

Molecular Markers of Embryo Quality

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Evaluation of the optimal number of embryos, their quality, and the precise timing for transfer are critical determinants in reproductive success, although still remaining one of the main challenges in assisted reproduction technologies (ART). Indeed, the success of in vitro fertilization (IVF) treatments relies on a multitude of events and factors involving both the endometrium and the embryo. Despite concerted efforts on both fronts, the overall success rates of IVF techniques continue to range between 25% and 30%. The role of the endometrium in implantation has been recognized, leading to the hypothesis that both the “soil” and the “seed” play a central role in a successful pregnancy. In this respect, identification of the molecular signature of endometrial receptivity together with the selection of the best embryo for transfer become crucial in ART.

Keywords: IVF ; endometrial receptivity ; implantation ; blastocyst ; embryo ; ART ; AI ; extracellular vesicles

1. Introduction

Implantation in mammals relies on the activation of spatially and temporally regulated signals from both the embryo and the endometrium. Synchronization of the embryo-endometrium dialogue represents a limiting step for a successful pregnancy, and the rate of clinical pregnancy in normal cycles only reaches about 30–40% ^[1]. Despite the improvement of IVF techniques and preimplantation genetic testing (PGT) to assess embryo euploidy, implantation failure remains a challenge. Approximately 10–30% of patients referred to IVF clinics experience implantation failure ^[2], and attention has been focused on measures to improve pregnancy outcomes. Among these, the identification of difficult procedures of embryo transfer ^[3], methods of creating optimal embryo cultures ^{[4][5]}, the standardization of morphological criteria to classify blastocyst competency ^{[6][7]}, the improvement of PGT ^[8], and measures to identify the optimal day for embryo transfer ^{[9][10][11]}, have been reported. Nevertheless, despite efforts in both endometrial analysis and embryonic evaluation, our capacity for assessment remains limited. One of the main complications in assisted reproductive techniques is recurrent implantation failure (RIF), defined as the failure to achieve pregnancy after the transfer of at least 3 good-quality embryos ^[12]. While embryo quality can be assessed using morphological and molecular parameters, the evaluation of proper endometrial competency/receptivity is more challenging. Due to its role in limiting embryo implantation, the concept of the endometrium as the guardian of pregnancy has been proposed ^[13]. Indeed, the embryo can efficiently implant in any tissue, independent of the stage of the cycle, with great invasion ability, while in the endometrium, it can only implant during a short period of time called the window of implantation (WOI) or window of endometrial receptivity ^{[14][15]}. In a 28-day normal cycle, the WOI occurs around 6–10 days after the LH surge and lasts about 3–6 days ^{[14][16][17]}. In cases of artificial cycles, the WOI occurs 4–7 days after the administration of progesterone ^[2]. The WOI is finely regulated by a plethora of factors, which include hormones, such as estrogen and progesterone, cytokines, and growth and immunomodulatory factors, all driving a series of morphological and molecular changes fundamental for a correct blastocyst-endometrial dialogue. Although the boundaries of the WOI in a 28-day cycle have been identified, the accurate assessment of endometrial receptivity in women with irregular cycles undergoing IVF is needed in order to timely transfer the embryo and reduce the risk of RIF ^[18]. The routine procedure to identify the day of embryo transfer in IVF is mainly based on the measurement of endometrial thickness by ultrasound, which can be ineffective as a method of predicting the risk of RIF ^{[19][20]}. Histological dating according to the Noyes criteria has been previously exploited to evaluate the morphological changes in stromal and glandular compartments along the proliferative and secretory phase of the menstrual cycle, and to identify the WOI ^[21]. These parameters are no longer considered predictive of endometrial receptivity, mainly due to their operator dependency ^{[22][23]}. More recently, omics approaches have been proposed as tools to identify the WOI ^{[24][25][26][27][28]}. Among these, the Endometrial Receptivity Assay (ERA) has been developed to assess the gene expression signature characterizing the receptive endometrium. However, the limits of the ERA include the assumption of signature reproducibility among cycles, the high costs, and the relatively small number of patients used to validate the assay ^{[29][30][31]}.

