



Circulating cell-free DNA for response evaluation of intravascular lymphoma

Dries Deeren¹ · Malaïka Van Der Linden² · Francesca Dedeurwaerdere³ · Lien Deleu¹ · Caressa Meert¹ · Björn Menten⁴ · Jo Van Dorpe²

Received: 20 February 2019 / Accepted: 17 March 2019 / Published online: 6 April 2019
© Springer-Verlag GmbH Germany, part of Springer Nature 2019

Dear Editor,

Circulating cell-free tumor DNA (ctDNA) is detectable in the plasma of cancer patients. It has been shown that copy number aberrations (CNAs) can be detected by shallow whole-genome sequencing (sWGS) of circulating cell-free DNA (cfDNA) from patients with Hodgkin lymphoma [1]. Changes in the levels of cfDNA have been associated with tumor burden [2]. Liquid biopsies in the form of blood draws to analyze cfDNA may potentially provide diagnostic, prognostic, and therapeutic value.

Intravascular large B cell lymphoma (IVLBCL) is characterized by the predominant growth of large cells within the lumen of small blood vessels [3]. It is rapidly progressive, but prone to diagnostic delay because of the nonspecific nature of presenting symptoms [4].

Sites of lymphoma may not be apparent on imaging studies. Since lymphoma cells are difficult to detect at diagnosis, it is not clear how response evaluation should be performed. Its location within the bloodstream and its high proliferative index [3] make liquid biopsy an attractive option to monitor therapy efficacy.

We treated a 61-year-old patient with IVLBCL, diagnosed on kidney biopsy and presenting with high fever, with six cycles R-DA-EPOCH and two cycles of high-dose methotrexate. Genome-wide copy number profiles and pathology are shown in Figs. 1 and 2. Liquid biopsy after three cycles of R-DA-EPOCH and after completion of therapy could not demonstrate ctDNA. This was confirmed by repeated kidney biopsy (Fig. 2d). One year after therapy, the patient is still in complete remission.

✉ Dries Deeren
dries.deeren@azdelta.be

¹ Department of Hematology, AZ Delta, Wilgenstraat 2, B-8800 Roeselare, Belgium

² Department of Pathology, Ghent University Hospital, C. Heymanslaan 10, B-9000 Ghent, Belgium

³ Department of Pathology, AZ Delta, Wilgenstraat 2, B-8800 Roeselare, Belgium

⁴ Center for Medical Genetics, Ghent University Hospital, C. Heymanslaan 10, B-9000 Ghent, Belgium

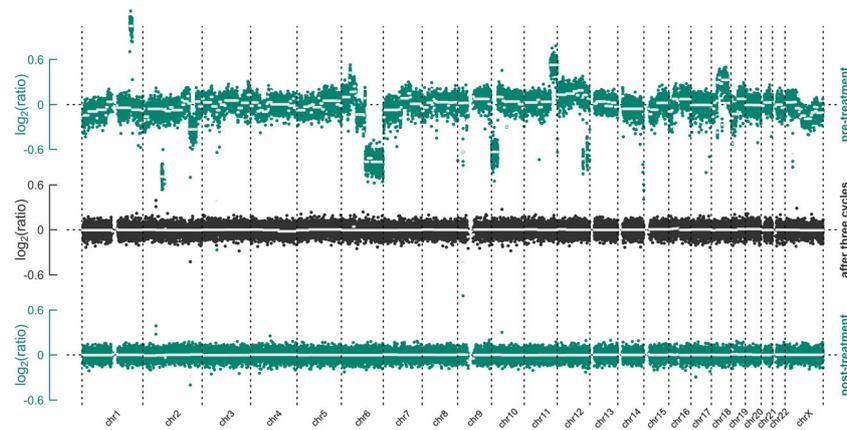
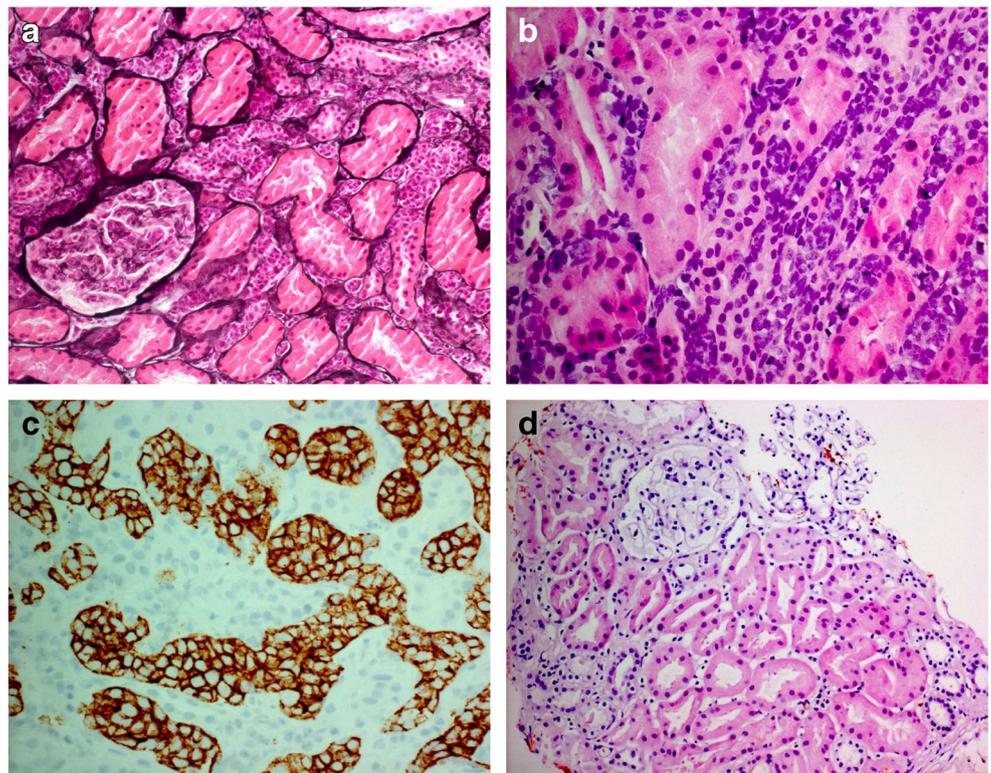


