Cellular Narratives in / Nuclear Time: On Epigenetic Memory as a Multi-Temporal Interpretive Mechanism/On (or as) the Molecular Mechanism of Cellular Narratives

Abstract

With the imminent threat of a nuclear arms race acceleration, and in the context of the existing implications of colonial nuclear violences, this paper seeks to trace the biological consequences for lives altered by the atom bomb, through Karen Barad's Agential Realist ontology. To do this, I first present the paradigmatic development in the field researching the effects of radiation exposure, from direct genetic mutagenesis to the contribution of epigenetic responsivity. Based on the congruence of the epigenetic model with agential realism, I continue by following the experience of Kyōko Hayashi as it is told in her semi-autobiographical atomic bomb novella *From Trinity to Trinity*, to consider what might be happening in her cells as her story unfolds. This is based on Barad's own diffractive reading of Hayashi's novella through their understanding of time as ontologically thick and multiple. Through this reading, I forward a speculative, yet scientifically informed interpretation of epigenetic function as materially and agentially manifesting such a temporality. By introducing a different conceptualization of epigenetic function, my aim is to stir new imaginings congruent with the relational, entangled nature of epigenetic mechanisms.

Keywords: Barad, Agential realism, nuclear, Kyoko Hayashi, epigenetics, epigenetic memory, chromatin, nucleus, Walter Benjamin.

Without sustained remembrance, we cannot learn to live with ghosts and so cannot think.

Donna J. Haraway, *Staying with the Trouble* (2016, p. 39)

As a rule, the more abstract the science, the greater the challenge for both critique and revision. (Weasel 1997, The cell in relation: an ecofeminist revision of cell and molecular biology, p. 51)

Prologue

On the morning of August 9, 1945, 14-year-old Kyōko Hayashi was working at the Mitsubishi Weaponry Ōhashi Factory in Nagasaki, where she and her peers were mobilized for the Japanese war effort. At 11:02, the 4.5-ton plutonium bomb dropped by the US Air Force 1.3 kilometers away was detonated at around 500 meters above ground for maximal damage (Kerr et al. 2005). More than 500,000 people were exposed to the two atom bombs dropped three days apart in August 1945, on Hiroshima and Nagasaki. Many thousands perished immediately from the tremendous heat, impact and radiation of the nuclear blast. Within 5 months, more than 210,000 people died of injuries and radiation poisoning. "[M]ore than 210,000 remaining victims… survived the first five months of death and agony and became *hibakusha*" (Tomonaga 2019, 493), literally, "persons who experienced the explosions". Among them the by-now 15-year-old Hayashi.

Introduction

The list of symptoms suffered by *hibakusha* in the aftermath of the explosions is long and excruciating. Symptoms including the significant increase in cases of leukemia in the years immediately following the bombing (Folley et al. 1952; Preston et al. 1994), and a significant increase in cases of solid tumors in the following years (Thompson et al. 1994; Tomonaga

2019), were attributed to the mutagenic effects of ionizing radiation (IR).[1] This effect, first recognized in the 1920s (Muller 1927; Stadler 1928a, 1928b), had become a matter of popular knowledge and continued to be the focus of scientific research for decades—it was, after all, *The Century of the Gene* (Keller 2002; Calabrese 2015).

In what follows, I briefly present the traditional linear model of mutagenic radiation effects, noting its incongruence with both empirical data, and the physics that produced the effects it aims to explain. Subsequently, I introduce a relatively recent alternative epigenetic model, with better explanatory rigor and emergent empirical support. This model implicates the involvement of complex reactive mechanisms guiding cellular responsivity to IR. Following a short discussion of epigenetic function, the promise this holds and some of the problems that epigenetic research has encountered are raised.

Having dedicated over a decade in my scientific past to processes that take place in cellular nuclei, and given the wealth of data and discussion, I wish to propose a different understanding of epigenetic function. This alternative analysis draws on the existing conceptualization of epigenetic mechanisms as materially bearing the impressions of experiences, read through Karen Barad's (2007) Agential Realist ontology. In this, my intention is to unsettle the reductionist and determinist paradigmatic hold on epigenetic research, by demonstrating that it is possible to come up with radical interpretations, with reformulations of causality, which are interdisciplinarily informed, including by molecular biology itself. In this I also seek to share my own appreciation of the richness of cellular biology, in which the "resolutely unpoetic language" of epigenetics (Margaret Lock 2015), criticized for its reductionist translation of life experiences to indistinguishable molecular marks (e.g., Landecker 2016), is not a feature but rather an articulating choice of the science and the scientists who research it.

To do this, I turn to Hayashi's detailed work as a chronicler of August 9, and to Barad's diffractive reading of her novella, *From Trinity to Trinity* (Hayashi 2008, 2010; Barad 2017a). Through their quantum theory based agential realist reading, I introduce a speculative story of what might be happening in cell nuclei as they negotiate living within this world.

The Biology of Radiation Exposure

The linear model

According to the linear no threshold (LNT) genetic model, the extent of DNA damage and corresponding health consequences following IR-exposure are directly and linearly linked to the level of radiation exposure. Furthermore, this model determines that the resulting damage occurs immediately or shortly after radiation, and is confined to directly exposed cells. Under this framework, prolonged effects may only be caused by unrepaired mutations which are then clonally passed to progeny (cells or offspring; Schofield and Kondratowicz 2018; Belli and Tabocchini 2020). In other words, the LNT model assumes that the effects of radiation remain local and discrete, both spatially and temporally.

