARS-CoV-2 genomic surveillance in Taiwan was timely

Sensitivity

- The median number of genomic sequencing in locally-acquired cases:

48 per week (interquartile range: 17–99)

- ECDC's guideline

Positive SARS-CoV-2 cases per time unit	Sample size needed to detect a change in the proportion of a certain variant from 1%–10%
<500–5,000	68–77
> 5,000	78

→ 2 weeks to detect variants with proportion change from 1% to 10%

Representativeness

- **Sampling methods:**
 - targeted sampling of re-infection cases
 - random sampling in few cases
- **Re-infection: 53%** of the locally-acquired cases sequenced, even though only 0.55% of locally-acquired cases were re-infections

Conclusion

- SARS-CoV-2 genomic surveillance was **timely**
- **2 weeks needed** to detect a change in proportion of a certain variant from 1% to 10%
- Majority of sequenced viruses were from re-infected cases, **not random sampling**

Recommendation

- Increase the number of specimens from locally-acquired cases to at least 78 per week to shorten the time needed to detect changes in emerging SARS-CoV-2 variants
- Do random sampling

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