

INTRODUCTION

Lyme borreliosis is the most common tickborne disease caused by the bacteria Borrelia burgdorferi. It is transmitted by the Ixodes ticks

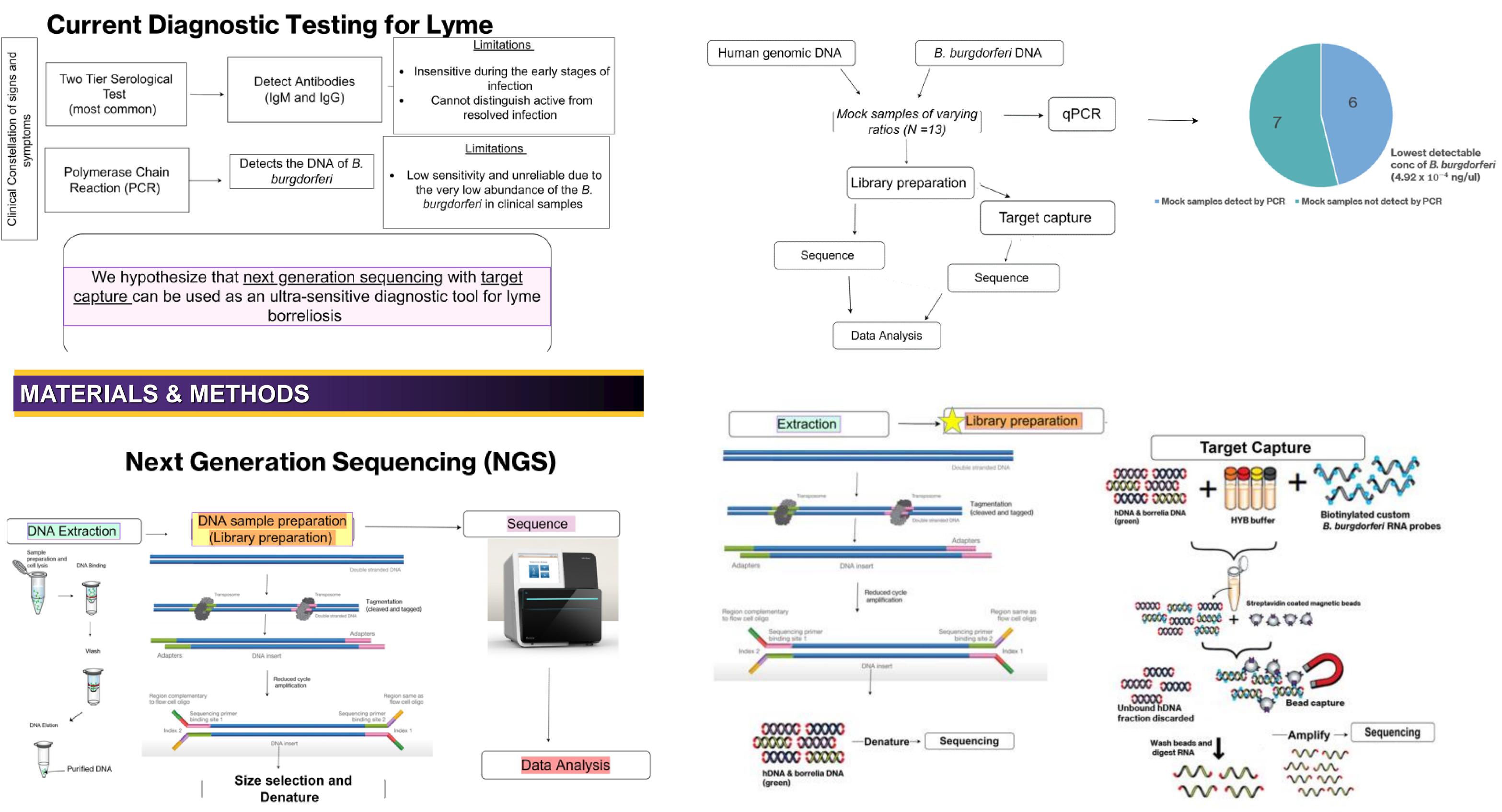


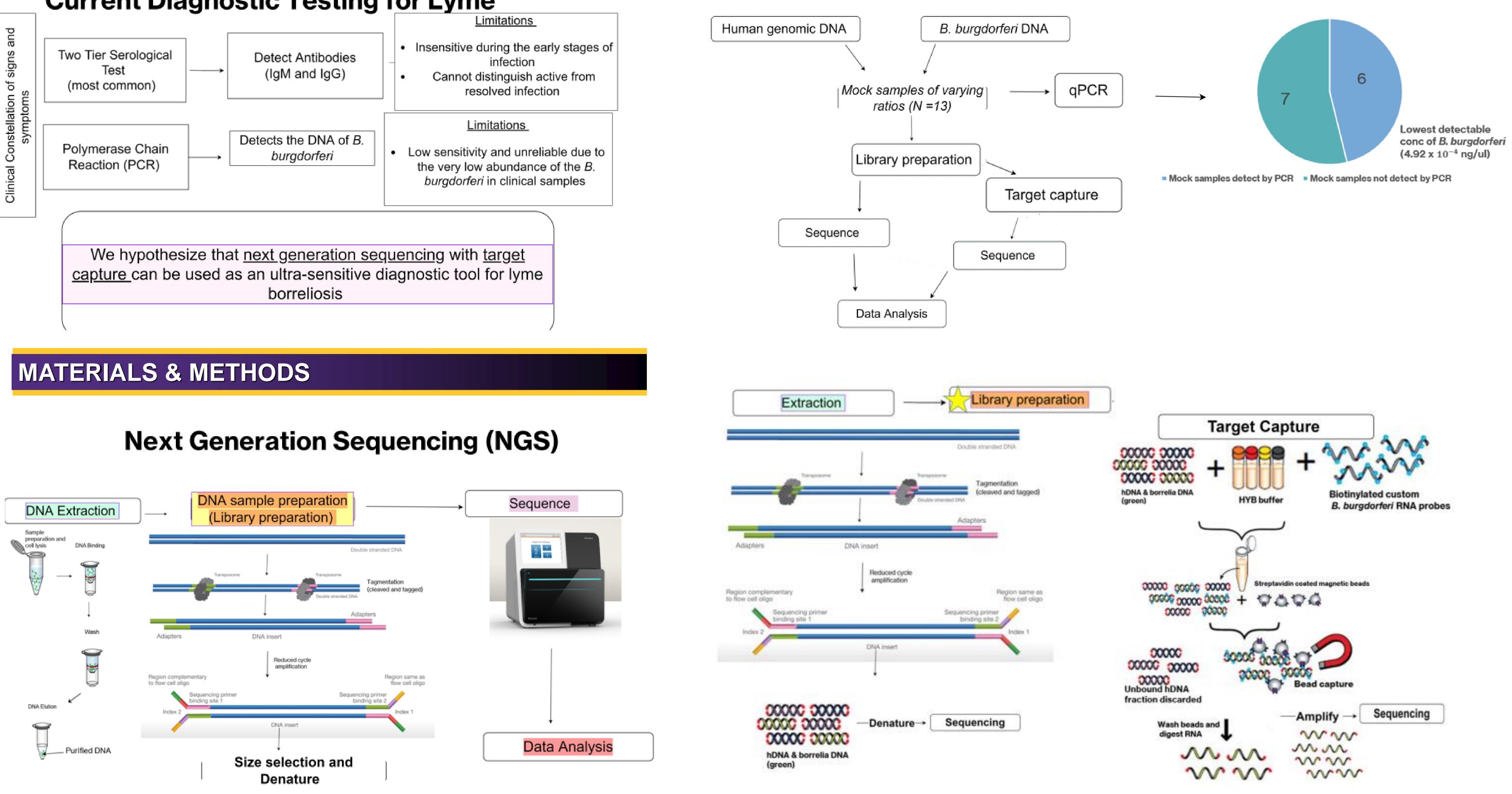


Stage 2: Neurological abnormalities or Carditis

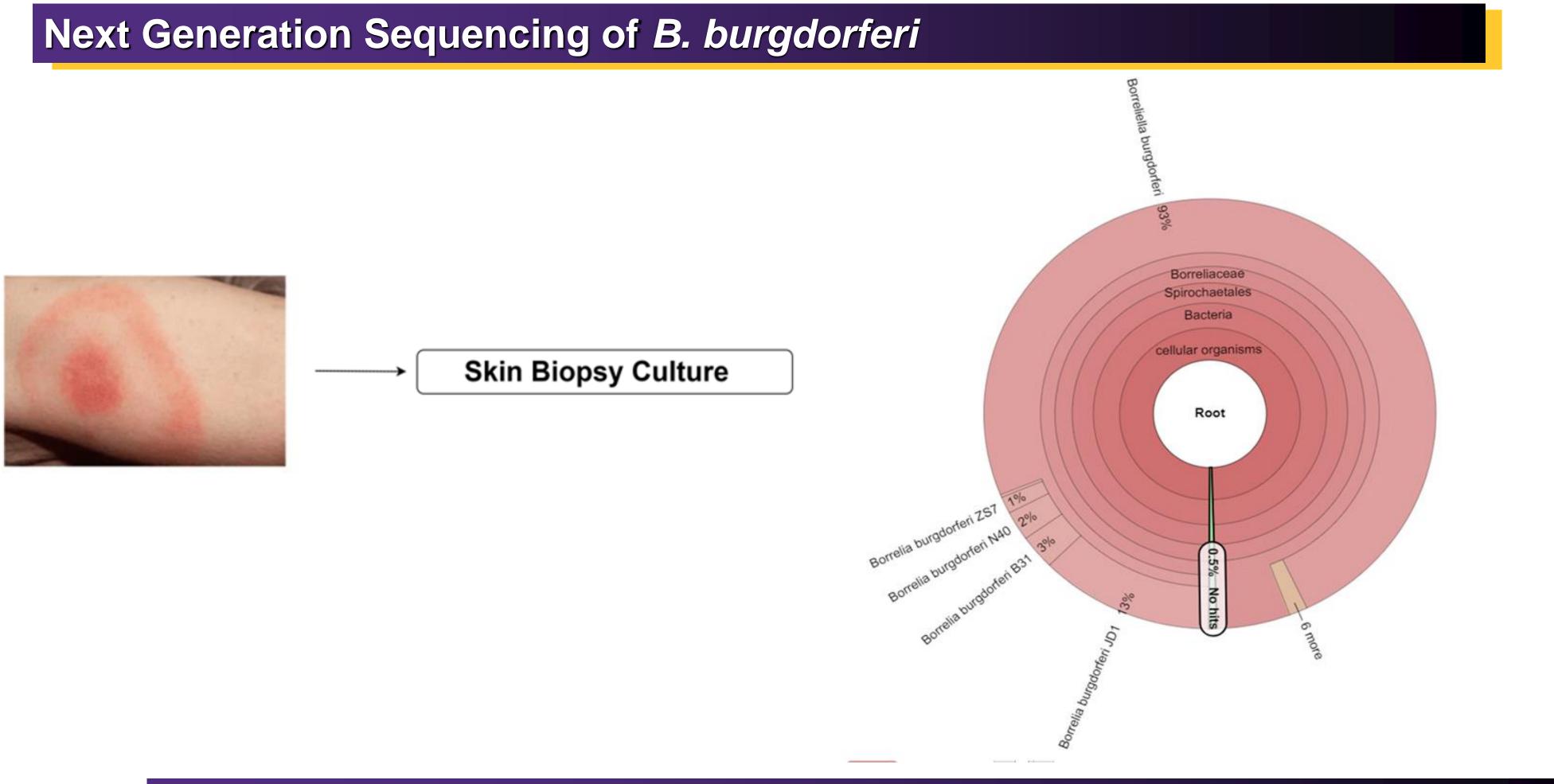
Stage 3: Arthritis

- The CDC reports about 30,000 annual cases of Lyme disease but the true estimate is about 500,000
- Next Generation Sequencing (NGS) is a technology sequence DNA and RNA





Next Generation Sequencing: An Ultrasensitive Diagnostic Tool for Lyme Borreliosis



Target Capture Enrichment to Increase the Sensitivity of NGS

Vanessa Amabo, Nolan Holbrook, Gordon Adams and Jacob Lemieux MD, PhD

DISCUSSION