Right from the onset of research, however, the biology seemed to be telling a more intricate story (MotherSill and Seymour 2012; Calabrese 2013, 2017). The findings of decades of laboratory as well as epidemiological studies[2] simply did not fit the LNT model (Calabrese and Golden 2019). Unlike the model's predictions, radiation can have delayed, carcinogenic as well as other detrimental effects sometimes taking years or decades to develop, and even present only generations later (Tamminga et al. 2008; Kamstra et al. 2018; Dubrova and Sarapultseva 2020). At lower doses, IR can actually induce adaptive and hormetic[3] effects (Averbeck et al. 2018; Shibamoto and Nakamura 2018; Ghosh 2022).

Furthermore, and inconsistent with this model, cells and tissues not directly exposed to radiation are often affected, through bystander and abscopal effects (Swati and Chadha 2021, MotherSill and Seymour 2022). Bystander effects have even been observed at the inter-organism level, for example in crustaceans, fish and rodents (MotherSill and Seymour 2012; Reis et al. 2018), demonstrating that radiation can impact neighboring, non-exposed individuals, and even invoke IR responses of entire (not directly exposed) ecosystem (MotherSill and Seymour 2009; Smith et al. 2013; Reis et al. 2018; Matarèse et al. 2020). Such effects simply cannot be accounted for by the LNT paradigm.

The interpretation of these observations is further complicated by the considerable variability in observed phenotypes depending on the characteristics of the individual organisms (or tissues) exposed (Paunesku et al. 2021; MotherSill and Seymour 2022). While accounting for much of this variability remains a point of profound paradigmatic dispute in the field, its existence underscores the complexity and contextual nature of biological responses to IR. Yet, despite repeated contestation, the LNT has remained in use, and is still commonly employed to guide radiation risk assessment (UNSCEAR 2022; Jones 2019; Wojcik 2022).[4]

Accounting for non-linearity: Epigenetic involvement in response to IR exposure

While IR has been traditionally associated with mutagenesis, epigenetic changes have been recurrently suggested since the mid-2000s, as the "missing link" able to account for the observed effects of IR exposure beyond direct mutagenesis, particularly in low and medium radiation doses (Baverstock and Belyakov 2005).[5] Epigenetic responsivity to IR has since become a distinct research avenue within the broader field of epigenetics.

Epigenetic mechanisms play a vital role in the development, morphology, physiology and health of essentially all organisms (Willbanks et al. 2016).[6] They function in response to

environmental changes by modifying the context of DNA, its organizing structures-known as chromatin (the stuff of chromosomes). This is mediated (mostly) through a range of specific marks added to chromatin to alter the physical characteristics and accessibility of genomic loci and thus regulate their function (Soshnev, Josefowicz and Allis 2016).[7] By functioning interrelatedly, epigenetic mechanisms orchestrate complex nuanced responses to (intrasomatic and extrasomatic) environmental cues: from our internal temperature, the air we breathe and the food we eat to our social experiences (Jablonka and Lamb 2014).

In recent years many of the observed IR effects have been shown to correlate with significant epigenetic changes, and in some cases, the involvement of such mechanisms has been directly demonstrated (Schofield and Kondratowicz 2018; Dubrova and Sarapultseva 2020; Belli and Tabocchini 2020; Swati and Chadha 2021). The epigenetic modifications found to occur in response to IR exposure are associated with various cellular pathways, including DNA repair, and many are thought to be involved in cell signaling-related gene regulation, such as cell cycle arrest and programmed cell death (apoptosis). The involvement of these pathways can be expected as cells cope with the damage they incurred. Importantly, certain observed modifications are related to intercellular signaling and to adaptive changes in cell radiosensitivity, offering a possible mechanistic explanation for the observed phenomena (Tharmalingam et al. 2019; Ghosh 2020). Thus, contrary to the LNT model, the data as well as the epigenetic model suggest active cellular responses to radiation at less-than-acute doses. That is, cells not only attempt to repair the damage caused by IR, but also undergo changes and reorganization to rearticulate themselves as cells and bodies that have experienced radiation.

The implications are of course not merely theoretical, nor limited to the past. Some researchers have raised their concern that the continued reliance on the LNT model may

have led both researchers and regulating agencies to underestimate the risk of radiation, with devastating effects (e.g., Burgio, Piscitelli and Migliore 2018; cf. Tharmalingam et al. 2019). They are referring for example to the increase in infant leukemia across Western Europe following the Chernobyl accident in 1986, even though the increase in radioactivity levels was deemed negligible (Busby 2009). They are also referring to the apparent increase in solid tumors and leukemia among children of families living near nuclear installations (Fairlie 2010, 2014; Laurier et al. 2014; Fairlie and Körblein 2015; cf. Boulton 2019). Naturally, local increases in radiation levels affects not only the human population but the entire surrounding ecosystem (Körblein and Hesse-Honegger 2018; Hancock et al. 2019; Cannon and Kiang 2022).

Epigenetic memory: The Promises and Pitfalls of Epigenetic Research

What are the implications of epigenetic involvement in the response to IR? Importantly, unlike the relative stability of DNA and its inheritance, epigenetic marks may be temporary and reversible (epigenetic plasticity), but may also be transmitted to daughter cells and even offspring,[8] a phenomenon known as *Epigenetic Inheritance*, or *Epigenetic Memory*. At the most fundamental level, epigenetic memory refers to the maintenance and transmission of altered gene expression states and/or the correlating epigenetic patterns and chromatin structures long after the initiating signal has passed (Cavalli and Heard 2019). This process is essential for epigenetic function, and seems to account for the extended effects of exposure to IR, while the contingency and plasticity of epigenetic functions may contribute to the variability in observed phenomena.

