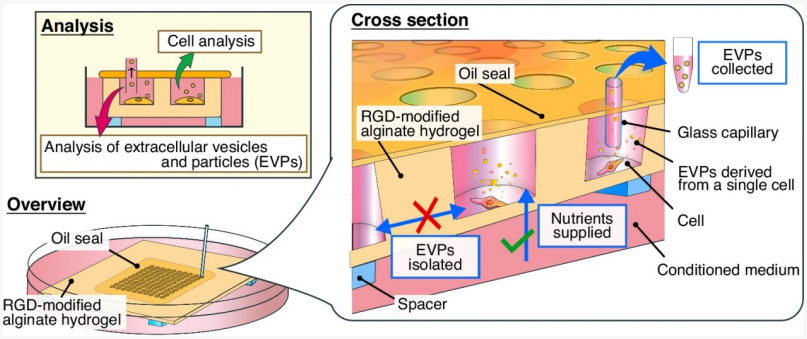
How individual cells reveal their hidden messages

GA, UNITED STATES, February 4, 2026 /EINPresswire.com/ -- Cells constantly release tiny particles that carry signals linked to disease, treatment response, and biological identity. Yet most studies blur these signals together by measuring large cell populations. This research introduces a new platform that isolates single cells and captures the particles each cell releases over time. The system keeps cells alive for weeks while preventing their secreted vesicles from mixing with others. Using this approach, researchers directly analyzed vesicles produced by individual cells and found striking differences from one cell to the next. The results show that even genetically similar cells can communicate in different ways, revealing hidden layers of biological diversity.



Concept of the oil-sealed, RGD-modified alginate hydrogel microwell array. The system enables the collection of EVPs secreted by single cells by culturing them in oil-sealed microwells. Single-cell culture is achieved by the size-selective permeability of

Extracellular vesicles and particles are central to how cells communicate, especially in cancer, where they help shape metastasis and treatment resistance. However, most existing methods analyze vesicles in bulk, masking differences between individual cells. Some single-vesicle techniques offer particle-level detail but lose information about the cell that produced them. Other single-cell platforms face practical limits, such as short culture times or signal mixing between cells. These limitations make it difficult to study how individual cells behave over time. Based on these challenges, there is a clear need for technologies that can culture single cells long-term while isolating and analyzing the vesicles each cell produces.

In a study published in Microsystems & Nanoengineering in 2025, researchers from Keio University and collaborating institutions report a microdevice designed to do exactly that. The team developed a sealed microwell platform that cultures individual adherent cells for more than 19 days while trapping the extracellular vesicles they release. The system allows researchers to collect vesicles from each cell separately and analyze their molecular features. This approach makes it possible to link vesicle profiles directly to single cells, something previous

technologies struggled to achieve.

The key advance lies in how the microwells are engineered. Each well forms a tiny, sealed space that holds one cell. Nutrients can flow in, keeping the cell healthy, but larger vesicles cannot escape. This design prevents cross-contamination and preserves a complete record of what each cell secretes.

Using this system, the researchers cultured individual cancer cells and tracked their growth over nearly three weeks. Some cells divided rapidly, while others grew slowly, even though they started from the same cell line. Vesicles released by each cell were collected one well at a time and analyzed for surface proteins and size. The results showed large differences between cells. Some cells released many vesicles, others far fewer. Marker composition and size profiles also varied and did not simply reflect how many cells were present.

These findings demonstrate that vesicle production is highly cell-specific. By capturing vesicles at their source, the platform reveals biological variability that bulk methods cannot detect.

“This platform lets us connect extracellular vesicles back to the exact cells that produced them,” the authors explain. By combining long-term single-cell culture with sealed isolation, the system captures the full secretion profile of each cell. The researchers emphasize that this level of resolution is critical for understanding why cells that look similar can behave so differently. Such differences, they note, are likely to play major roles in disease progression, therapy resistance, and patient-to-patient variability.

The new platform opens doors for research and clinical applications that depend on cellular heterogeneity. It could improve studies of cancer metastasis, drug response, and biomarker discovery by revealing how individual cells communicate. Beyond vesicle analysis, the system may also support RNA or protein studies from the same single cells, enabling integrated analyses over time. With further scaling and automation, the approach could analyze hundreds or thousands of cells in parallel. This would support precision medicine strategies that move beyond averages and focus on the behavior of individual cells.

References

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Lucy Wang
BioDesign Research
email us here