2. Morphological Criteria to Identify the Best Embryo

2.1. Static and Morphological Embryonic Features–Cleavage Stage Embryo

Assessment of a cleavage stage embryo by using morphological characteristics considers several parameters, including cell number, the degree of fragmentation, the presence of multinucleation, and blastomere size and symmetry. Numerous studies have been conducted on the correlation between the morphology of embryos at the cleavage stage and their subsequent implantation outcomes [7]. According to the Istanbul consensus [32], the characteristics of 'good' embryos included 4 blastomeres on Day 2, and at least 8 blastomeres on Day 3, depending on the time elapsed post-insemination. Furthermore, blastomeres should be even sized. Moreover, embryos had to exhibit <10% fragmentation and show no signs of multinucleation. On the other hand, some studies reported a positive correlation between the live birth rate and an increment in cell count up to 8, while noting a reduction in live birth rates in embryos with more than 8 cells [33][34]. Therefore, there is a general consensus about the reduced developmental potential of slow-cleaving embryos, but the developmental competence of fast-cleaving embryos remains a controversial issue.

The presence of multinucleated blastomeres in human embryos is widely recognized as a factor associated with a diminished potential of embryo development, manifested by reduced blastocyst formation, significantly lower implantation, and decreased live birth rates [35][36][37][38][39]. Therefore, the recording of this morphological characteristic should be integrated into embryo grading schemes.

2.2. Static and Morphological Embryonic Features–Blastocyst

The evaluation of embryo morphology is the predominant method for assessing human blastocysts worldwide [40][41][42]. This grading system incorporates various parameters such as blastocyst expansion and hatching, the appearance of the inner cell mass (ICM), and trophectoderm (TE) cohesiveness [32]. Significantly, many studies have identified a correlation between the chromosomal status of the embryo and the blastocyst morphology, with higher-quality ICM and TE being linked to increased rates of euploidy [43][44][45][46][47][48][49][50][51]. Conversely, poor quality ICM and TE are associated with elevated rates of complex aneuploidy, affecting multiple chromosomes [43][44]. In the context of embryo transfers involving vitrified-warmed embryos without genetic testing, factors such as blastocyst expansion and the grading of the TE and ICM have been linked to pregnancy outcomes. However, there remains a lack of consensus regarding the predictive value of each of these parameters, with studies yielding conflicting results about which parameter serves as the strongest predictor. Some studies showed that ICM grade had the best predictive effect [52][53][54], while others indicated that expansion stage and TE grade were stronger predictors [55][56][57]. A recent systematic review and meta-analysis revealed that embryos with a grade C ICM were correlated with a decreased rate of live births per euploid transfer compared to those with grade A/B ICM. Similarly, embryos with a grade C TE exhibited a lower live birth rate per euploid transfer compared to those with grade A/B TE. Additionally, poor quality blastocysts (<BB) were associated with reduced live birth rates per euploid transfer in comparison to high-quality blastocysts [58].

2.3. Morphokinetic Embryonic Features

The implementation of time-lapse technology (TLT) has facilitated an enhancement in both the frequency of observations and the dynamic monitoring of embryo development [59]. Various timings are recorded, mainly following ESHRE guidelines [60], such as the time of pronuclear fading (tPNf) and cleavage times at various stages (t2, t3, t4, etc.). Consequently, the durations of the initial three cell cycles (CC1, CC2, and CC3), as well as the period of blastocyst expansion, can be deduced from these observations. Numerous studies have explored whether these developmental timings are indicative of embryonic competence. Rienzi and coworkers observed that the duration until morulation and the quality of TE are substantial indicators for predicting live births following the transfer of euploid embryos [61]. Moreover, a recent meta-analysis, including 58 studies and over 40,000 embryos, examined a potential link between ploidy status and morphokinetic characteristics observed via TLT [62]. It was noted that aneuploid blastocysts exhibited extended durations for t8, t9, and the initiation of expansion (tEB), in addition to higher grades of fragmentation, persistent multinucleation at the four-cell stage, and blastocyst contractions. Nevertheless, due to the diverse nature of these results and the low quality of evidence, the authors recommended further research. Lastly, a retrospective study examined timings such as tPNf, t2, t3, t4, t8, tM, and tB in relation to 192 euploid single embryo transfers. Embryos resulting in live birth, euploid pregnancy loss, or no pregnancy have nearly identical morphokinetic parameters after monitoring with TLT [63].

3. Developmental Timing to Identify the Best Blastocyst

Full blastocyst expansion should be assessed at 116 ± 2 h post-insemination [32]. However, it has been observed that a significant number of blastocysts continue to develop beyond Day 5, with their development extending up to Day 7. Some

systematic review and meta-analyses reported that clinical pregnancy and live birth rates were significantly higher following transfers of fresh or frozen-thawed blastocysts developed on Day 5 compared to Day 6/Day 7, demonstrating that blastocysts with a slower development can be of top morphological grade, euploid, and result in a healthy live birth [58][64][65]. A summary of the morphological criteria so far discussed is reported in **Table 1**.