As the inheritance of epigenetic modifications can be highly dynamic, responsive and interrelated, we might ask *what* exactly is being transmitted? An important clue comes from

what is known as epigenetic priming, where the transmitted epigenetic pattern differs from the initial epigenetic response. What is transmitted, then, is neither an activated response nor a reversion to the pre-exposed state. Instead, it is a distinct, “primed” pattern that may facilitate, for example, a robust or rapid reactivation of genes to recurring environmental challenges, including IR (Ghosh 2022; MotherSill and Seymour 2022). In other words, in extending the epigenetic response to environmental conditions through time and cellular lineages, what is passed on is not simply an epigenetic pattern, nor necessarily a change in gene expression, but an epigenetic encoding and memory of particular *experiences*, or the impressions of experiences already enfolded with anticipation (Levenson and Sweatt 2006; Davis 2014, 2017; Lappé and Landecker 2015; Mansfield 2017; Meloni 2019; Aristizabal et al. 2020).

Bodies thus seem to carry the memories of a wide range of personal and lineal experiences. Jörg Niewöhner describes these somatic memory effects as "extend[ing] the embedded body in time and across generations in ways that molecular biology has not produced before" (2011, 290). This embedded body is "heavily impregnated by its own past and by the social and material environment within which it dwells. It is a body that is imprinted by evolutionary and transgenerational time, by ‘early-life,’ and a body that is highly susceptible to changes in its social and material environment” (289–290; but see Sarah Richardson 2021 for important feminist critique). This relationally situates the genome (and body) in time and space, bringing it to life (Keller 2005; Lappé and Landecker 2015; Lock 2015; Chung et al. 2016).

This embeddedness was initially celebrated in the social sciences and humanities for its promise to extricate biological research from the confining determinism of the genetic code. Epigenetic function added relationality to the biological framework itself, suggested

the entanglement of the biological and social, nature and culture, self and environment, as well as past, present and future (e.g., Jablonka and Lamb 1998; Stotz 2008; Niewöhner 2011; Carey 2012; Guthman and Mansfield, 2012; Lock 2013; Keller 2014). However, in analyzing epigenetic research, both science and technology studies (STS) and other social sciences scholars find that it fails to meet these early expectations, reducing the much-anticipated plurality of epigenetics, and incorporating it into the existing biomedical framework of binary and mechanistic determinism (for a review see Dupras, Saulnier and Joly 2019). Socio-environmental complexity collapses in research practice, both in the construction of uncritical, oversimplified causation inquiries (e.g., Kenney and Müller, 2017; Chiapperino 2021; Meloni et al. 2022), and through the "molecularization of biography and milieu" (Niewöhner 2011, 291), flattening and reducing profoundly different types of experiences to molecular mechanisms acting on chromatin (Landecker and Panofsky 2013; Meloni and Testa 2014; Landecker 2016; Lloyd and Raikhel 2018; Chiapperino and Panese 2018), and ultimately serving as “volume controls for genes” (Kuzawa and Sweet 2009, 5). In this formulation genes remain the functional center, and the focus for both examination and the possibility of delivering change.

As with the specific case of IR exposure, this debate is more than theoretical. Life circumstances, including living environments and lived experiences are strongly related to geo-socioeconomic distribution. The biological mechanisms that react to environments, and possibly transmit their influences over generations, are thus inherently of political importance, making environmental epigenetics and related research inherently political, in its potential to shed light on local and global conditions of health inequalities (Lock 2015; Richardson and Stevens 2015; Meloni 2016; Pentecost and Cousin 2017; Meloni et al. 2018; Niewöhner and Lock 2018; Penkler et al. 2019, 2021). However, in its present formulation,

epigenetic research and related health policies may lead to new forms of social discrimination, including equally problematic environmental- and epigenetic-determinism (Landecker 2011; Mansfield 2012; Lock 2013; Mansfield and Guthman 2015; Waggoner and Uller 2015; Richardson 2015, 2017; Meloni 2016, 2017, 2019; Müller et al. 2017; Saldaña-Tejeda and Wade 2019; Valdez 2021).

Researching Otherwise: The Potential Contribution of Agential Realism

Given these challenges, epigenetic research has reached a sort of impasse, struggling both to draw concrete meaning from the complexity of functions it studies (Chiapperino and Paneni 2022), and to fulfil its political potential. Looking for alternative paths of exploration, I move away from the contemporary debate, to rethink epigenetic molecular materiality through Karen Barad's agential realist ontology (2007, 2017a, 2017b). *Agential Realism* rearticulates the concepts of materiality, entanglement and indeterminacy, all central to epigenetic discourse, through its firm (yet both creative and critical) grounding in scientific knowledge. Together with its political implications (Barad and Gandorfer2021), this makes it a particularly relevant and fruitful framework for exploring epigenetic function.

Indeed, the potential contribution of Barad's work to the field of epigenetics has been recognized by several scholars (e.g., Niewöhner 2011; Åsberg 2013; Weasel 2016; Warin and Hammarstrom 2018; Warin and Martin 2018; Roberts Sanz 2018; Warin et al. 2022; see below the analyses of Davis 2014, 2017). In Barad's ontology entities are only determined through their relationships, their intra-actions (rather than interactions) within phenomena, in acts that are at once entangling/differentiating, which Barad named *agential cuts*. This understanding contributed to a powerful reading of epigenetic function as embodying the entanglement of the material-discursive, and the relational cultural-biological coproduction of bodies. As relata do not preexist the relations that constitute

them in agential realism, boundaries, properties and meaning remain indeterminate outside particular relations. Radically, this means that indeterminacy is not an epistemological uncertainty but a fundamental quality of the world. This understanding resonates not only with the contingency of epigenetic enacted agential cuts in relationally determining organismic traits, but also with the possibility for institutions and researchers, to make more ethical cuts.