Fig. 1 Genome-wide copy number profiles obtained from shallow whole-genome sequencing of cell-free DNA (cfDNA). The methodology used here is essentially the same as for non-invasive prenatal testing (NIPT) for fetal aneuploidies [5]. Log₂-transformed ratios between the observed and expected (for the normal diploid state) number of reads per window (bin) of 100 kb are plotted across all chromosomes and are represented as a dot. A positive log₂ ratio

indicates a chromosomal gain (blue), while a negative log₂ ratio indicates a loss (red). Analysis of cfDNA at diagnosis showed many copy number aberrations, gains as well as losses (CNAs) (top panel). After three cycles R-DA-EPOCH no CNAs could be detected (middle panel). Analysis of cfDNA after treatment shows again a flat profile (bottom panel)

Fig. 2 **a** Renal biopsy, Jones stain, × 20: Glomeruli and tubules show no abnormalities. The interstitial capillaries are filled with atypical lymphoid cells. **b** Renal biopsy, H&E stain, × 40: The atypical lymphoid cells are medium-sized with irregular, slightly hyperchromatic nuclei. **c** Renal biopsy, immunohistochemical stain for CD20, × 40: the atypical lymphoid cells show strong membranous staining for CD20. Most cells display weak membranous positivity for CD5 (not shown). They are negative for myeloperoxidase, CD3, CD10, CD56, TDT, SOX11, and cyclin D1. **d**: Renal biopsy, H&E, × 40: after treatment, no residual atypical lymphoid cells are morphologically recognizable



Compliance with ethical standards

Ethics All human and animal studies have been approved by the appropriate ethics committee and have therefore been performed in accordance with the ethical standards laid down in the 1964 Declaration of Helsinki and its later amendments. All procedures followed were in accordance with the ethical standards of the responsible committee on human experimentation (institutional

and national) and with the Helsinki Declaration of 1975, as revised in 2008 (5).

Informed consent Informed consent was obtained from all patients for being included in the study.

Conflict of interest The authors declare that they have no conflicts of interest.

References

1. Vandenberghe P, Wlodarska I, Tousseyn T, Dehaspe L, Dierickx D, Verheecke M, Uyttendaele A, Bechter O, Delforge M, Vandecaveye V, Brison N, Verhoef GE, Legius E, Amant F, Vermeesch JR (2015) Non-invasive detection of genomic imbalances in Hodgkin/Reed-Sternberg cells in early and advanced stage Hodgkin's lymphoma by sequencing of circulating cell-free DNA: a technical proof-of-principle study. *Lancet Haematol* 2(2):e55–e65. [https://doi.org/10.1016/S2352-3026\(14\)00039-8](https://doi.org/10.1016/S2352-3026(14)00039-8)
2. Akca H, Demiray A, Yaren A, Bir F, Koseler A, Iwakawa R, Bagci G, Yokota J (2013) Utility of serum DNA and pyrosequencing for the detection of EGFR mutations in non-small cell lung cancer. *Cancer Gene Ther* 20(3):73–80. <https://doi.org/10.1016/j.cancergen.2013.01.005>
3. Ponzoni M, Campo E, Nakamura S (2018) Intravascular large B-cell lymphoma: a chameleon with multiple faces and many masks. *Blood* 132(15):1561–1567. <https://doi.org/10.1182/blood-2017-04-737445>
4. Handy Marshall C, Nahas-Vigon J, Manesh R, Gelber AC (2018) Just beneath the surface. *N Engl J Med* 379(10):968–973. <https://doi.org/10.1056/NEJMcp1802664>
5. Van Roy N, Van Der Linden M, Menten B, Dheedene A, Vandeputte C, Van Dorpe J, Laureys G, Renard M, Sante T, Lammens T, De Wilde B, Speleman F, De Preter K (2017) Shallow whole genome sequencing on circulating cell-free DNA allows reliable noninvasive copy-number profiling in neuroblastoma patients. *Clin Cancer Res* 23(20):6305–6314. <https://doi.org/10.1158/1078-0432.ccr-17-0675>

Publisher's note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.