Table 1. Summary of the morphological criteria available to identify the best embryo and for endometrial receptivity assessment.

	Criteria	Description	Evidence in Support	Evidence Against
Embryo	Good embryo according to Istanbul consensus	At least 8 blastomeres even sized on Day 3, <10% fragmentation and no signs of multinucleation	[7][33]	[34]
	Multinucleated blastomeres	A multinucleation in Day 2 and Day 3 cleavage embryos		[35][36][37][38][39]
	ICM grading	The grading scale for ICM quality of the blastocyst	[52][53][54]	
	Expansion stage and TE grading	The grading scale for expansion and TE quality of the blastocyst	[55][56][57]	
	Developmental timing	Full blastocyst expansion should be assessed at 116 ± 2 h post-insemination	[58][64][65]	
Endometrium	Endometrial Thickness (EndT)	Optimal thickness for receptive endometrium of about 16–18 mm (evaluated by transvaginal ultrasound)	[66][67][68][69][70]	[71][72][73][74][75]
	Noyes Criteria	Histological criteria identifying gland mitosis and tortuosity, apical position of secretory vesicles in cells of the glandular epithelium, secreted material in the glandular lumen, stromal edema, pseudo-decidual reaction, and leukocyte infiltration	[76]	[18][22][23][77][78][79]
	Pinopodes	Evaluation of density and morphology of plasma membrane protrusions on epithelial cells projecting toward the uterine lumen on days 20–22 of a natural menstrual cycle	[80][81][82][83][84][85]	[86][87]

4. Molecular Markers of Embryo Quality

4.1. Mitochondrial DNA (mtDNA)

The concentration of mitochondrial DNA (mtDNA) within embryonic cells has been postulated to play a key role in determining embryonic competence. Given that mitochondria originate from the oocyte and considering the established influence of oocyte quality on early embryonic development, it is plausible to suggest that mitochondrial function could significantly impact embryonic competence. This perspective aligns with the hypothesis that elevated mtDNA levels may indicate suboptimal energy production and compromised homeostasis within the embryo [88]. In fact, Fragouli et al. [89] observed a significant correlation between increased levels of mtDNA content above a threshold level and dramatically diminished clinical outcomes among euploid blastocysts. Concurrently, Diez-Juan et al. [90] confirmed these findings, suggesting a model where rising mtDNA copy numbers correlate with diminishing implantation potential.

However, these observations are not universally accepted, as other studies have reported contrasting results [91]. Victor and coworkers [92] were unable to find a relationship between mtDNA content and clinical outcomes in euploid embryos. Likewise, other studies did not identify any implantation benefits in embryos with reduced mtDNA content [93][94][95]. Moreover, the analysis of TE samples from 615 euploid human blastocysts showed that mtDNA content was not predictive of euploid human embryo reproductive competence [96]. Recently, an attempt was made to conduct a meta-analysis, but the heterogeneity in study designs, characteristics of experimental groups, analytical methodologies, and outcome measures hindered direct comparisons across studies and a real understanding of the impact of mtDNA levels on the reproductive competence of embryos [59]. These data do not support the use of mitochondrial DNA copy number in clinical decision making when selecting which embryo to transfer.

4.2. Cumulus Cells or Spent Media Molecular Analyses

Cumulus cells (CCs) are somatic cells closely associated with the oocyte, playing crucial roles in metabolic and signaling functions during folliculogenesis and oocyte maturation [97]. Given that oocyte competence is achieved through

bidirectional signaling between the oocyte and the surrounding cumulus cells [98], and that these cells are typically discarded after oocyte retrieval, they represent a compelling and non-invasive focal point for in-depth investigation into the factors influencing preimplantation embryo quality.