Building on this existing scholarship, I consider the very materiality of epigenetic function by following Barad's (2007, 2010) neo-material appreciation of matter as meaningful and agentive, not a thing but a ceaselessly generating and generated relational process. I take Barad's lead into this field of knowledge to think, what epi/genomes *do in their materiality*, outside their known and acknowledged functions as replicating, regulating, transcribing, expressing and silencing genes. Shifting away from the conventional framing of epigenetic function as regulating gene expression, yet carefully following recent scientific studies, I consider how the existing understanding of epigenetic marks as bearing the memories of personal and lineal experiences may be tied with the very materiality of chromatin. In doing this I offer a speculative, affirmative exploration of molecular function,[9] perhaps even a molecular fable of response-ability of sorts, an attempt at a formulation that accounts for lives already altered by violences (Kenney 2019; Meloni and Müller 2018). To do this, I follow Barad's own methodology of diffraction, which involves "reading insights through rather than against each other" (2017a, 64), revealing trans-disciplinary entanglements that are already materially there. Diffraction, by its very nature, is a performative troubling of analogically presupposed binaries and boundaries, holding the potential to be at once affirmative and profound, in rigorously working with multiple knowledges (Van der Tuin 2011; Juelskjær, Plauborg and Adrian 2020). I return to Kyōko

Hayashi, introduced at the beginning, and the memory of August 9 she has been carrying throughout her life.

Staying with the Trouble: Living with August 9

Having survived the atom bomb, the data briefly presented above suggests that Kyōko Hayashi's memories of the blast and of her continued exposure to radioactive fallout and to internal radiation (Hayashi 2007) left epigenetic imprints on her body. Research into the biological response to trauma (Ramo-Fernández et al. 2015; Morrison et al. 2019; Mehta et al. 2020; Neves, Dinis-Oliveira and Magalhães 2021; Smeeth, Karam and Pluess 2021; Richter and Hunter 2021), suggests that the devastation and loss she experienced following the atomic blast not only haunted her mind, were not only etched, scarring her irradiated body, but were also marked on her chromatin as her cells rearticulated themselves as cells that have experienced the bomb, cells that could never stop anticipating the bomb. From the nuclei of plutonium isotopes to the nuclei of her cells, what else can a body do with such memories?

Committed to the memory of classmates "who were robbed of their own deaths by unspeakable violence" (Barad 2017, 70), and to fellow *hibakusha*, Hayashi devoted her adult life to chronicling 9 August in its entanglements. Her stories reveal the most intimate, devastating details of lives altered by the bomb, including those of mental and physical health soaked in the personal and political implications of surviving or not the a-bomb (e.g., Hirosuke 1993; Hayashi 2005, 2008, 2010, 2017; Hayashi and Selden 2015). In the novella, *From Trinity to Trinity* (2008, 2010), we meet Hayashi 54 years after Nagasaki, now an elderly *hibakusha*, as she embarks on a political-spiritual pilgrimage to the site of the first atomic bomb test, Trinity, New Mexico, where a plutonium bomb was detonated on July 16, 1945.

Hayashi's narrating style is multitemporal, her protagonist "'travel hops' from one spacetime point to another, circling back, re-turning and turning our attention to a multiplicity of entangled colonial histories condensed into 9 August" (Barad 2017a, 69).

Barad's diffractive reading of the novella reveals this multi-temporality as not merely an epistemological stance but as an onto-epistemological feature of this world. Time, rather than a simple blank axis along which events and phenomena unfold, is itself part of the radical indeterminacy of the world, contingent on the intra-actions that articulate it and its intra-actions within phenomena, evolving in an open ongoing becoming (Barad 2007, 2010, 2017a; Schrader 2010). "[I}ntra-actions", explains Barad (2007), "are [thus] temporal not in the sense that the values of particular properties change in time; rather, which property comes to matter is re(con)figured in the very making/marking of time" (180). Hayashi's travel hopping, attentively traces specific entanglements of August 9, and in that asserts their mattering.

Barad also introduces the concept of a *thick now*, invoking a "thick sense of multiple historicities and temporalities" (2017b, 76) through their entanglements, and the quantum field theory (QFT) understanding of "each moment as a condensation of other beings, places, and times" (2015a, 416). This multiplicity of entanglements is not simply an alignment of events constituting a coherent story; rather, moments are ontologically threaded through each other, living inside each other, formed by and contingent upon each other (Barad 2017b). In Hayashi's recounting too, events become meaningful through diffraction, threaded through August 9 and through each other. When she arrives at Trinity's Ground Zero, this super-positioning of specific space-time points, this travel hopping, this particular thick-now, allows her narrator to undergo a profound transformation. She writes:

> I have always been aware of being a *hibakusha*. But as soon as I started walking through the small passage…. my always-present awareness of being a victim disappeared from my mind. It was as if I became a fourteen-year-old again…. it was when I stood in front of the memorial that I was truly exposed to the atomic bomb.
>
> Looking back, I did not shed a tear on August 9. As I ran with the pack of people whose hands, feet, faces no longer looked human, no tears came to me. . . .
>
> For the first time here at Trinity, however, I might be crying with the human tears that I did not shed on August 9. Standing on the land that speaks no words, I shivered, feeling its pain. Until today, I have lived with merciless pains that hurt my mind and body. But it could have been the pain of the skin that grew from August 9. Here in this desert I had momentarily forgotten my life as a *hibakusha* (Hayashi 2010, 50-51).