- Next Generati to sequence the Borrelia burgo
- Target capture overcome the *burgdorferi* in We anticipate
- NGS with Target

Capture

REFERENCES

- Tatum R, Pearsor StatPearls [Interne [Figure, Borrelia a MD] Available from https://www.ncbi.
- Centers for Disea 2 Zoonotic Infectiou Lyme diseases (J Behjati S, Tarpey
- Educ Pract Ed. 20 Epub 2013 Aug 28
- Melnikov A, Galin pathogen genome Aug;12(8):R73. D PMC3245613.
- https://microbeon

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ion Sequencing was successfully used he genome of a cultured sample of <i>dorferi</i> . e enrichment of pathogen DNA can help low abundance of the <i>Borrelia</i> blood that:
NGS w/o target capture
 Shaver AL. Borrelia Burgdorferi. [Updated 2021 Jul 19]. In: et]. Treasure Island (FL): StatPearls Publishing; 2022 Jan oppearance in dark field microscopy. Image courtesy S Bhimj. m: <u>hlm.nih.gov/books/NBK532894/figure/article-18460.image.f1/</u> se Control and Prevention, National Center for Emerging and is Diseases (NCEZID), Division of Vector-Borne Diseases . uly 25, 2022). <u>https://www.cdc.gov/lyme/index.html</u> PS. What is next generation sequencing? Arch Dis Child 013 Dec;98(6):236-8. doi: 10.1136/archdischild-2013-304340 8. PMID: 23986538; PMCID: PMC3841808 sky K, Rogov P, et al. Hybrid selection for sequencing es from clinical samples. Genome Biology. 2011 OI: 10.1186/gb-2011-12-8-r73. PMID: 21835008; PMCID:
ine.com/borrrelia-burgdorferi-lyme-disease/

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