Looking for molecular markers of oocyte competence in CCs constitutes a way to enhance the predictive value of conventional embryo selection. To enhance the predictive value currently obtained from standard embryo morphology assessments, these molecular markers should be able to identify oocytes which, after ART, have progressed to the blastocyst stage. More specifically, these markers should have the ability to discern those oocytes that have not only reached the blastocyst stage but are also capable of successfully establishing a pregnancy. Some studies have indicated a correlation between CCs function and embryo development. Seven genes related to CCs metabolism (CCND2, CXCR4, GPX3, CTNND1, DHCR7, DVL3, HSPB1, and TRIM28) were found to be altered at the cleavage stage in genome-wide gene expression studies [99]. Moreover, ANG, RGS2, and PLIN2 were indicated as potential predictors of blastocyst development [100]. Scarica and coworkers [101] investigated the association of CCs-related expression of a selected cluster of genes (PTGS2, CAMK1D, HAS2, STC1, and EFNB2) with embryo development to blastocyst. In particular, a strong association between the CAMK1D expression level and blastocyst formation was observed [102][103].

Other studies have explored gene expression in CCs and its relation to embryonic competence. EFNB2 and CAMK1D were suggested to be promising genes that could help to choose EFNB2 and CAMK1D were suggested to be promising genes that could help to select for transfer the embryo with the highest chance to give a pregnancy [104]. Assou et al. [105] associated NFIB reduction and BCL2L11 and PCK1 upregulation with CCs of embryos resulting in live births. Moreover, the upregulation of VCAN, PTGS2, GREM1 and PFKP in CCs of oocytes was observed in embryos leading to successful pregnancy [106]. Similarly, Wathlet and colleagues [104] described an association between pregnancy success and EFNB2, CAMK1D, STC1, and STC2 gene expression in CCs of embryos leading to successful pregnancy. Lastly, prediction models based on CCs gene expression showed upregulation of FGF12, GPR137B, SLC2A9, ARID1B, NR2F6, ZNF132, and FAM36A, and down-regulation of ZNF93, RHBDL2, DNAJC15, MTUS1, and NUP133 in the CCs of oocytes that resulted in a successful pregnancy after IVF [107].

It is noteworthy that these studies assessed pregnancy outcomes after multiple embryo transfers, without adequately accounting for the ploidy status of the embryos, limiting the applicability of these findings to current practices. In contrast, two studies conducted transcriptomic analysis on CCs from oocytes that developed into either implanting or non-implanting euploid blastocysts [108][109]. One study examined five cases per group, while another investigated 17 double embryo transfers of sibling blastocysts, yielding conflicting outcomes. Both studies identified several differentially expressed genes, but none reached statistical significance, so these genes cannot serve as reliable biomarkers of blastocyst competence.

The failure to identify transcriptome biomarkers in this analysis aligns with the results reported by Burnik Papler et al. [110]. This study, conducted using a microarray platform, similarly found no discernible differences in gene expression that could predict either oocyte fertilization or embryo implantation [110]. Moreover, recently, Sachs and colleagues [111] compared the transcriptome of CCs obtained from oocytes that resulted in pregnancy, did not result in pregnancy, led to live birth, or did not result in live birth. Although the RNA sequencing analysis did not uncover differentially expressed genes (DEGs) when comparing the transcriptomic profiles of the groups “no pregnancy” with “pregnancy”, they identified 139 DEGs when comparing the subset of “pregnancy only” with “live birth”. Notably, 28 of these differentially expressed genes were associated with clusters crucial for successful ART outcomes, such as CTGF, SERPINE2, PCK1, HHIP, HS3ST, and BIRC5 [111].

Emerging omics methodologies, including proteomics and metabolomics, are increasingly revealing distinct molecular signatures in viable gametes and embryos. These unique profiles offer potential biomarkers that may be harnessed for the purposes of developmental or viability assessment and selection. Of particular interest in ART is the secretome, those proteins that are produced within the embryo and secreted into the surrounding environment. Defining the embryonic secretome will also provide a deeper understanding of the distinctive series of events crucial for successful implantation, encompassing the essential prerequisites of the blastocyst. Given the intricate and diverse nature of the human embryo, it appears rational to anticipate a collaborative ‘omics’ approach in characterizing the human embryonic secretome [112].

Moreover, in recent years an expanding body of literature has emerged to explore the clinical applicability of spent embryo culture media (SCM) in the context of PGT-A [113][114][115][116]. Different studies demonstrated the ability to detect, extract, and amplify cell-free DNA (cfDNA) from SCM at both the cleavage and blastocyst stages. Belandres and colleagues [117] suggested enhancements to increase the precision and sensitivity of the assay prior to integrating PGT-A with SCM into clinical practice.

Additionally, it has been shown that microRNA (miRNAs) can be detected in IVF culture media, and that some of them are differentially expressed according to the fertilization method, chromosomal status, and pregnancy outcome, which makes them potential biomarkers for predicting euploidy as well as IVF success [118][119][120].