Memories orient us in the world, allowing us to interpret it and ourselves within it; without them, the present is undifferentiated. But in themselves, memories too are indeterminate. It is not only that each present becomes meaningful through its contextualization within the memories threaded through it, but memories too gain meaning only when they are contextualized within other memories and within the present. The same memory, the same event, can have disparate significance depending on the context within which it is entangled. We tend to relate to memories as determining features of our lives, and indeed they are, but because our lives are open phenomena, how memories will determine us and our behavior remains open as we are continuously rearticulated.

We are dealing here with trauma. Trauma victims are often uncontrollably and excruciatingly sucked into those moments that changed their lives forever (Ehlers, Hackmann and Michael 2004). But what Hayashi allows us to witness is profoundly different.

In the short essay accompanying her 2008 English translation of the novella, Kyoko Selden writes: "Having completed the journey that was at once real and symbolic, Hayashi takes a new direction. Not that she no longer writes about Nagasaki, but she handles the theme differently…" (Hayashi 2008, 28-29). The significance lies not solely in her painful return to August 9, but in her diligence in tracing its entanglements. Arriving at this site thick with the memories of its own reconfigurations including its nuclear and other colonial histories (Barad 2017a; Engelmann 2022), Hayashi realizes with her marked and wounded body the entanglement of Nagasaki and Trinity, beyond linear time, as she re-members. Reconfiguring her own phenomenon, together with the phenomena of which she is part, August 9 is contextualized, and experiencing its pain, Hayashi goes through the heavy transformation from victim to survivor.

This re-membering is articulated not only in her cognition, but throughout her body. "Hayashi's… body does not represent the story;" reiterates Annouchka Bayley, "her body *is* the story" (2019, 82). Barad's ontology tells us that the world carries the memory of its past articulations within its very materiality. Science tells us that surviving Nagasaki is written into her chromatin, along with and related to her complicated medical history. But what of this superpositioned event? If her materiality carries the history of her phenomenon, and epigenetic mechanisms biologically mark her experiences, surely this is one to remember!?

Epigenetic Temporality

In its present performative state, the science of epigenetics is unable to address the complexity of intricate layering of experiences, the effects of a personal, epistemic, yet colossal and ontological, transformative journey. Epigenetics therefore gives me no answer and so, I am left speculating… But, although she lived, to her own surprise, to (die of) old age

(Hayashi 2017), there is nothing I can say about the correlation between Hayashi's experience, epigenetic markings, and health. I cannot speak of the probability of malignancies, the possibility of a heart attack, known to occur with increased rates in elderly *hibakusha*, or of any of the disorders associated with early trauma. Instead, I wish to consider epigenetic memories and their temporality. If this thickness of dis/continuous multiplicity of temporalities is ontological, if Hayashi's act of recontextualizing her history through tracing the entanglements of this thick-now is, as Barad claims, ontological, might we also trace its manifestation in epigenetics?

That the epi/genome's materiality does not embody a linear temporality is clear. Changes to DNA and to epigenetic patterns are not organized along chromosomes in chronological order. In Baradian terms, we might say that chromosomes *are* entangled memories of events and experiences of different timescales and different times (Niewöhner and Lock 2018), nonlinearly organized. Indeed, several scholars have elaborated on the non-linearity of epigenetic temporality. Julie Livingston, for example, asserts: "epigenetic time is hard to hold onto... It is layered, accelerant, recursive, contingent, scalar, linear, and circular all at once… we will need ways of thinking and talking about time that allow for its embodied florescence" (Lock 2015, 166-167).

While this paper aims to contribute precisely to this effort, it is crucial to recognize that scientific conceptualizations are never politically naïve. Becky Mansfield (2017), for example, describes how the folding of past and future into the present, as perceived in mainstream epigenetic inheritance research, results in the formulation of interventionist reproduction policies. Through these, an ever-receding future of next generations–vulnerable fetuses that *do not* and *may not* exist–becomes privileged over the present, and in particular over the present of women and girls, of (potential) mothers. Conversely,

indigenous Australian scholars (Pember 2015, 2016; Warbrick et al. 2016; Conching and Thayer 2019; Paul 2020), utilize the resonance of epigenetic temporality with Indigenous ontologies to "transmut[e]… scientific knowledge through decolonial imagery" (Warin et al. 2022, 19). They thus articulate a nondeterministic, situated, postcolonial postgenomics “as a model of collective embodiment and distributed responsibility" (1). This, in turn, serves as the ground for ongoing community collaborative health initiatives.

Noela Davis specifically elaborates on epigenetic temporality through agential realism (2014, 2017). She identifies epigenetic mechanisms as agential realist apparatuses performing agential cuts, making determinate specific phenotypes from the indeterminacy of the genome. Davis thus elegantly reverses the proclaimed determinism of the genetic code, and creatively demonstrates the contingency of a virtually undisputed scientific conceptualization.[10] In their agentive function, states Davis, epigenetic mechanisms also materialize the particular cause-and-effect relations within the phenomenon under investigation, enfolding and materializing experiences and memories of the past, as well as the anticipatory preparation for future possibilities (for example of a stressful life).

Epigenetic Materiality: Chromatin Organization

As epigenetics is first and foremost a material phenomenon, here I seek to extend our understanding of this complex temporality by exploring epigenetics' molecular materiality. While research looking into the epigenetic embedding of experience and memory primarily focuses on the changes in epigenetic composition in response to exposures, it is important to note that these changes do not simply mark loci on linear genomes. Rather, they induce alterations in the specific and even overall organization of chromatin (Maeshima, Lida and Tamura 2021). "This", notes Maurizio Meloni (2018), "is

where epigenetics really matters: not so much as ‘tags’ or ‘bookmarks’ added to linear DNA sequences but as the complex machinery that spatially rearranges and regulates chromatin…" (22). Together with recent technological advancements, this insight drives a thriving 3D genomics research front, involved in understanding this materiality–its structures, regulation and functional effect (e.g., Quinodoz et al. 2018; Saintillan, Shelley and Zidovska. 2018; Sun et al. 2021; Amiad-Pavlov et al. 2022; Nollmann et al. 2022). And while the functional significance of chromosomes as long linear segments is undeniable, it is increasingly chromatin's *in vivo* non-linear features, its loops and folds, which are at the center of investigation.

Nuclear architecture research reveals a structured hierarchy in chromatin organization, starting with *nucleosomes*, consisting of DNA wrapped around core histones, and progressing through increasing orders of controlled looping and folding to chromatic mega structures called *chromatin compartments*, which are further organized into *chromosomal territories*. This controlled yet dynamic spatial organization produces biological function and meaning through regulating gene expression and other nuclear processes (Magaña-Acosta and Valadez-Graham 2020). For example, within chromosomal territories active genes tend to be grouped together in certain compartments, while non-active regions are grouped in others. Changing the transcription level of a gene may cause its relocalization (Brueckner et al. 2020) and vice versa: experimentally inducing a shift in a gene’s position within the nucleus may change its expression profile (Reddy et al. 2008). As changes in epigenetic composition over time and circumstances bring about structural reconfiguration (Cavalli and Heard 2019; Bourbousse, Barneche and Laloi 2020; Harabula and Pombo 2021), this allocates the genome with both a lifespan and a dynamic physical body (Lappé and Landecker 2015).

This dynamic spatial segregation makes, of course, functional sense in regulating gene expression.[11] But the importance of the overall regulation of nuclear architecture seems to exceed this. For example, in nearly every type of cancer studied, this regulation goes astray: studies find massive epigenetic changes, beginning prior to cancer development, and continuing as cancer progresses. Importantly, these changes seem to have little direct effect on gene expression, but greatly impact chromatin organization itself (Madakashira and Sadler 2017; Xu et al. 2020).

Accounting for the materiality of epigenetic memory: chromatin constellations

To consider the material architecture of chromatin, its folding and looping, through agential realist ontology, I turn to a recent paper, in which Barad (2017b) diffractively reads their articulation of QFT-based temporality through Walter Benjamin's notion of *Now-Time* (*Jetztzeit*; 2006). Now-time describes the present moment, shot through with a specific multiplicity of temporalities, together forming a crystalline *constellation* of temporalities or events that gives the moment its meaning (e.g., ibid., 1999). Of the various metaphors Benjamin uses, the image of constellations becomes particularly meaningful when thinking about chromatin. Gazing into the night sky, constellations "seem to be purely spatial arrangements, but Benjamin uses them in a temporal modality" (Barad 2017b, 34). This is because the stars we see are not only *of* space but also *of* time. Since the speed of light is constant, the more distant the star–the further into the star's past we are looking. As the stars within a constellation are at different distances from us, "constellations are… images of a specific array of past events, a configuration of multiple temporalities" (ibid.).

The image of spatio-temporal-material constellation aligns beautifully with Barad's (2017b) articulation of the thick-now. Hayashi's (2010) multi-spatio-temporal tracing of entanglement can also be thought of as forming a constellation that produces meaning. This

perspective extends to chromatin formations governed by epigenetic mechanisms, not only as spatial but also temporal arrangements. As epigenetic marks are understood *in science* as a form of memory, epigenetic regulation of chromatin structures can be thought of as functioning through integrating, storing, sorting and relaying memory via shape (Jablonka and Lamb 1998; Lappé and Landeker 2015). Therefore, chromatin formations governed by epigenetic mechanisms are not only spatial, but also temporal arrangements. Furthermore, when chromatic sections are held together, they functionally influence each other, more than that–they become entangled, contingent upon each other and continuously rearticulated by their multiple entanglements. These entangled chromatic constellations articulate a particular thick-now of bound memories that produces biological and functional meaning, in driving cellular activity.

Although, as suggested above, scholars have been thinking both about epigenetic memory and about the related loopy arrangements of chromatin, no published work has so far addressed the joint significance of both attributes. Conceptualized this way, chromatin clusters can be understood as constellations aligning and entangling particular memories in an individual's life, or even from earlier lineal time. This view offers a different explanation for chromatin organization, and a different yet not mutually exclusive system of causation. The identity and functionality of a cell can be said to be determined by the genes that it activates, which for purposes of efficiency it groups together. The identity and functionality of a cell can also be understood as dependent on the choices it makes in grouping *memories* together, to create a reference system, a context, a narrative even, through which it understands itself within the world, and interacts (or more precisely, intra-acts) with it. Claiming that cellular responses to the environment are dependent on their past experiences and the epigenetic memories they carry may prove insufficient to explain existing variability,

for example. Thus, cellular responses may also depend on which of these memories and in what constellations come to *matter now*. As with our cognitive organization, as with Hayashi's act of recontextualization, the interpretation of the present depends on those memories that cells may deem relevant, and for every life-story, for every present, there are multitudes of possibilities.