Three studies focused on miRNAs released in the SCM of euploid blastocysts, comparing those that implanted to those that did not [121][122][123]. Initially, a study involving 53 euploid single embryo transfers (SETs) found increased expression of miR-20a and miR-30c in the SCM of implanted blastocysts [122]. Nevertheless, a subsequent multicenter study that employed a tailored plate and protocol for the analysis of 10 miRNAs in 221 euploid SETs did not corroborate these findings. Although the latter study reported significant differences between non-implanted and implanted euploid blastocysts in terms of both miRNA detection and relative quantitation, when the data were adjusted for embryo morphology and day of biopsy, no significant association was confirmed [123]. The expression of miR-372 and miR-191 in embryo culture medium was found to be related to implantation failure [118], while miR-661 was successfully detected in embryonic blastocyst medium, with a higher expression in blastocysts that failed to implant [119]. Moreover, Borges and coworkers found that the expression of miR-142-3p was higher in successfully implanted embryos compared with embryos that failed to implant [124].

Recent studies have focused on the possibility of conducting PGT-A on SCM, aiming to set up a workflow to conduct non-invasive aneuploidy testing [125]. Two studies assessed outcomes following the SET of blastocysts classified as euploid via PGT-A of TE biopsy, but as either euploid or aneuploid in the SCM analysis [126][127]. A recent meta-analysis showed that SCM reported as aneuploid or euploid were associated with similar live birth and miscarriage rates per clinical pregnancy.

An additional study adopted a similar approach but complemented TE analysis with the outcome of DNA amplification from blastocoel fluid collected via blastocentesis [128]. Intriguingly, among 53 euploid SETs, the detection of DNA in the blastocoel correlated with a significantly lower live birth rate (31.5% versus 67.6%), although the miscarriage rate remained comparable. The authors suggested that this cost-effective analysis might act as a biomarker of embryo reproductive potential, indirectly revealing the impact of apoptosis or necrosis in embryonic cells, which release DNA into the blastocoel fluid. However, further research is required to substantiate this hypothesis.

In the context of spent media, extracellular vesicles (EVs) have been identified as interesting candidates able to modulate embryo development, as well as to be released by the embryos [129]. These small, membrane-bound entities released by cells have been identified in various bodily fluids, including the spent media from human embryos [130]. EVs have the capability to transport regulatory molecules such as miRNAs, mRNAs, lipids, metabolites, and proteins [131][132], reflecting the genetic makeup of the originating cells, such as the developing embryo. The membrane of EVs effectively shields enclosed cargo contents, rendering miRNAs derived from EVs more stable and reliable than free-floating miRNAs, owing to protection against RNase present in the medium [133][134].

Until now, only a few studies conducted on animal models investigated miRNAs isolated from conditioned media generated by group cultured blastocysts or degenerated embryos. These studies suggested a link with embryo quality and development [120][135]. Recent studies by Pavani et al. [136] have shed light on the selective enrichment of specific miRNAs in EVs secreted by bovine embryos reaching the blastocyst stage. The administration of synthetic forms of these miRNAs significantly enhanced the hatching capacity of blastocysts, showcasing the potential of EV-associated genetic material in influencing embryonic development. Moreover, in a study conducted by Giacomini and coworkers [130], it was demonstrated that EVs derived from human embryos obtained from ICSI carry a distinct molecular cargo, and they are internalized by endometrial cells. Additionally, EVs released by individually cultured preimplantation bovine embryos can alter the gene expression of oviduct epithelial cells [137] and endometrial cells [138]. Masoumeh Es-Haghi and colleagues demonstrated that three RNA transcripts in EVs secreted by human trophoblast spheroids were directly transferred to endometrial cells [139]. These data underline the crucial role of embryo-derived EVs in embryo–embryo and embryo–maternal communication and in the establishment of endometrial receptivity. Considering the implications for genetic diagnostics, the cargo within EVs secreted by embryos becomes a valuable source for potential biomarkers indicative of genetic health and abnormalities.

In the context of PGT, the genetic content encapsulated within EVs could provide a non-invasive and informative means of assessing the genetic status of embryos, potentially enhancing the accuracy and comprehensiveness of PGT results. By leveraging the molecular cargo of EVs secreted by human embryos, researchers may unveil new possibilities for advancing genetic diagnostics in the field of assisted reproductive technologies, paving the way for more precise and insightful genetic assessments during the preimplantation phase.

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