What has been labeled as epigenetic memory, starting from the transmission of epigenetic marks on particular DNA sequences, becomes complex, highly dynamic and contextualized, dependent on both an entire historical background—manifest by the nuclear landscape, on particular historical memories inscribed at specific loci, and on the particular spatio-temporal entanglement with other such loci. Thus, the cellular ongoing becoming is entangled not only with its environment at the present, nor simply with the integrated context of the past—that had been and passed (Chung et al. 2016; Pitts-Taylor 2018). Rather, it is also impacted by the living entanglement of the present with specific memories and anticipations, particular re-collections, as they are materially articulated through chromatic constellations. This organization may determine which memories *matter* in driving a particular cellular onto-epistemological response to and in the present.

Every cell nucleus (as an open indeterminacy) holds within it a multitude of possible chromatic constellations, possible stories in telling itself. Enacting particular ones performatively configures the phenomena–a reality. Crucially, chromatin dynamics suggests that chromatin not only contextualizes memories and events, but holds an inherent ability to recontextualize them. Thus, the agential cuts that epigenetic mechanisms enact, which as Davis (2014, 2017) elaborates, configure causation itself, are not only of the functional-biological choice, but of its framing, the context within which it is made. In this reading, it is not only experiences that matter, but also their onto-epistemological context, the way in

which they are configured, and may be continuously recontextualized and reconfigured within dynamic chromatic structures. These structures participate in (re)determining cellular activity, and therefore cellular and organismic intra-action within the world. This reading presents a different structure of causation and cellular decision making, grounded in living experiences, beyond the traditional linearity and universality in scientific narratives.

Discussion and Conclusions: The Implications of Chromatin Constellations

The world according to agential realism is thick with the memories of all its previous articulations, entangled with its own prior iterations. These iterations can be traced through their entanglements, and in the very act of tracing, the traced phenomenon is rearticulated, open to further reconfigurations. In this, agential realist ontology holds the potential and hope for more just iterations. Kyōko Hayashi's unwavering commitment to tracing entanglements, as evident in her journey and overall oeuvre, allows her to place the memory of August 9 within context. It is no less devastating, but as some of its entanglements are realized– so is its place in and of this world. This act of tracing caries an ontological impact—a reconfiguring of phenomena. It is, Barad insists, an embodied labor, and I propose further that it involves the agency of all bodily scales, including the molecular arrangements of cellular nuclei.

This thickness of time is not a fanciful theoretical interjection. For Benjamin, the rejection of progress as a founding concept of history (Benjamin 1999), his conceptualization of the now-time, and the related image of constellations, are theologically-inspired, politically charged formulations of resistance to fascism (ibid.). Like Benjamin, Barad understands time-being "as a specifically political and material practice… attuned to the possibilities for liberation, for justice, in the now of the present moment" (2017b, 38).

Crucially, although their work is a call for *us* to realize the thick-now, for both Benjamin and Barad, the potential for justice is not in itself a human actant, but an ontological feature of the world, traversing each moment, each *Now* (Butler 2016; Barad 2017b).[12] Barad (2010) gives us a sense of the ontological thickness of now, through which the world articulates itself, by "following" an electron in superposition as it "experiences" particular entangled events "at once". Here, I suggest that *through its very structure and function*, chromatin manifests this as well. Chromatin constellations are the material embodiment of epigenetic multi-temporality and non-trivial causality. They demonstrate one way in which our bodies are continuously materially (re)articulated in particular, yet multiple thick-nows. Following Barad's ontology, and the contingency of time, we might say that in its organization and dynamism, chromatin agentively participates in materializing time itself. If chronological, linear or progressive time plays a part here, it is only one of many.

Like Benjamin's now-time and Barad's thick-now, epigenetic marks are politically significant (e.g., Guthman and Mansfield 2015; Müller and Samaras 2018; Murray 2018; Dubois and Guaspare 2020; Taki and de Melo-Martin 2021; Valdez 2021). They mark inequalities, and in bearing the molecular histories of acts of violence, they further increase the risk of those oppressed, discriminated and marginalized, and the risk of their descendants for developing detrimental health conditions (Hanson and Gluckman 2014). The reading presented here also suggests their potential—not in eliminating or erasing these marked memories, but in reconfiguring them, recontextualizing them through actions taken *now*. Within this framing, the epigenetic and overall wisdom of those whose lives have been altered by violences can be appreciated and celebrated, without diminishing the demand for accountability and change.[13]

In order to heed these memories and the potential present in the thickness of chromatin constellations, biomedical research itself has to extend beyond existing linear and binary thought modes. In the "pragmatically reductionist" search for clear universal causal rules, along with the tendency to label whole populations as "damaged" (Tuck 2009; Saulnier and Dupras 2017; Pentecost 2021), memories that can serve as the ontological foundation for change are conceptualized as needing to be reversed (i.e., erased). Existing population diversity, bearing particular, intersectional rearticulated knowledges of harm, of resilience and growth, remains mostly outside scientific enquiry, which instead is focused unsuccessfully on finding simple, unified epigenetic records of damage (Meloni 2016; Müller and Kenney 2021). This lacuna highlights the shift agential realism calls for in science, in appreciating ontological indeterminacy and entanglement as "the conditions for responsible and objective science" (Schrader 2010, 275; see also Hendrickx 2022), including acknowledging the limiting conditions we enact. In the case of epigenetics, too often research and derived public health policies fail to trace and address the entangled overarching discriminatory conditions that produce health inequality, including those of science itself (e.g., Landecker 2011; Mansfield 2012; Lock 2015; Dupras and Ravitsky 2016; Müller et al. 2017; Meloni and Müller 2018; Murray 2018; Müller 2020; Mancilla et al. 2020;Lawson-Boyd and Meloni 2021; Richardson 2021; Saulnier et al. 2022).

Epilogue: The Possibilities for Living and Dying Otherwise

This paper began with the biological effects of nuclear radiation exposure, and followed the story of one woman, a *hibakusha*, Kyōko Hayashi. Her novella reveals how the courageous and diligent tracing of the entanglements of August 9, allowed her to face its full devastating impact, and grieve. Returning to Japan, Hayashi continued to write about August 9; the title of her 2005 publication *Kibō*, means Hope (Hayashi and Selden 2008, 28).

By diffractively reading available epigenetic data through the insights expressed in Hayashi's work, and through Barad's own reading of her novella, this paper proposes that the ontological impact of tracing entanglement may exist in the materiality of our cells, enabling the rearticulation of cellular function and responsivity to the world. This speculative proposal comes in response to the impasse that epigenetic research finds itself, as expressed in existing critique briefly laid out above, despite the fact that the premise of epigenetic mechanisms as contributing to cellular responsivity to the environment holds true. Perhaps Hayashi's documented labor of mourning, relentlessly revealing the entanglements of human cruelty and violence, and from this devastation finding hope, can serve as a fitting guiding imperative to (re)think through both epigenetic research and derived public health policies.

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[1] Ionizing radiation (IR), consists of subatomic particles or electromagnetic waves that have sufficient energy to ionize atoms or molecules by detaching electrons from them. Types of IR include alpha, beta, and neutron particles, gamma rays, X-rays and the higher-energy ultraviolet part of the electromagnetic spectrum (Reis et al. 2018).

[2] Laboratory research has been conducted on cultured cells and model organisms, most notably rodents. Epidemiological research collected data not only of the victims of Hiroshima and Nagasaki, but of the growing numbers of populations exposed to higher levels of radiation: from nuclear weapons testing, nuclear power stations–including leakages and accidents, professional and medical exposures, and from naturally occurring localized high-level background radiation, see UNSCEAR 2022.

[3] Having beneficial effects at low levels of exposure (Shibamoto and Nakamura 2018).

[4] For critical analyses of the science politics through which the LNT model was selected to guide radiation risk assessment, see Calabrese 2013, 2015, 2017; Williams 2019; Folkers 2021.

[5] See Mothersill, Cocchetto, and Seymour 2022 for the more recent suggestions for the possible involvement of bio-electric signaling.

[6] Strikingly, epigenetic mechanisms play a key role in cognitive processes of learning and memory, and the evolution of memory formation and human cognition is thought to have occurred through the nervous

system's co-opting of this ancient, successful and evolutionarily conserved form of cellular memory (neuroepigenetics - Levenson and Sweatt 2006).

[7] Epigenetics has many, sometimes contradictory definitions (Cavalli and Heard 2019). Here, I follow Adrian Bird's (2007) biochemical, chromatin-centered definition. The range of modifications includes those added to DNA itself–such as cytosine methylation, by far the most studied, but other modifications are known, and changes to the molecular complexes around which DNA is arranged, such as histone variants and various histone modifications. Epigenetic mechanisms also include the function of noncoding RNAs (ncRNAs), not all of them function directly at the DNA level. RNA molecules themselves can also serve as substrates for (epigenetic) modification. For more details see Wei et al. 2017; Piexoto et al. 2020. For the involvement of ncRNA in response to IR see May et al. 2021.

[8] The existence and extent of inter- and trans-generational epigenetic inheritance in humans is the subject of ongoing heated debate, with important social implications. The implications for second generation *hibakusha* and their descendants are also of pressing importance (Hayashi 2008, 2010; Hayashi and Selden 2015; Tomonaga 2019; Dubrova and Sarapultseva 2020). Due to space limitations, I restrict my discussion to the effects on those directly exposed, remembering that the impact of experiences does not begin with one's birth nor end with one's death.

[9] See Le Goff, Allard and Landecker 2021 for an analysis of the conceptual legacy of negative definitions in epigenetic research.

[10] Genetic determinism has been profusely challenged by many, but here Davis challenges the conceptualization of the genetic code as in itself determinist.

[11] It is energetically beneficial, for example, to place genomic loci that require the same apparatuses together.

[12] Agential realist inherent ethics (its ethico-onto-epistemology) is expressed throughout Barad's writing. For a detailed explanation see Barad 2007, chapter 8.

[13] Not least for those who suffered under nuclear aggression and nuclear colonialism. Following the test, it is estimated that the inhabitants who lived downwind of the Trinity explosion site, were exposed to X10,000 higher radiation levels than those currently allowed (Tucker and Alvarez 2019). They were not warned of the approaching blast, nor of the dangers in remaining on their land covered in fallout, in consuming their now radioactive collected water, and land-grown produce. Despite a documented sharp increase in infant mortality rate in the following three months, no measures were taken to protect them (ibid.). Despite the compelling life stories of many dealing with radiation related illness, to this day, they are still denied reparation, and are excluded from the Radiation Exposure Compensation Act (Tularosa Basin Downwinders Consortium n.d.). This paper is dedicated to them.

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Bio

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